

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	82	44.3	36	4	US-09-894-882-3	Sequence 3, Appli
2	79	42.7	36	4	US-09-894-882-4	Sequence 4, Appli
3	75	40.5	36	1	US-08-682-485A-7	Sequence 7, Appli
4	75	40.5	36	2	US-08-933-314-7	Sequence 6, Appli
5	75	40.5	37	2	US-08-682-485A-6	Sequence 7, Appli
6	75	40.5	37	2	US-08-933-314-6	Sequence 6, Appli
7	72.5	39.2	37	4	US-09-894-882-5	Sequence 5, Appli
8	69	37.3	31	4	US-09-894-882-461	Sequence 461, App
9	69	37.3	39	4	US-09-894-882-497	Sequence 247, App
10	69	37.3	67	4	US-09-894-882-247	Sequence 247, App
11	67	36.2	32	4	US-09-894-882-470	Sequence 470, App
12	67	36.2	40	4	US-09-894-882-498	Sequence 498, App
13	67	36.2	68	4	US-09-894-882-274	Sequence 274, App
14	59	31.9	155	4	US-09-252-991A-28474	Sequence 28474, A
15	59	31.9	211	4	US-09-902-540-15694	Sequence 15694, A
16	59	31.9	2471	1	US-08-185-432-16	Sequence 16, Appl
17	59	31.9	2471	1	US-08-083-590A-19	Sequence 19, Appl
18	59	31.9	2471	3	US-08-532-384-19	Sequence 19, Appl
19	59	31.9	2471	4	US-08-899-233-1	Sequence 1, Appli
20	59	31.9	2471	4	US-09-121-457-1	Sequence 1, Appli
21	58.5	31.6	34	1	US-08-117-080-5	Sequence 5, Appli
22	58.5	31.6	34	1	US-08-471-329-5	Sequence 5, Appli
23	58.5	31.6	34	2	US-08-915-142-5	Sequence 5, Appli
24	58.5	31.6	908	4	US-08-714-741-44	Sequence 44, Appl
25	58	31.4	39	4	US-09-894-882-248	Sequence 248, App
26	57.5	31.1	180	4	US-09-510-238A-286	Sequence 286, App
27	57.5	31.1	981	4	US-09-252-991A-23962	Sequence 23962, A

```

: GENERAL INFORMATION:
: APPLICANT: University of Utah Research Foundation
: APPLICANT: Cognetix, Inc.
: APPLICANT: Walker, Craig S.
: APPLICANT: Shetty, Reshma
: APPLICANT: Jimenez, Elsie C.
: APPLICANT: McIntosh, J. Michael
: APPLICANT: Olivera, Baldomero M.
: APPLICANT: Watkins, Maren
: APPLICANT: Jones, Robert M.
: APPLICANT: Shen, Greg S.
: TITLE OF INVENTION: I-Superfamily Conotoxins
: FILE REFERENCE: 2314-238
: CURRENT APPLICATION NUMBER: US/09/894,882
: CURRENT FILING DATE: 2001-06-29
: PRIOR APPLICATION NUMBER: US 60/
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 60/243,410
: PRIOR FILING DATE: 2000-10-27
: PRIOR APPLICATION NUMBER: US 60/246,591
: PRIOR FILING DATE: 2000-11-08
: PRIOR APPLICATION NUMBER: US 60/247,714
: PRIOR FILING DATE: 2000-11-14
: PRIOR APPLICATION NUMBER: US 60/264,356
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 506
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 4
: LENGTH: 36
: TYPE: PRT
: ORGANISM: Hadronyche versuta
: US-09-894-882-4

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Query Match 42.7%; Score 79; DB 4; Length 36;  
Best Local Similarity 51.5%; Pred. No. 0.0092;  
Matches 17; Conservative 0; Mismatches 14; Indels

RESULT 3  
US-08-682-485A-7  
; Sequence 7, Application US/08682485A  
; Patent No. 5763568  
; GENERAL INFORMATION:  
; APPLICANT: ATKINSON, RONALD K  
; APPLICANT: HOWDEN, MERLIN E.H.  
; APPLICANT: TYLER, MARGARET I  
; APPLICANT: VONARX, EDWARD J  
; TITLE OF INVENTION: Insecticidal Toxins Derived From  
; TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Zeneca, Inc.  
; STREET: 1200 South 47th Street  
; CITY: Richmond  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/682,485A  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/682,485  
; FILING DATE: 17-JULY-1996

APPLICATION NUMBER: US/08/256,933  
FILING DATE: 27-JULY-1994  
APPLICATION NUMBER: WO 93/15108  
FILING DATE: 29-JAN-1993  
APPLICATION NUMBER: AU PL0722  
FILING DATE: 31-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Shaw, Melissa A.  
REGISTRATION NUMBER: 38,301  
REFERENCE/DOCKET NUMBER: PPD 5099/DI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-231-1542  
TELEFAX: 510-231-1112  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Atrax formidabilis  
US-08-682-485A-7

Query Match 40.5%; Score 75; DB 1; Length 36;  
Best Local Similarity 50.0%; Pred. No. 0.027;  
Matches 16; Conservative 0; Mismatches 14; Indels 2

QY 4 CTPGVKCPAALPCCGRLRCIGGVNNKV--CR 33  
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DB 4 CTGADRPCAACCCPGCTSGCKGPBFGVSYCR 35

RESULT 4  
US-08-933-314-7  
Sequence 7, Application US/08933314  
Patent No. 5959182  
GENERAL INFORMATION:  
APPLICANT: ATKINSON, RONALD K  
APPLICANT: HOWDEN, MERLIN E.H.  
APPLICANT: TYLER, MARGARET I  
APPLICANT: VONARX, EDWARD J  
TITLE OF INVENTION: Insecticidal Toxins Derived From  
Funnel Web (Atrax or Hadronyche Spiders)  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zeneca, Inc.  
STREET: 1200 South 47th Street  
CITY: Richmond  
STATE: California  
COUNTRY: USA  
ZIP: 94804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,314  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/682,485  
FILING DATE: 17-JULY-1996  
APPLICATION NUMBER: US/08/256,933  
FILING DATE: 27-JULY-1994  
APPLICATION NUMBER: WO 93/15108  
FILING DATE: 29-JAN-1993  
APPLICATION NUMBER: AU PL0722  
FILING DATE: 31-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Shaw, Melissa A.



```

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/682.485
FILING DATE: 17-JULY-1996
APPLICATION NUMBER: US/08/256.933
FILING DATE: 27-JULY-1994
APPLICATION NUMBER: WO 93/15108
FILING DATE: 29-JAN-1993
APPLICATION NUMBER: AU P0722
FILING DATE: 31-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Shaw, Melissa A.
REGISTRATION NUMBER: 38,301
REFERENCE/DOCKET NUMBER: PPD 5099
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-231-1542
TELEFAX: 510-231-1112
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
TOPOLOGY: linear

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; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Atrax formidabilis
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 37
; OTHER INFORMATION: /label=a
; OTHER INFORMATION: /note="this site may be amidated without loss
; OTHER INFORMATION: of biological activity"
US-08-933-314-6

Query Match          40.5%; Score 75; DB 2; Length 37;
Best Local Similarity 50.0%; Pred. No. 0.028;
Matches 16; Conservative 0; Mismatches 14; Indels 2; Gaps 1;

Qy 4 CTGAGVKCPAALPCCPGLCIGGVNKC--CR 33
Db 4 CTGADRPCAACCCPGTSGCKGPEPVGVSICR 35

RESULT 7
US-09-894-882-5
; Sequence 5, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 461
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-461

Query Match          37.3%; Score 69; DB 4; Length 31;
Best Local Similarity 44.8%; Pred. No. 0.12;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

Qy 4 CTGAGVKCPAALPCCPGLCIGGVNKC 32
Db 1 CFPFGIVCTPPLPCWIGCC--GTCRNVC 27

RESULT 9
US-09-894-882-497
; Sequence 497, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497

Query Match          39.2%; Score 72.5; DB 4; Length 37;
Best Local Similarity 46.9%; Pred. No. 0.054;
Matches 15; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

Qy 3 ICTGAGVKCPAALPCCPGLCIGGVN--KVC 33
Db 2 ICTGADRPCAACCCPGTSGCKAESNGVSYCR 33

RESULT 8
US-09-894-882-461
; Sequence 461, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:

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; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

Query Match          37.3%; Score 69; DB 4; Length 39;
Best Local Similarity 44.8%; Pred. No. 0.14;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGLCIGVNNKVC 32
Db 1 CFPFGIVCTPYLPCCWIGCC--GTCRNVC 27

RESULT 10
US-09-894-882-247
; Sequence 247, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: 1-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-247

Query Match          37.3%; Score 69; DB 4; Length 67;
Best Local Similarity 44.8%; Pred. No. 0.24;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGLCIGVNNKVC 32
Db 29 CFPFGIVCTPYLPCCWIGCC--GTCRNVC 55

RESULT 11
US-09-894-882-470
; Sequence 470, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: 1-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-247

Query Match          37.3%; Score 69; DB 4; Length 67;
Best Local Similarity 44.8%; Pred. No. 0.24;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGLCIGVNNKVC 32
Db 29 CFPFGIVCTPYLPCCWIGCC--GTCRNVC 55

RESULT 12
US-09-894-882-498
; Sequence 498, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: 1-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 498
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-498

Query Match          36.2%; Score 67; DB 4; Length 40;
Best Local Similarity 50.0%; Pred. No. 0.25;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
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Qy 4 CTPAGVKCPAALPCCPGLRCIG 25  
Db 1 CFPLGTFCRSYLPCCSGMCCSG 22

## RESULT 13

US-09-894-882-274  
; Sequence 274, Application US/09894882  
; Patent No. 6767895

## GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation

; APPLICANT: Cognetix, Inc.

; APPLICANT: Walker, Craig S.

; APPLICANT: Shetty, Reshma

; APPLICANT: Jimenez, Elsie C.

; APPLICANT: McIntosh, J. Michael

; APPLICANT: Olivera, Baldomero M.

; APPLICANT: Watkins, Maren

; APPLICANT: Jones, Robert M.

; APPLICANT: Shen, Greg S.

; TITLE OF INVENTION: I-Superfamily Conotoxins

; FILE REFERENCE: 2314-238

; CURRENT APPLICATION NUMBER: US/09/894,882

; CURRENT FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: US 60/

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 60/243,410

; PRIOR FILING DATE: 2000-10-27

; PRIOR APPLICATION NUMBER: US 60/246,581

; PRIOR FILING DATE: 2000-11-08

; PRIOR APPLICATION NUMBER: US 60/247,714

; PRIOR FILING DATE: 2000-11-14

; PRIOR APPLICATION NUMBER: US 60/264,256

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 506

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 274

; LENGTH: 68

; TYPE: PRT

; ORGANISM: Conus virgo

US-09-894-882-274

Query Match 36.2%; Score 67; DB 4; Length 68;  
Best Local Similarity 50.0%; Pred. No. 0.41;  
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 4 CTPAGVKCPAALPCCPGLRCIG 25  
Db 29 CFPLGTFCRSYLPCCSGMCCSG 50

## RESULT 14

US-09-252-991A-28474

; Sequence 28474, Application US/09252991A

; Patent No. 6551795

## GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 28474

; LENGTH: 155

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-28474

Query Match 31.9%; Score 59; DB 4; Length 155;  
Best Local Similarity 52.6%; Pred. No. 7.5;  
Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 5 TPAGVKCPAALPCCPGLRC 23  
Db 7 TPASPRPSTAWCCPGRRC 25

## RESULT 15

US-09-902-540-15694

; Sequence 15694, Application US/09902540

; Patent No. 6833447

## GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 15694

; LENGTH: 211

; TYPE: PRT

; ORGANISM: Myxococcus xanthus

US-09-902-540-15694

Query Match 31.9%; Score 59; DB 4; Length 211;  
Best Local Similarity 42.9%; Pred. No. 10;  
Matches 9; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 3 ICTPAGVKCPAALPCCPGLRC 23  
Db 180 VCAPIGEACGESAAACCLGLMC 200

Search completed: March 9, 2005, 17:27:34  
Job time : 2.06257 secs

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OM protein - protein search, using sw model

Run on: March 9, 2005, 17:22:50 ; Search time 3.24047 Seconds  
(without alignments)  
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Title: US-10-019-823B-1  
Perfect score: 185  
Sequence: 1 XXICTPAGVKCPALPCCPGLCIGVGNKVCVR 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*  
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17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	44.3	36	9	US-09-894-882-3
2	79	42.7	36	9	US-09-894-882-4
3	73	39.5	35	14	US-10-072-602B-571
4	73	39.5	82	14	US-10-072-602B-140
5	72.5	39.2	37	9	US-09-894-882-5
6	69.5	37.6	30	14	US-10-072-602B-570
7	69.5	37.6	37	14	US-10-072-602B-137
8	69	37.3	31	9	US-09-894-882-461
9	69	37.3	37	9	US-09-894-882-497
10	69	37.3	69	9	US-09-894-882-247
11	67	36.2	32	9	US-09-894-882-470
12	67	36.2	32	14	US-10-072-602B-581
13	67	36.2	40	9	US-09-894-882-498

14	67	36.2	68	9	US-09-894-882-274
15	67	36.2	79	14	US-10-072-602B-255
16	64.5	34.9	86	15	US-10-424-599-240605
17	64	34.6	30	14	US-10-072-602B-576
18	64	34.6	77	14	US-10-072-602B-191
19	64	34.6	566	10	US-09-900-449A-6
20	64	34.6	572	10	US-09-900-449A-7
21	64	34.6	601	10	US-09-900-449A-5
22	64	34.6	639	10	US-09-900-449A-4
23	64	34.6	1064	14	US-10-173-461-5
24	64	34.6	3501	14	US-10-123-155-37
25	64	34.6	3501	14	US-10-146-731-37
26	64	34.6	3501	14	US-10-140-472-37
27	64	34.6	3501	14	US-10-141-761-37
28	64	34.6	3501	14	US-10-142-885-37
29	64	34.6	3501	14	US-10-158-790-37
30	64	34.6	3501	15	US-10-137-871-37
31	64	34.6	3501	15	US-10-140-923-37
32	64	34.6	3501	15	US-10-141-756-37
33	64	34.6	3501	15	US-10-141-759-37
34	64	34.6	3501	15	US-10-140-805-37
35	64	34.6	3501	15	US-10-140-864-37
36	64	34.6	3501	15	US-10-142-426-37
37	63	34.1	1971	14	US-10-123-155-139
38	63	34.1	1971	14	US-10-146-731-139
39	63	34.1	1971	14	US-10-140-472-139
40	63	34.1	1971	14	US-10-141-761-139
41	63	34.1	1971	14	US-10-142-885-139
42	63	34.1	1971	14	US-10-158-790-139
43	63	34.1	1971	15	US-10-137-871-139
44	63	34.1	1971	15	US-10-140-523-139
45	63	34.1	1971	15	US-10-141-756-139

## ALIGNMENTS

RESULT 1  
US-09-894-882-3  
; Sequence 3, Application US/09894882  
; Patent No. US20020102607A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jimenez, Elsie C.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Oliveira, Baldomero M.  
; APPLICANT: Watkins, Maren  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Shen, Greg S.  
; TITLE OF INVENTION: I-Superfamily Conotoxins  
; FILE REFERENCE: 2314-238  
; CURRENT APPLICATION NUMBER: US/09/894,882  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/243,410  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/246,581  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: US 60/247,714  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/264,256  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Hadronyche versuta  
US-09-894-882-3

Query Match 44.3%; Score 82; DB 9; Length 36;  
Best Local Similarity 51.5%; Pred. No. 0.018;  
Matches 17; Conservative 1; Mismatches 13; Indels 2; Gaps 1;

QY 3 ICTPAGVKCPAALPCCPGRLRCIGGVNNKY--CR 33  
||| | | | | | | | | | | | | | | | | | | |  
DB 2 ICTGADRPCAACCCPGTSCQGPESNGVGYCR 34

## RESULT 2

US-09-894-882-4  
; Sequence 4, Application US/09894882  
; Patent No. US20020102607A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jimenez, Elsie C.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: Watkins, Maren  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Shen, Greg S.  
; TITLE OF INVENTION: I-Superfamily Conotoxins  
; FILE REFERENCE: 2314-238  
; CURRENT APPLICATION NUMBER: US/09/894,882  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/243,410  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/246,581  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: US 60/247,714  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/264,256  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; TYPE: PRT  
; ORGANISM: Hadronyche versuta  
US-09-894-882-4

Query Match 42.7%; Score 79; DB 9; Length 36;  
Best Local Similarity 51.5%; Pred. No. 0.039;  
Matches 17; Conservative 0; Mismatches 14; Indels 2; Gaps 1;

QY 3 ICTPAGVKCPAALPCCPGRLRCIGGVNNKY--CR 33  
||| | | | | | | | | | | | | | | | | | | |  
DB 2 ICTGADRPCAACCCPGTSCQGPENGVGYCR 34

## RESULT 3

US-10-072-602B-571  
; Sequence 571, Application US/10072602B  
; Publication No. US20030109670A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Watkins, Maren  
; APPLICANT: Garrett, James E.  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Grille, Michelle  
; APPLICANT: Schoenfeld, Robert M.  
; APPLICANT: Walker, Craig  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jones, Robert M.

; TITLE OF INVENTION: Cone Snail Peptides  
; FILE REFERENCE: 2314-249  
; CURRENT APPLICATION NUMBER: US/10/072,602B  
; CURRENT FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: US 60/267,408  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 571  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Conus lividus  
US-10-072-602B-571

Query Match 39.5%; Score 73; DB 14; Length 35;  
Best Local Similarity 43.3%; Pred. No. 0.18;  
Matches 13; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 4 CTPAGVKCPAALPCCPGRLRCIGGVNNKYCR 33  
| | | | | | | | | | | | | | | | | | | |  
DB 2 CGESGGGCYSVRPCPGGLICKGTGGGLCR 31

## RESULT 4

US-10-072-602B-140  
; Sequence 140, Application US/10072602B  
; Publication No. US20030109670A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Watkins, Maren  
; APPLICANT: Garrett, James E.  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Grille, Michelle  
; APPLICANT: Schoenfeld, Robert M.  
; APPLICANT: Walker, Craig  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jones, Robert M.  
; TITLE OF INVENTION: Cone Snail Peptides  
; FILE REFERENCE: 2314-249  
; CURRENT APPLICATION NUMBER: US/10/072,602B  
; CURRENT FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: US 60/267,408  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 140  
; LENGTH: 82  
; TYPE: PRT  
; ORGANISM: Conus lividus  
US-10-072-602B-140

Query Match 39.5%; Score 73; DB 14; Length 82;  
Best Local Similarity 43.3%; Pred. No. 0.39;  
Matches 13; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 4 CTPAGVKCPAALPCCPGRLRCIGGVNNKYCR 33  
| | | | | | | | | | | | | | | | | | | |  
DB 49 CGESGGGCYSVRPCPGGLICKGTGGGLCR 78

## RESULT 5

US-09-894-882-5  
; Sequence 5, Application US/09894882  
; Patent No. US20020102607A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jimenez, Elsie C.

Db 2 CGHSGAGC-YTRCCPGLHCSGGQAGGLC 29

RESULT 7

US-10-072-602B-137

; Sequence 137, Application US/10072602B

; Publication No. US20030109670A1

; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation

; APPLICANT: Cognetix, Inc.

; APPLICANT: Olivera, Baldomero M.

; APPLICANT: McIntosh, J. Michael

; APPLICANT: Watkins, Maren

; APPLICANT: Garrett, James E.

; APPLICANT: Cruz, Lourdes J.

; APPLICANT: Grilley, Michelle

; APPLICANT: Schoenfeld, Robert M.

; APPLICANT: Walker, Craig

; APPLICANT: Shetty, Reshma

; APPLICANT: Jones, Robert M.

; TITLE OF INVENTION: Cone Snail Peptides

; FILE REFERENCE: 2314-249

; CURRENT APPLICATION NUMBER: US/10/072,602B

; CURRENT FILING DATE: 2002-02-11

; PRIOR APPLICATION NUMBER: US 60/267,408

; PRIOR FILING DATE: 2001-02-09

; NUMBER OF SEQ ID NOS: 638

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 137

; LENGTH: 77

; TYPE: PRT

; ORGANISM: Conus lividus

US-10-072-602B-137

Query Match 37.6%; Score 69.5; DB 14; Length 77;

Best Local Similarity 44.8%; Pred. No. 0.93; 13; Indels 1; Gaps 1;

Matches 13; Conservative 2; Mismatches 13; Indels 1; Gaps 1;

QY 4 CTGAGKCPAALPCCPGLRCIGGVNKKVC 32

Db 49 CGHSGAGC-YTRCCPGLHCSGGQAGGLC 76

US-09-894-882-461

; Sequence 461, Application US/09894882

; Patent No. US20020102607A1

; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation

; APPLICANT: Cognetix, Inc.

; APPLICANT: Walker, Craig S.

; APPLICANT: Shetty, Reshma

; APPLICANT: Jimenez, Elsie C.

; APPLICANT: McIntosh, J. Michael

; APPLICANT: Olivera, Baldomero M.

; APPLICANT: Watkins, Maren

; APPLICANT: Jones, Robert M.

; APPLICANT: Shen, Greg S.

; TITLE OF INVENTION: I-Superfamily Conotoxins

; FILE REFERENCE: 2314-238

; CURRENT APPLICATION NUMBER: US/09/894,882

; CURRENT FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: US 60/

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 60/243,410

; PRIOR FILING DATE: 2000-10-27

; PRIOR APPLICATION NUMBER: US 60/246,581

; PRIOR FILING DATE: 2000-11-08

; PRIOR APPLICATION NUMBER: US 60/247,714

; PRIOR FILING DATE: 2000-11-14

; PRIOR APPLICATION NUMBER: US 60/264,256

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 506

; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 461  
; LENGTH: 31  
; TYPE: PRT  
; ORGANISM: Conus emaciatus  
US-09-894-882-461

Query Match 37.3%; Score 69; DB 9; Length 31;  
Best Local Similarity 44.8%; Pred. No. 0.48;  
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32  
Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

RESULT 9

US-09-894-882-497  
; Sequence 497, Application US/09894882  
; Patent No. US20020102607A1

; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jimenez, Elsie C.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: Watkins, Maren  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Shen, Greg S.  
; TITLE OF INVENTION: I-Superfamily Conotoxins

; FILE REFERENCE: 2314-238

; CURRENT APPLICATION NUMBER: US/09/894,882

; PRIOR FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: US 60/

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 60/243,410

; PRIOR FILING DATE: 2000-10-27

; PRIOR APPLICATION NUMBER: US 60/246,581

; PRIOR FILING DATE: 2000-11-08

; PRIOR APPLICATION NUMBER: US 60/247,714

; PRIOR FILING DATE: 2000-11-14

; PRIOR APPLICATION NUMBER: US 60/264,256

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 506

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 497

; LENGTH: 39

; TYPE: PRT

; ORGANISM: Conus emaciatus

US-09-894-882-497

Query Match 37.3%; Score 69; DB 9; Length 39;  
Best Local Similarity 44.8%; Pred. No. 0.58;  
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32  
Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

RESULT 10

US-09-894-882-247  
; Sequence 247, Application US/09894882  
; Patent No. US20020102607A1

; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jimenez, Elsie C.  
; APPLICANT: McIntosh, J. Michael

; FILE REFERENCE: 2314-238

; CURRENT APPLICATION NUMBER: US/09/894,882

; PRIOR FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: US 60/

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 60/243,410

; PRIOR FILING DATE: 2000-10-27

; PRIOR APPLICATION NUMBER: US 60/246,581

; PRIOR FILING DATE: 2000-11-08

; PRIOR APPLICATION NUMBER: US 60/247,714

; PRIOR FILING DATE: 2000-11-14

; PRIOR APPLICATION NUMBER: US 60/264,256

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 506

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 470

; LENGTH: 32

; TYPE: PRT

; ORGANISM: Conus virgo

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32

Db 1 CFPFGIYCTPLPCCWGICC--GTCRNV 27

US-09-894-882-470

Query Match 36.2%; Score 67; DB 9; Length 32;

Qy 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32



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Best Local Similarity 50.0%; Pred. No. 0.83;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 4 CTPAGVKCPAALPCCPGLRGIG 25
Db 1 CFPLGTFCSRVLPCCSGMCCSG 22

RESULT 12
US-10-072-602B-581
; Sequence 581, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 581
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Conus virgo
US-10-072-602B-581

Query Match 36.2%; Score 67; DB 14; Length 32;
Best Local Similarity 48.4%; Pred. No. 0.83;
Matches 15; Conservative 1; Mismatches 13; Indels 2; Gaps 2;

Qy 4 CTPAGVKCPAALPCCPGLRGIG 33
Db 2 CGGQGECC-YTQPCPCGLRCRGGTGGVCQ 31

RESULT 13
US-09-894-882-498
; Sequence 498, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 274
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-498

Query Match 36.2%; Score 67; DB 9; Length 68;
Best Local Similarity 50.0%; Pred. No. 1.6;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 4 CTPAGVKCPAALPCCPGLRGIG 25
Db 29 CFPLGTFCSRVLPCCSGMCCSG 50

RESULT 15
US-10-072-602B-255
; Sequence 255, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
```

Thu Mar 10 14:26:01 2005

```

; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 255
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Conus virgo
US-10-072-602B-255

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Query Match      36.2%; Score 67; DB 14; Length 79;
Best Local Similarity 48.4%; Pred. No. 1.8;
Matches 15; Conservative 1; Mismatches 13; Indels 2; Gaps 2;

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QY      4 CTPAGVKCPAALPCCPLRCI-GGVNKKVC 33
Db      49 CGGQEGC-YTPCCPLRCRGGGTGGVCQ 78

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Search completed: March 9, 2005, 18:08:02  
Job time : 4.24047 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:50:50 ; Search time 176 Seconds  
(without alignments)  
96.015 Million cell updates/sec

Title: US-10-019-823B-1

Perfect score: 185

Sequence: 1 XICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	44.9	36	1	TXJB_HADVE
2	80	43.2	36	1	TXJB_HADVE
3	73.5	39.7	37	1	TXJC_HADVE
4	73	39.5	72	2	Q9TVN1
5	73	39.5	72	2	Q9UA22
6	73	39.5	72	2	Q9UA43
7	73	39.5	72	2	Q9UAA4
8	73	39.5	72	2	Q9UAA5
9	73	39.5	72	2	Q9UAA7
10	73	39.5	72	2	Q9UAB0
11	73	39.5	72	2	Q9UAB1
12	72	38.9	2524	2	Q9GPAS
13	71.5	38.6	33	1	TXCS_PHONI
14	71.5	38.6	3775	2	Q7PMF9
15	69	37.3	67	1	CKX_CONVR
16	68	36.8	71	2	Q9UAA9
17	66	35.7	71	2	Q9UAB3
18	66	35.7	1064	1	FBI1_STRPU
19	65	35.1	71	2	Q9TW08
20	65	35.1	71	2	Q9UAA0
21	65	35.1	71	2	Q9UAA1
22	65	35.1	71	2	Q9UAA6
23	65	35.1	71	2	Q9UAA8
24	65	35.1	71	2	Q9UAB2
25	64.5	34.9	76	2	Q9BP93
26	64	34.6	77	2	Q75WH6
27	63	34.1	233	2	Q946V8
28	62.5	33.8	80	2	Q9BP85
29	62	33.5	328	2	Q8TVF0
30	61.5	33.2	77	2	Q75WH3
31	61.5	33.2	494	2	Q6FN08

32 61.5 33.2 496 2 Q6CL87  
33 61 33.0 1317 2 Q6IQ50  
34 61 33.0 2471 1 NTC2\_HUMAN  
35 60 32.4 406 2 Q25059  
36 60 32.4 422 2 Q05790  
37 60 32.4 570 1 FBP3\_STRPU  
38 59.5 32.2 120 2 Q8N820  
39 59 31.9 259 1 DKX2\_MOUSE  
40 59 31.9 259 2 Q8BFW0  
41 59 31.9 1529 2 Q7XIQ7  
42 58.5 31.6 34 1 CXGS\_CONGE  
43 58.5 31.6 72 2 Q9BP95  
44 58.5 31.6 75 2 Q9BP94  
45 58.5 31.6 1390 1 INSR\_AEDAE

#### ALIGNMENTS

RESULT 1  
TXJA\_HADVE  
ID TXJA\_HADVE STANDARD; PRT; 36 AA.  
AC P82227;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Janus-atracotoxin-Hv1a (J-ActX-Hv1a).  
OS Hadronyche versuta (Blue mountains funnel-web spider) (Atrax versutus).  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
OC Mygalomorphae; Hexathelidae; Hadronyche.  
OX NCBI\_TaxID=6904;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=20343014; PubMed=10881200; DOI=10.1038/75921;  
RA Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H., Nicholson G.M., Christie M.J., King G.F.;  
RT "Discovery and characterization of a family of insecticidal neurotoxins with a rare vicinal disulfide bridge."  
RL Nat. Struct. Biol. 7:505-513(2000).  
CC -1- FUNCTION: Insecticidal neurotoxin.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.  
DR HSSP; P82228; IDLO.  
KW Direct protein sequencing; Neurotoxin; Toxin.  
FT DISULFID 3 17 By similarity.  
FT DISULFID 10 22 By similarity.  
FT DISULFID 13 14 By similarity.  
FT DISULFID 16 33 By similarity.  
SQ SEQUENCE 36 AA; 3685 MW; D1598B2560BFE997 CRC64;  
Query Match 44.9%; Score 83; DB 1; Length 36;  
Best Local Similarity 50.0%; Pred. No. 0.0046;  
Matches 17; Conservative 2; Mismatches 13; Indels 2; Gaps 1;  
QY 2 XICTPAGVKCPAALPCCPGLRCIGGVNNKV--CR 33  
:|||||:|||||:|||||:|||||:|||||:  
Db 1 TICTGADRPCAACCCPCGTCQGPESNGVVYCR 34  
RESULT 2  
TXJB\_HADVE  
ID TXJB\_HADVE STANDARD; PRT; 36 AA.  
AC P82226;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Janus-atracotoxin-Hv1b (J-ActX-Hv1b).  
OS Hadronyche versuta (Blue mountains funnel-web spider) (Atrax versutus).  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
OC Mygalomorphae; Hexathelidae; Hadronyche.

OX NCBI\_TaxID=6904;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=20343014; PubMed=10881200; DOI=10.1038/75921;

RA Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H.,

RA Nicholson G.M., Christie M.J., King G.F.;

RT "Discovery and characterization of a family of insecticidal

RT neurotoxins with a rare vicinal disulfide bridge.";

RL Nat. Struct. Biol. 7:505-513(2000).

CC -1- FUNCTION: Insecticidal neurotoxin.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.

DR HSP; P82228; IDL0.

KW Direct protein sequencing; Neurotoxin; Toxin.

FT DISULFID 3 17 By similarity.

FT DISULFID 10 22 By similarity.

FT DISULFID 13 24 By similarity.

FT DISULFID 16 33 By similarity.

SQ SEQUENCE 36 AA; 3651 MW; D23A442560B89997 CRC64;

Query Match 43.2%; Score 80; DB 1; Length 36;

Best Local Similarity 50.0%; Pred. No. 0.011; Indels 2; Gaps 1;

Matches 17; Conservative 1; Mismatches 14; Indels 2; Gaps 1;

QY 2 XICTPAGVKCPAALPCCPGLRCIGGVNNK--CR 33

Db 1 TICTGADRPCAACCCPCPGTSCQGPENGVS YCR 34

RESULT 3

TXJC HADVE

ID TXJC HADVE STANDARD; PRT; 37 AA.

AC P82228;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Janus-atracotoxin-Hvic (J-Actx-Hvic).

OS Hadronyche versuta (Blue mountains funnel-web spider) (Atrax

OS versuta).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;

OC Mygalomorphae; Hexathelidae; Hadronyche.

ON NCBI\_TaxID=6904;

RN [1]

RP SEQUENCE, FUNCTION, AND STRUCTURE BY NMR.

RC TISSUE=Venom;

RX MEDLINE=20343014; PubMed=10881200; DOI=10.1038/75921;

RA Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H.,

RA Nicholson G.M., Christie M.J., King G.F.;

RT "Discovery and characterization of a family of insecticidal

RT neurotoxins with a rare vicinal disulfide bridge.";

RL Nat. Struct. Biol. 7:505-513(2000).

CC -1- FUNCTION: Insecticidal neurotoxin.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.

DR PDB; IDL0; NMR; A=1-37.

KW 3D-structure; Direct protein sequencing; Neurotoxin; Toxin.

FT DISULFID 3 17

FT DISULFID 10 22

FT DISULFID 13 14

FT DISULFID 16 32

FT TURN 6 7

FT TURN 9 9

FT TURN 18 19

FT TURN 20 24

FT TURN 26 27

FT STRAND 30 34

SQ SEQUENCE 37 AA; 3768 MW; E4DDF046CC750FFC CRC64;

Query Match

Best Local Similarity 39.7%; Score 73.5; DB 1; Length 37;

Matches 15; Conservative 1; Mismatches 16; Indels 1; Gaps 1;

QY 2 XICTPAGVKCPAALPCCPGLRCIGGVNNK--KVC 33

Db 1 AICTGADRPCAACCCPCPGTSCQGPENGVS YCR 33

RESULT 4

Q9TVN1

ID Q9TVN1 PRELIMINARY; PRT; 72 AA.

AC Q9TVN1;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)

DE Four-loop conotoxin LVVIA (Four-loop conotoxin LVVIB)

DE (Fragment).

OS Conus lividus.

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.

ON NCBI\_TaxID=89426;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99289555; PubMed=10359796; DOI=10.1073/pnas.96.12.6820;

RA Duda T.F. Jr., Palumbi S.R.;

RT "Molecular genetics of ecological diversification: duplication and

RT rapid evolution of toxin genes of the venomous gastropod Conus.";

RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).

DR EMBL; AF089958; AAD48213.1; -

DR EMBL; AF089902; AAD48158.1; -

DR EMBL; AF089906; AAD48162.1; -

DR EMBL; AF089907; AAD48163.1; -

DR EMBL; AF089910; AAD48165.1; -

DR EMBL; AF089913; AAD48168.1; -

DR EMBL; AF089914; AAD48169.1; -

DR EMBL; AF089915; AAD48170.1; -

DR EMBL; AF089916; AAD48171.1; -

DR EMBL; AF089917; AAD48172.1; -

DR EMBL; AF089918; AAD48173.1; -

DR EMBL; AF089919; AAD48174.1; -

DR EMBL; AF089920; AAD48175.1; -

DR EMBL; AF089921; AAD48176.1; -

DR EMBL; AF089922; AAD48177.1; -

DR EMBL; AF089923; AAD48178.1; -

DR EMBL; AF089924; AAD48179.1; -

DR EMBL; AF089925; AAD48180.1; -

DR EMBL; AF089926; AAD48181.1; -

DR EMBL; AF089927; AAD48182.1; -

DR EMBL; AF089928; AAD48183.1; -

DR EMBL; AF089929; AAD48184.1; -

DR EMBL; AF089930; AAD48185.1; -

DR EMBL; AF089931; AAD48186.1; -

DR EMBL; AF089932; AAD48187.1; -

DR EMBL; AF089933; AAD48188.1; -

DR EMBL; AF089941; AAD48196.1; -

DR EMBL; AF089942; AAD48197.1; -

DR EMBL; AF089943; AAD48198.1; -

DR EMBL; AF089944; AAD48199.1; -

DR EMBL; AF089945; AAD48200.1; -

DR EMBL; AF089946; AAD48201.1; -

DR EMBL; AF089947; AAD48202.1; -

DR EMBL; AF089948; AAD48203.1; -

DR EMBL; AF089949; AAD48204.1; -

DR EMBL; AF089950; AAD48205.1; -

DR EMBL; AF089951; AAD48206.1; -

DR EMBL; AF089953; AAD48208.1; -

DR EMBL; AF089954; AAD48209.1; -

GO; GO:000576; C:extracellular; IEA.

GO; GO:0008200; F:ion channel inhibitor activity; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

InterPro; IPR004214; Conotoxin.

Pfam; PF02950; Conotoxin; 1.

NON TER 1

SEQUENCE 72 AA; 7984 MW; B2057DDC87553B8D CRC64;

FT	NON TER	1	1
SQ	SEQUENCE	72 AA; 8014 MW;	C2757DDC87553EDD CRC64;
	Query Match	39.5%;	Score 73; DB 2; Length 72;
	Best Local Similarity	44.8%;	Pred. No. 0.14;
	Matches 13; Conservative	5; Mismatches	9; Indels 2; Gaps 1;
QY	1 XXICTPAGVKCPAALPCCPGLRC--IGGV 27	:	: ::   :
DB	41 TWTCSPAGEVCTSKSPCCGTGFLSHIGGM 69	:	: ::   :
RESULT 7			
Q9UAA4	PRELIMINARY;	PRT;	72 AA.
ID	Q9UAA4;		
AC	Q9UAA4;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Four-loop conotoxin LVVIA (Fragment).		
OS	Conus lividus.		
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;		
OC	Apoagastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;		
OC	Necogastropoda; Conoidea; Conidae; Conus.		
OX	NCBI_TaxID=89426;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RP	MEDLINE=99289555; PubMed=10359796; DOI=10.1073/pnas.96.12.6820;		
RA	Duda T.F. Jr., Palumbi S.R.;		
RT	"Molecular genetics of ecological diversification: duplication and rapid evolution of toxin genes of the venomous gastropod Conus.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).		
DR	EMBL; AF089955; AAD48210.1; -.		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0008200; F:ion channel inhibitor activity; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR004214; Conotoxin.		
DR	Pfam; PF02950; Conotoxin; 1.		
FT	NON TER	1	1
SQ	SEQUENCE	72 AA; 7998 MW; B4DE7DDC87553B8D CRC64;	
	Query Match	39.5%;	Score 73; DB 2; Length 72;
	Best Local Similarity	44.8%;	Pred. No. 0.14;
	Matches 13; Conservative	5; Mismatches	9; Indels 2; Gaps 1;
QY	1 XXICTPAGVKCPAALPCCPGLRC--IGGV 27	:	: ::   :
DB	41 TRTCSPAGEVCTSKSPCCGTGFLTHIGGM 69	:	: ::   :
RESULT 8			
Q9UAA5	PRELIMINARY;	PRT;	72 AA.
ID	Q9UAA5;		
AC	Q9UAA5;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Four-loop conotoxin LVVIA (Fragment).		
OS	Conus lividus.		
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;		
OC	Apoagastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;		
OC	Necogastropoda; Conoidea; Conidae; Conus.		
OX	NCBI_TaxID=89426;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RP	MEDLINE=99289555; PubMed=10359796; DOI=10.1073/pnas.96.12.6820;		
RA	Duda T.F. Jr., Palumbi S.R.;		
RT	"Molecular genetics of ecological diversification: duplication and rapid evolution of toxin genes of the venomous gastropod Conus.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).		
DR	EMBL; AF089952; AAD48207.1; -.		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0008200; F:ion channel inhibitor activity; IEA.		

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DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 72 AA; 7915 MW; D9757DCD87553EDC CRC64;
Query Match 39.5%; Score 73; DB 2; Length 72;
Best Local Similarity 44.8%; Pred. No. 0.14;
Matches 13; Conservative 5; Mismatches 9; Indels 2; Gaps 1;
Qy 1 XXICTPAGVKCPAALPCCPGIIRC--IGGV 27
Db 41 TGTCSPAGEVCTSKSPCCCTGFLCSHIGGM 69
RESULT 9
Q9UAA7
ID Q9UAA7 PRELIMINARY; PRT; 72 AA.
AC Q9UAA7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Four-loop conotoxin LVVIA (Fragment).
OS Conus lividus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89426;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9289555; PubMed=10359796; DOI=10.1073/pnas.96.12.6820;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RT rapid evolution of toxin genes of the venomous gastropod Conus.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823 (1999).
DR EMBL; AF089912; AAD48167.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 72 AA; 7970 MW; B7A0DDC87533B8D CRC64;
Query Match 39.5%; Score 73; DB 2; Length 72;
Best Local Similarity 44.8%; Pred. No. 0.14;
Matches 13; Conservative 5; Mismatches 9; Indels 2; Gaps 1;
Qy 1 XXICTPAGVKCPAALPCCPGIIRC--IGGV 27
Db 41 TGTCSPAGEVCTSKSPCCCTGFLCSHIGGM 69
RESULT 10
Q9UAB0
ID Q9UAB0 PRELIMINARY; PRT; 72 AA.
AC Q9UAB0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Four-loop conotoxin LVVIA (Fragment).
OS Conus lividus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89426;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9289555; PubMed=10359796; DOI=10.1073/pnas.96.12.6820;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RT rapid evolution of toxin genes of the venomous gastropod Conus.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823 (1999).
DR EMBL; AF089912; AAD48167.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 72 AA; 7970 MW; B7A0DDC87533B8D CRC64;
Query Match 39.5%; Score 73; DB 2; Length 72;
Best Local Similarity 44.8%; Pred. No. 0.14;
Matches 13; Conservative 5; Mismatches 9; Indels 2; Gaps 1;
Qy 1 XXICTPAGVKCPAALPCCPGIIRC--IGGV 27
Db 41 TGTCSPAGEVCTSKSPCCCTGFLCSHIGGM 69
RESULT 11
Q9UAB1
ID Q9UAB1 PRELIMINARY; PRT; 72 AA.
AC Q9UAB1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Four-loop conotoxin LVVIA (Fragment).
OS Conus lividus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89426;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9289555; PubMed=10359796; DOI=10.1073/pnas.96.12.6820;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RT rapid evolution of toxin genes of the venomous gastropod Conus.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823 (1999).
DR EMBL; AF089904; AAD48160.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 72 AA; 7935 MW; 64C72DDC8755282F CRC64;
Query Match 39.5%; Score 73; DB 2; Length 72;
Best Local Similarity 44.8%; Pred. No. 0.14;
Matches 13; Conservative 5; Mismatches 9; Indels 2; Gaps 1;
Qy 1 XXICTPAGVKCPAALPCCPGIIRC--IGGV 27
Db 41 TGTCSPAGEVCTSKSPCCCTGFLCSHIGGM 69
RESULT 12
Q9GPA5
ID Q9GPA5 PRELIMINARY; PRT; 2524 AA.
AC Q9GPA5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative notch receptor protein.
GN Name-notch;
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7739;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Whole larvae;
RA Holland L.Z., Burgdorf C., Holland N.D., Lehrach H., Tamme R.,
```

RA Abi-Rached L., Pontarotti P., Lardelli M.;  
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Whole larvae;  
RA Lardelli M.T.;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Y12539; CAC19873.1; -;  
DR HSP; P07207; IOT8.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0030154; P:cell differentiation; IEA.  
DR InterPro; IPR002110; ANK.  
DR InterPro; IPR001012; Asx\_hydroxyl\_S.  
DR InterPro; IPR008985; ConA like lec\_gl.  
DR InterPro; IPR000345; CytC\_heme\_BS.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001438; EGF\_II.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR008000; Notch\_region.  
DR Pfam; PF00023; Ank; 6.  
DR Pfam; PF00008; EGF; 34.  
DR Pfam; PF07645; EGF\_Ca; 2.  
DR Pfam; PF00066; Notch; 3.  
DR PRINTS; PR01415; ANKYRIN.  
DR PRINTS; PR01452; NOTCH.  
DR SMART; SM00248; ANK; 6.  
DR SMART; SM00179; EGF\_Ca; 21.  
DR SMART; SM00004; NL; 3.  
DR PROSITE; PS50088; ANK\_REPEAT; 4.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
DR PROSITE; PS0010; ASX\_HYDROXYL; 23.  
DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; 34.  
DR PROSITE; PS01186; EGF\_2; 28.  
DR PROSITE; PS50026; EGF\_3; 36.  
DR PROSITE; PS01187; EGF\_Ca; 22.  
KW ANK repeat; EGF-like domain; Receptor.  
SQ SEQUENCE 2524 AA; 270970 MW; CCA57E306D23EC9 CRC64;

Query Match 38.9%; Score 72; DB 2; Length 2524;  
Best Local Similarity 45.9%; Pred. No. 4.5;  
Matches 17; Conservative 2; Mismatches 10; Indels 8; Gaps 2;

QY 4 CTPA--GVKCP-----AALPCCPGLCIGGVNNKVC 32  
DB 768 CLPGYGVNCDINTDECASNPCQNGRCLDGVNNYVC 804

RESULT 13  
TXCS\_PHONI

ID TXCS\_PHONI STANDARD; PRT; 33 AA.  
AC P84015;  
DT 25-OCT-2004 (Rel. 45, Created)  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Venom protein PN10C5.  
OS Phoneutria nigriventer (Brazilian armed spider).  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.  
OX NCBI\_TaxID=6918;  
RN [1]  
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS  
RC SPECTROMETRY.  
RC TISSUE=Venom;  
RA Richardson M., Pimenta A.M.C., Bemquerer M.P., Santoro M.M.,  
RA Figueiredo S.G., Cordeiro M.N.;  
RT "New peptide PN10C5 from venom of Brazilian armed spider Phoneutria  
RT nigriventer has sequence similarities with snake disintegrins,  
RT vasotocin-neurophysins and other spider toxins.";

RL Submitted (JUN-2004) to Swiss-Prot.  
CC -!- FUNCTION: Non-toxic to mice.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.  
CC -!- MASS SPECTROMETRY: MW=3672.7; METHOD=Electrospray; RANGE=1-33;  
CC NOTE=Ref.1.  
KW Direct protein sequencing.  
SQ SEQUENCE 33 AA; 3679 MW; 77F1127D4785D6E1 CRC64;

Query Match 38.6%; Score 71.5; DB 1; Length 33;  
Best Local Similarity 37.5%; Pred. No. 0.11;  
Matches 12; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 2 XICTPAGVKCPAALPCCPGLCIGGVNNKVC 33  
DB 1 GFCAQKGKIC-HDIHCCTNLKCVREGSNVCR 31

## RESULT 14

Q7PMF9  
ID Q7PMF9 PRELIMINARY; PRT; 3775 AA.  
AC Q7PMF9;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE ENSANGP00000011881 (Fragment).  
GN Name=ENGANGG00000009392;  
OS Anopheles gambiae str. PEST.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.  
OX NCBI\_TaxID=180454;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PEST.  
RA Anopheles Genome Sequencing Consortium;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AAB01008980; EAA13897.2; -;  
DR HSSP; P16109; 1FSB.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR000345; CytC\_heme\_BS.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF00008; EGF; 3.  
DR Pfam; PF07645; EGF\_Ca; 16.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 17.  
DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
DR PROSITE; PS00615; C\_TYPE\_LLECTIN\_1; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; 25.  
DR PROSITE; PS50026; EGF\_3; 25.  
DR PROSITE; PS01187; EGF\_Ca; 16.  
KW EGF-like domain.  
FT NON\_TER 1  
FT NON\_TER 3775  
SQ SEQUENCE 3775 AA; 396198 MW; 51C4106F6E9908F4 CRC64;

Query Match 38.6%; Score 71.5; DB 2; Length 3775;  
Best Local Similarity 39.4%; Pred. No. 7.5;  
Matches 13; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 1 XXICT-PAGVKCPAALPCCPGLCIGGVNNKVC 32  
DB 1351 KTVCTNPQCQGANQCPCPGYGVGVNCLC 1383

RESULT 15  
CXK\_CONVR

```
ID  CXK  CONVR  STANDARD;  PRT;  67 AA.
AC  Q7YZS9;
DT  29-MAR-2004 (Rel. 43, Created)
DT  29-MAR-2004 (Rel. 43, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Kappa-conotoxin ViTx precursor.
GN  Name=ViTx;
OS  Conus virgo (Virgin cone).
OC  Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC  Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypogastropoda;
OC  Neogastropoda; Conoidea; Conidae; Conus.
OX  NCBI_TaxID=89427;
RN  [1]
RP  SEQUENCE FROM N.A., SEQUENCE OF 27-53, SYNTHESIS OF 27-60, AND MASS
RP  SPECTROMETRY.
RC  TISSUE=Venom, and Venom duct;
RX  PubMed=12893060; DOI=10.1016/S0041-0101(03)00099-0;
RA  Kaferstein S., Huys I., Lamthanh H., Stocklin R., Sotto F., Menez A.,
RA  Tytgat J., Mebs D.;
RT  "A novel conotoxin inhibiting vertebrate voltage-sensitive potassium
RT  channels.";
RL  Toxicon 42:43-52(2003).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Venom duct;
RA  Kaferstein S.;
RL  Thesis (2001), University of Darmstadt, Germany.
CC  -!- FUNCTION: Kappa-conotoxins bind and inhibit voltage-sensitive
CC  potassium channels. This toxin inhibits the vertebrate potassium
CC  channels Kvi.1 and Kvi.3, but not Kvi.2. It has no effect on HERG-
CC  type channels, sodium hH1 channels and Kir-type channels (IRK1).
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC  -!- PTM: Contains four disulfide bonds.
CC  -!- MASS SPECTROMETRY: MW=3933.3; METHOD=Electrospray; RANGE=27-60;
CC  NOTE=Ref.1.
CC  -!- SIMILARITY: Belongs to the conotoxin O-superfamily. Kappa-type
CC  family.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AJ560778; CAD90965.1; -
KW  Direct protein sequencing; Signal; Toxin.
FT  SIGNAL 1 26
FT  CHAIN 27 60 Kappa-conotoxin ViTx.
FT  PROPEP 61 67
FT  CONFLICT 38 38 P -> S (in Ref. 1).
FT  CONFLICT 49 49 G -> S (in Ref. 1).
SQ  SEQUENCE 67 AA; 7599 MW; 46671D012446F62D CRC64;

Query Match 37.3%; Score 69; DB 1; Length 67;
Best Local Similarity 44.8%; Pred. No. 0.41;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

Qy 4 CTPAGVKCPAALPCCGLRICIGGVNNKVC 32
Db 29 CFPPICTVPLPCGWGCC--GTCRNV 55
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Search completed: February 14, 2005, 21:04:58  
Job time : 176 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:56:55 ; Search time 39 Seconds  
(without alignments)  
81.414 Million cell updates/sec

Title: US-10-019-823B-1

Perfect score: 185

Sequence: 1 XXICTPAGVKCPAALPCFGLRCIGGVNNKVC 33

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: piri:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	35.7	1064	2 A40136	fibropellin Ia - s
2	60	32.4	422	2 S48564	probable membrane
3	60	32.4	570	2 A48336	fibropellin C prec
4	58.5	31.6	34	2 A31043	mu-conotoxin GS -
5	58.5	31.6	1390	2 T30346	insulin receptor -
6	58	31.4	37	2 E44007	aptotoxin III - tr
7	58	31.4	1221	2 T23472	hypothetical prote
8	57	30.8	2531	2 S18188	notch protein homo
9	57	30.8	2531	2 A46019	notch-1 protein -
10	56.5	30.5	4543	1 A53102	alpha-2-macroglobu
11	56	30.3	197	2 T10081	sperm mitochondria
12	56	30.3	585	2 S43572	COSB5.5 protein (c
13	56	30.3	585	2 E88571	protein COSB5.5 [i
14	56	30.3	2352	2 T30201	Notch homolog prot
15	55.5	30.0	788	2 A87722	protein ZC123.1 [i
16	55	29.7	132	2 H75335	hypothetical prote
17	55	29.7	238	2 T04166	thauematic-like pro
18	55	29.7	2139	2 A45672	crumbs protein - f
19	55	29.7	2318	2 A45306	notch 3 protein -
20	55	29.7	2321	2 S78549	notch3 protein - h
21	54.5	29.5	417	2 T08724	hypothetical prote
22	54.5	29.5	601	2 T22025	hypothetical prote
23	54.5	29.5	601	2 D89711	protein F40E10.4 [
24	54.5	29.5	4544	1 S02392	alpha-2-macroglobu
25	54.5	29.5	4545	1 S25111	alpha-2-macroglobu
26	54	29.2	73	2 H43019	platelet aggregati
27	54	29.2	269	2 T26957	hypothetical prote
28	54	29.2	283	2 E88597	protein Y47D38.6 [
29	54	29.2	596	2 T26950	hypothetical prote

30 54 29.2 1203 2 A49175 Motch B protein -  
31 54 29.2 1449 2 S47423 E2 glycoprotein pr  
32 54 29.2 2437 2 S42612 transmembrane prot  
33 54 29.2 2524 2 A35844 Xotch protein - Af  
34 53 28.6 456 1 KXBO protein C (activat  
35 53 28.6 1447 1 VGIHE3 E2 glycoprotein pr  
36 53 28.6 1447 1 VGIHE2 E2 glycoprotein pr  
37 53 28.6 1449 1 A43573 E2 glycoprotein pr  
38 53 28.6 1449 1 VGIHFS E2 glycoprotein pr  
39 53 28.6 1451 1 JQ1719 E2 glycoprotein pr  
40 53 28.6 1453 2 S41453 spike protein - ca  
41 52 28.1 64 2 A25775 metallochionein A  
42 52 28.1 64 2 A33825 metallochionein A  
43 52 28.1 71 2 G43019 platelet aggregati  
44 52 28.1 134 2 AD0652 conserved hypothet  
45 52 28.1 249 2 T32060 hypothetical prote

#### ALIGNMENTS

##### RESULT 1

A40136  
fibropellin Ia - sea urchin (Strongylocentrotus purpuratus)  
N/Alternate names: epidermal growth factor homolog precursor  
N/Contains: alternatively spliced fibropellin Ib (EGFI)  
C/Species: Strongylocentrotus purpuratus (purple urchin)  
C/Date: 13-May-1992 #sequence revision 17-Sep-1997 #text\_change 09-Jul-2004  
C/Accession: A40136; B40136; C40136; A29316; A43131  
R/Delgadillo-Reynoso, M.G.; Rollo, D.R.; Hersh, D.A.; Raff, R.A.  
J. Mol. Evol. 29, 314-327, 1989  
A/Title: Structural analysis of the uegf gene in the sea urchin Strongylocentrotus purpuratus  
A/Reference number: A40136; MUID:90112459; PMID:2514273  
A/Accession: A40136  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-114 <DEL>  
A/Cross-references: UNIPROT:P10079; GB:X17530; NID:gi0225; PID:g667061  
A/Accession: B40136  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 181-251,329-370,'R',372-408,'RA',411-441 <DE2>  
A/Accession: C40136  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 'K',747-821,898-978 <DE3>  
R/Hersh, D.A.; Andrews, M.E.; Raff, R.A.  
Science 237, 1487-1490, 1987  
A/Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.  
A/Reference number: A29316; MUID:87319677; PMID:3498216  
A/Accession: A29316  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 'S',280-481,786-1064 <HUR>  
A/Cross-references: GB:M17421; NID:gl61474; PIDN:AAA30050.1; PID:G552260  
R/Hunt, L.T.; Barker, W.C.  
FASEB J. 3, 1760-1764, 1989  
A/Title: Avidin-like domain in an epidermal growth factor homolog from a sea urchin.  
A/Reference number: A43131; MUID:89196806; PMID:2784773  
A/Contents: annotation  
C/Comment: EGF homology repeats 10-17 are spliced out in the short form (fibropellin Ib)  
F:1-13/Domain: signal sequence #status predicted <SIG>  
F:20-1064/Product: fibropellin I #status predicted <FIB>  
F:23-54/Domain: EGF homology <EG01>  
F:57-175/Domain: Ctr/Cis repeat homology <CLR>  
F:180-211/Domain: EGF homology <EG02>  
F:218-249/Domain: EGF homology <EG03>  
F:256-287/Domain: EGF homology <EG04>  
F:294-325/Domain: EGF homology <EG05>  
F:332-363/Domain: EGF homology <EG06>  
F:370-401/Domain: EGF homology <EG07>  
F:408-439/Domain: EGF homology <EG08>  
F:446-477/Domain: EGF homology <EG09>





C:Genetics:  
A:Gene: notch-1  
A:Map position: 2  
A:Note: proximal region of chromosome 2  
C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology  
F:106-138/Domain: EGF homology <EGF1>  
F:144-175/Domain: EGF homology <EG01>  
F:222-254/Domain: EGF homology <EGF2>  
F:261-292/Domain: EGF homology <EG02>  
F:339-370/Domain: EGF homology <EG03>  
F:416-449/Domain: EGF homology <EGF3>  
F:456-487/Domain: EGF homology <EG04>  
F:494-525/Domain: EGF homology <EG05>  
F:532-563/Domain: EGF homology <EG06>  
F:607-638/Domain: EGF homology <EG07>  
F:682-713/Domain: EGF homology <EG08>  
F:757-788/Domain: EGF homology <EG09>  
F:795-826/Domain: EGF homology <EG10>  
F:873-904/Domain: EGF homology <EG11>  
F:911-942/Domain: EGF homology <EG12>  
F:949-980/Domain: EGF homology <EG13>  
F:987-1018/Domain: EGF homology <EG14>  
F:1025-1056/Domain: EGF homology <EG15>  
F:1063-1094/Domain: EGF homology <EG16>  
F:1149-1180/Domain: EGF homology <EG17>  
F:1187-1218/Domain: EGF homology <EG18>  
F:1233-1264/Domain: EGF homology <EGF4>  
F:1352-1383/Domain: EGF homology <EG19>  
F:1391-1425/Domain: EGF homology <EGF>  
F:1917-1948/Domain: ankyrin repeat homology <AN1>  
F:1949-1981/Domain: ankyrin repeat homology <AN2>  
F:1983-2015/Domain: ankyrin repeat homology <AN3>  
F:2016-2048/Domain: ankyrin repeat homology <AN4>  
F:2049-2081/Domain: ankyrin repeat homology <AN5>  
Query Match 30.8%; Score 57; DB 2; Length 2531;  
Best Local Similarity 34.1%; Pred. No. 79;  
Matches 14; Conservative 4; Mismatches 15; Indels 8; Gaps 2;  
Qy 1 XXICTP-AGVKCPAALPCCPQLR-----CIGGVNKKVC 33  
Db 242 ECALUFGAGQCNENVDPCFNCKNGGACVGVNTVNCR 282  
RESULT 10  
A53102  
alpha-2-macroglobulin receptor precursor - chicken  
N:Alternate names: CB91; LDL receptor-related protein 1; low density lipoprotein receptor  
C:Species: Gallus gallus (chicken)  
C:Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 09-Jul-2004  
C:Accession: A53102  
R:Nimpf, J.; Stifani, S.; Bilous, P.T.; Schneider, W.J.  
J. Biol. Chem. 269, 212-219, 1994  
A:Title: The somatic cell-specific low density lipoprotein receptor-related protein of t  
A:Reference number: A53102; MUID:94103212; PMID:7506255  
A:Accession: A53102  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-4543 <NTM>  
A:Cross-references: UNIPROT:p98157; GB:X74904; NID:g438006; PIDN:CAA52870.1; PID:g438007  
C:Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associated protein.  
C:Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding  
C:Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; glycopro  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-3942/Domain: alpha-2-macroglobulin receptor 515K chain #status predicted <515K>  
F:18-3942,3943-4543/Product: alpha-2-macroglobulin receptor #status predicted <MAT>  
F:29-66/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
F:74-110/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
F:117-150/Domain: EGF homology <EG>  
F:156-190/Domain: EGF homology <EG2>  
F:200-241/Domain: LDL receptor YWTD-containing repeat homology <YW01>  
F:242-283/Domain: LDL receptor YWTD-containing repeat homology <YW02>  
F:294-336/Domain: LDL receptor YWTD-containing repeat homology <YW03>  
F:337-380/Domain: LDL receptor YWTD-containing repeat homology <YW04>  
F:381-422/Domain: LDL receptor YWTD-containing repeat homology <YW05>  
F:423-470/Domain: LDL receptor YWTD-containing repeat homology <YW06>  
F:480-521/Domain: EGF homology <EG3>  
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F:616-661/Domain: LDL receptor YWTD-containing repeat homology <YW08>  
F:662-712/Domain: LDL receptor YWTD-containing repeat homology <YW09>  
F:713-754/Domain: LDL receptor YWTD-containing repeat homology <YW10>  
F:755-797/Domain: LDL receptor YWTD-containing repeat homology <YW11>  
F:805-840/Domain: EGF homology <EG4>  
F:852-888/Domain: LDL receptor ligand-binding repeat homology <LDL3>  
F:893-929/Domain: LDL receptor ligand-binding repeat homology <LDL4>  
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F:974-1009/Domain: LDL receptor ligand-binding repeat homology <LDL6>  
F:1013-1045/Domain: LDL receptor ligand-binding repeat homology <LDL7>  
F:1060-1095/Domain: LDL receptor ligand-binding repeat homology <LDL8>  
F:1102-1138/Domain: LDL receptor ligand-binding repeat homology <LDL9>  
F:1143-1180/Domain: LDL receptor ligand-binding repeat homology <LDL10>  
F:1183-1219/Domain: EGF homology <EG5>  
F:1225-1259/Domain: EGF homology <EG6>  
F:1267-1306/Domain: LDL receptor YWTD-containing repeat homology <YW12>  
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F:1487-1529/Domain: LDL receptor YWTD-containing repeat homology <YW17>  
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F:1625-1667/Domain: LDL receptor YWTD-containing repeat homology <YW19>  
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F:1752-1794/Domain: LDL receptor YWTD-containing repeat homology <YW22>  
F:1795-1842/Domain: LDL receptor YWTD-containing repeat homology <YW23>  
F:1846-1882/Domain: EGF homology <EG8>  
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F:1973-2015/Domain: LDL receptor YWTD-containing repeat homology <YW25>  
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F:2102-2147/Domain: LDL receptor YWTD-containing repeat homology <YW28>  
F:2155-2190/Domain: EGF homology <EG9>  
F:2195-2237/Domain: LDL receptor YWTD-containing repeat homology <YW29>  
F:2247-2288/Domain: LDL receptor YWTD-containing repeat homology <YW30>  
F:2338-2382/Domain: LDL receptor YWTD-containing repeat homology <YW31>  
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F:2424-2467/Domain: LDL receptor YWTD-containing repeat homology <YW33>  
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F:2518-2555/Domain: LDL receptor ligand-binding repeat homology <LDL11>  
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F:2646-2682/Domain: LDL receptor ligand-binding repeat homology <LDL14>  
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F:2941-2977/Domain: EGF homology <EG11>  
F:2983-3018/Domain: EGF homology <EG12>  
F:3026-3065/Domain: LDL receptor YWTD-containing repeat homology <YW34>  
F:3066-3110/Domain: LDL receptor YWTD-containing repeat homology <YW35>  
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F:3154-3197/Domain: LDL receptor YWTD-containing repeat homology <YW37>  
F:3198-3238/Domain: LDL receptor YWTD-containing repeat homology <YW38>  
F:3239-3281/Domain: LDL receptor YWTD-containing repeat homology <YW39>  
F:3291-3327/Domain: EGF homology <EG13>  
F:3331-3366/Domain: LDL receptor ligand-binding repeat homology <LDL19>  
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F:3491-3528/Domain: LDL receptor ligand-binding repeat homology <LDL23>  
F:3533-3567/Domain: LDL receptor ligand-binding repeat homology <LDL24>  
F:3572-3606/Domain: LDL receptor ligand-binding repeat homology <LDL25>

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F;3692-3728/Domain: LDL receptor ligand-binding repeat homology <LDLU>  
F;3738-3774/Domain: LDL receptor ligand-binding repeat homology <LDLV>  
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F;3826-3858/Domain: EGF homology <EG15>  
F;3866-3909/Domain: LDL receptor WYTD-containing repeat homology <YW40>  
F;3910-3968/Domain: LDL receptor WYTD-containing repeat homology <YW41>  
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F;4235-4266/Domain: EGF homology <EG18>  
F;4271-4302/Domain: EGF homology <EG19>  
F;4307-4338/Domain: EGF homology <EG20>  
F;4343-4373/Domain: EGF homology <EG21>  
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F;4421-4443/Domain: transmembrane #status predicted <TMM>  
F;4444-4543/Domain: intracellular #status predicted <INT>  
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3485,3659,3786,3837,3952,4074,4124,4178,4278/Binding site: carbohydrate (Asn) (covalent)  
F;168,2995/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted  
F;2955/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

Query Match 30.5%; Score 56.5; DB 1; Length 4543;  
Best Local Similarity 33.3%; Pred. No. 1.4e+02;  
Matches 13; Conservative 6; Mismatches 13; Indels 7; Gaps 2;

QY 1 XXICTPAGVKCPAALPCGGL-RCIG-----GVNNKVC 32  
Db 3407 IHVCLPSQFKCTWNRICGIFRCNGQDNCDEDEKDC 3445

RESULT 11  
T10081  
sperm mitochondrial capsule selenoprotein - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 16-Jul-1999 #sequence\_revision 04-Mar-2000 #text\_change 09-Jul-2004  
C;Accession: T10081; A37199  
R;Kleene, K.C.; Smith, J.; Bozorgzadeh, A.; Harris, M.; Hahn, L.; Karimpour, I.; Gerstel  
Dev. Biol. 137, 395-402, 1990  
A;Title: Sequence and developmental expression of the mRNA encoding the seleno-protein c  
A;Reference number: A37199; MUID:90152148; PMID:2303168  
A;Accession: T10081  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-6,'X',8-16,'X',18-33,'X',35-197 <KLE1>  
A;Cross-references: UNIPROT:P15265; EMBL:M29603; NID:g199088; PIDN:AAA53045.1; PID:g5672  
A;Experimental source: strain CD-1  
A;Note: in Genbank entry MUSMCS, release 113.0, PIDN:AAA53045.1, the selenocysteine UGA  
A;Accession: A37199  
A;Molecule type: mRNA  
A;Residues: 55-197 <KLE2>  
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A;Note: the authors translated the codon TGT for residue 112 as Pro  
C;Genetics:  
A;Genome: nuclear  
C;Keywords: mitochondrion; selenocysteine; sperm  
F;7,17,34/Modified site: selenocysteine #status predicted

Query Match 30.3%; Score 56; DB 2; Length 197;  
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Matches 9; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 CTGAGVKCPAALPCGGLRC 23  
Db 87 CCPKSPCCPPKSPCCPKPC 106

us-10-019-823b-1.dx.rpr

## RESULT 12

S43572  
C05B5.5 protein (clone C05B5) - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 07-Sep-1994 #sequence\_revision 10-Nov-1995 #text\_change 10-Nov-1995  
C;Accession: S43572  
R;Northmore, B.  
submitted to the EMBL Data Library, April 1994  
A;Reference number: S43570  
A;Accession: S43572  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-585 <MOR>  
A;Cross-references: EMBL:Z32679  
C;Genetics:  
A;Introns: 35/2; 218/3; 292/2; 328/1; 442/2

Query Match 30.3%; Score 56; DB 2; Length 585;  
Best Local Similarity 33.3%; Pred. No. 33;  
Matches 12; Conservative 1; Mismatches 9; Indels 14; Gaps 1;

QY 6 PAGVKC-----PAALPCCGGLRCIGGV 27  
Db 541 PTGYQCIDGKCKTKRHFAPPCVACPPGTRCINGV 576

## RESULT 13

E88571  
protein C05B5.5 [imported] - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C;Accession: E88571  
R;anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
A;Reference number: A75000; MUID:99069613; PMID:9851916  
A;Note: see websites genome.wustl.edu/gsc/c\_elegans/ and www.sanger.ac.uk/projects/c\_eleg  
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A;Accession: E88571  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-585 <STO>  
A;Cross-references: UNIPROT:P34293; GB:chr\_III; PIDN:CAA83593.1; PID:g3873993; GSPDB:GN0  
C;Genetics:  
A;Gene: C05B5.5  
A;Map position: 3

Query Match 30.3%; Score 56; DB 2; Length 585;  
Best Local Similarity 33.3%; Pred. No. 33;  
Matches 12; Conservative 1; Mismatches 9; Indels 14; Gaps 1;

QY 6 PAGVKC-----PAALPCCGGLRCIGGV 27  
Db 541 PTGYQCIDGKCKTKRHFAPPCVACPPGTRCINGV 576

## RESULT 14

T30201  
Notch homolog protein - sea squirt (Halocynthia roretzi)  
C;Species: Halocynthia roretzi  
C;Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 08-Sep-2002  
C;Accession: T30201  
R;Hori, S.; Saichoh, T.; Matsumoto, M.; Makabe, K.W.; Nishida, H.  
Dev. Genes Evol. 207, 371-380, 1997  
A;Title: Notch homologue from Halocynthia roretzi is preferentially expressed in the cent  
A;Reference number: Z20775  
A;Accession: T30201  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-2352 <HOR>  
A;Cross-references: EMBL:AB001327; NID:d1204472; PID:d1026501; PIDN:BAA25571.1  
C;Genetics:

Search completed: February 14, 2005, 21:05:43  
Job time : 40 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 21:01:05 ; Search time 129 Seconds  
(without alignments)  
83.587 Million cell updates/sec

Title: US-10-019-823B-1

Perfect score: 185  
Sequence: 1 XXICTPAGVKCPAALPCCPLRCIGGVNKNKVR 33

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
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20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	44.9	36	9	US-09-894-882-3
2	80	43.2	36	9	US-09-894-882-4
3	73.5	39.7	37	9	US-09-894-882-5
4	73	39.5	35	14	US-10-072-602B-571
5	73	39.5	82	14	US-10-072-602B-140
6	69.5	37.6	30	14	US-10-072-602B-570
7	69.5	37.6	77	14	US-10-072-602B-137
8	69	37.3	31	9	US-09-894-882-461
9	69	37.3	39	9	US-09-894-882-497
10	69	37.3	67	9	US-09-894-882-247
11	67	36.2	32	9	US-09-894-882-470
12	67	36.2	32	14	US-10-072-602B-581
13	67	36.2	40	9	US-09-894-882-498

14	67	36.2	68	9	US-09-894-882-274	Sequence 274, App
15	67	36.2	79	14	US-10-072-602B-255	Sequence 255, App
16	66	35.7	566	10	US-09-900-449A-6	Sequence 6, Appli
17	66	35.7	572	10	US-09-900-449A-7	Sequence 7, Appli
18	66	35.7	601	10	US-09-900-449A-5	Sequence 5, Appli
19	66	35.7	639	10	US-09-900-449A-4	Sequence 4, Appli
20	66	35.7	1064	14	US-10-173-461-5	Sequence 5, Appli
21	65	35.1	77	14	US-10-072-602B-191	Sequence 191, App
22	65	35.1	3501	14	US-10-123-155-37	Sequence 37, Appl
23	65	35.1	3501	14	US-10-146-731-37	Sequence 37, Appl
24	65	35.1	3501	14	US-10-140-472-37	Sequence 37, Appl
25	65	35.1	3501	14	US-10-141-761-37	Sequence 37, Appl
26	65	35.1	3501	14	US-10-142-885-37	Sequence 37, Appl
27	65	35.1	3501	14	US-10-158-790-37	Sequence 37, Appl
28	65	35.1	3501	15	US-10-137-871-37	Sequence 37, Appl
29	65	35.1	3501	15	US-10-140-923-37	Sequence 37, Appl
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31	65	35.1	3501	15	US-10-141-759-37	Sequence 37, Appl
32	65	35.1	3501	15	US-10-140-805-37	Sequence 37, Appl
33	65	35.1	3501	15	US-10-140-864-37	Sequence 37, Appl
34	65	35.1	3501	15	US-10-142-426-37	Sequence 37, Appl
35	64.5	34.9	86	15	US-10-424-599-240605	Sequence 240605,
36	64	34.6	30	14	US-10-072-602B-576	Sequence 576, App
37	64	34.6	1971	14	US-10-123-155-139	Sequence 139, App
38	64	34.6	1971	14	US-10-146-731-139	Sequence 139, App
39	64	34.6	1971	14	US-10-140-472-139	Sequence 139, App
40	64	34.6	1971	14	US-10-141-761-139	Sequence 139, App
41	64	34.6	1971	14	US-10-142-885-139	Sequence 139, App
42	64	34.6	1971	14	US-10-158-790-139	Sequence 139, App
43	64	34.6	1971	15	US-10-137-871-139	Sequence 139, App
44	64	34.6	1971	15	US-10-140-923-139	Sequence 139, App
45	64	34.6	1971	15	US-10-141-756-139	Sequence 139, App

ALIGNMENTS

RESULT 1  
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; Sequence 3, Application US/09894882  
; Patent No. US20020102607A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jimenez, Elsie C.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: Watkins, Maren  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Shen, Greg S.  
; TITLE OF INVENTION: I-Superfamily Conotoxins  
; FILE REFERENCE: 2314-238  
; CURRENT APPLICATION NUMBER: US/09/894,882  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/243,410  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/246,581  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: US 60/247,714  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/264,256  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Hadronyche versuta  
US-09-894-882-3

REF ID: A61111



Qy 4 CTPAGVKCPAALPCCPGLRCIGGVNKKVC 32

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 461
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-461

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Best Local Similarity 44.8%; Pred. No. 0.59;
Matches 13; Conservative 2; Mismatches 12; Indels 12; Gaps 1;

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RESULT 9
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; Sequence 497, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

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Best Local Similarity 44.8%; Pred. No. 0.72;
Matches 13; Conservative 2; Mismatches 12; Indels 12; Gaps 1;

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Db      1 CFPFGIYCTPYLPCCWGICC--GTCRNVC 27

RESULT 10
US-09-894-882-427
; Sequence 247, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
```

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; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-247

Query Match      37.3%; Score 69; DB 9; Length 67;
Best Local Similarity 44.8%; Pred. No. 1.2;
Matches 13; Conservative 2; Mismatches 12; Indels 12; Gaps 1;

Qy      4 CTPAGVKCPAALPCPCGRLRCIGGVNNKVC 32
Db      29 CFPFGIYCTPYLPCCWGICC--GTCRNVC 55

RESULT 11
US-09-894-882-470
; Sequence 470, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 470
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-470

Query Match      36.2%; Score 67; DB 9; Length 32;
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Best Local Similarity 50.0%; Pred. No. 1;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 4 CTPAGVKCPAALPCCPGRLRCIG 25
Db 1 CPPLGTFCRSRYLPCCSGMCCSG 22

RESULT 12
US-10-072-602B-581
; Sequence 581, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 581
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Conus virgo
US-10-072-602B-581

Query Match 36.2%; Score 67; DB 14; Length 32;
Best Local Similarity 48.4%; Pred. No. 1;
Matches 15; Conservative 1; Mismatches 13; Indels 2; Gaps 2;

QY 4 CTPAGVKCPAALPCCPGRLRCI-GGVNKNKVC 33
Db 2 CGSQGEGC-YTQPCPGRLCRGGGTGGGVCQ 31

RESULT 13
US-09-894-882-498
; Sequence 498, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 274
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-498

Query Match 36.2%; Score 67; DB 9; Length 68;
Best Local Similarity 50.0%; Pred. No. 2;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 4 CTPAGVKCPAALPCCPGRLRCIG 25
Db 29 CPPLGTFCRSRYLPCCSGMCCSG 50

RESULT 15
US-10-072-602B-255
; Sequence 255, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
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; APPLICANT: Cognetix, Inc.  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J, Michael  
; APPLICANT: Watkins, Maren  
; APPLICANT: Garrett, James E.  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Grille, Michelle  
; APPLICANT: Schoenfeld, Robert M.  
; APPLICANT: Walker, Craig  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jones, Robert M.  
; TITLE OF INVENTION: Cone Snail Peptides  
; FILE REFERENCE: 2314-249  
; CURRENT APPLICATION NUMBER: US/10/072,602B  
; CURRENT FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: US 60/267,408  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 255  
; LENGTH: 79  
; TYPE: PRT  
; ORGANISM: Conus virgo  
US-10-072-602B-255

Query Match 36.2%; Score 67; DB 14; Length 79;  
Best Local Similarity 48.4%; Pred. No. 2.3;  
Matches 15; Conservative 1; Mismatches 13; Indels 2; Gaps 2;

QY 4 CTPAGVKCPAALPCCPGI-IGVNNKVC 33  
Db 49 CGGQEGC-YTPCCPGI-IGVNNKVC 78

Search completed: February 14, 2005, 21:08:47  
Job time : 129 secs

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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:59:16 ; Search time 43 Seconds  
(without alignments)  
57.289 Million cell updates/sec

Title: US-10-019-823B-1  
Perfect score: 185  
Sequence: 1 XICTPAGVKCPAALPCCPGLRCIGGVNKKVCR 33

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/PCUTUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	44.9	36	4	US-09-894-882-3
2	80	43.2	36	4	US-09-894-882-4
3	76	41.1	36	1	US-08-682-485A-7
4	76	41.1	36	2	US-08-933-314-7
5	76	41.1	37	1	US-08-682-485A-6
6	76	41.1	37	2	US-08-933-314-6
7	73.5	39.7	37	4	US-09-894-882-5
8	69	37.3	31	4	US-09-894-882-461
9	69	37.3	39	4	US-09-894-882-497
10	69	37.3	67	4	US-09-894-882-247
11	67	36.2	32	4	US-09-894-882-470
12	67	36.2	40	4	US-09-894-882-498
13	67	36.2	68	4	US-09-894-882-274
14	61	33.0	211	4	US-09-902-540-15694
15	61	33.0	2471	1	US-08-485-432-16
16	61	33.0	2471	1	US-08-083-590A-19
17	61	33.0	2471	3	US-08-532-384-19
18	61	33.0	2471	4	US-08-899-232-1
19	61	33.0	2471	4	US-09-121-457-1
20	59	31.9	155	4	US-09-452-991A-28474
21	59	31.9	259	3	US-09-161-241-11
22	58.5	31.6	34	1	US-08-117-080-5
23	58.5	31.6	34	1	US-08-471-329-5
24	58.5	31.6	34	2	US-08-915-142-5
25	58.5	31.6	180	4	US-09-510-238A-286
26	58.5	31.6	908	4	US-08-714-741-44
27	57.5	31.1	70	4	US-09-894-882-295

28	57.5	31.1	281	4	US-09-252-991A-23962
29	57	30.8	493	4	US-09-252-991A-16925
30	57	30.8	2732	4	US-09-086-436-30
31	56.5	30.5	30	4	US-09-894-882-474
32	56.5	30.5	44	4	US-09-894-882-502
33	56.5	30.5	291	4	US-09-902-540-15052
34	56	30.3	642	3	US-08-872-855-10
35	55.5	30.0	69	4	US-09-894-882-298
36	55.5	30.0	70	4	US-09-894-882-277
37	55.5	30.0	70	4	US-09-894-882-280
38	55.5	30.0	70	4	US-09-894-882-283
39	55.5	30.0	2211	3	US-09-738-884-1
40	55.5	30.0	2211	4	US-10-096-961A-1
41	55	29.7	717	4	US-09-644-460-37
42	55	29.7	2321	4	US-09-230-652-2
43	54.5	29.5	30	4	US-09-894-882-471
44	54.5	29.5	30	4	US-09-894-882-475
45	54.5	29.5	44	4	US-09-894-882-499

## ALIGNMENTS

RESULT 1  
US-09-894-882-3  
; Sequence 3, Application US/09894882  
; Patent No. 6767895  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jimenez, Elsie C.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: Watkins, Maren  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Shen, Greg S.  
; TITLE OF INVENTION: I-Superfamily Conotoxins  
; FILE REFERENCE: 2314-238  
; CURRENT APPLICATION NUMBER: US/09/894,882  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/243,410  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/246,581  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: US 60/247,714  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/264,256  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Hadronyche versuta  
US-09-894-882-3

Query Match 44.9%; Score 83; DB 4; Length 36;  
Best Local Similarity 50.0%; Pred. No. 0.0041;  
Matches 17; Conservative 2; Mismatches 13; Indels 2; Gaps 1;

Qy 2 XICTPAGVKCPAALPCCPGLRCIGGVNKKV--CR 33  
Db 1 TICTGADRPCAACCCPGTSCGPESNGVYCR 34

RESULT 2  
US-09-894-882-4  
; Sequence 4, Application US/09894882  
; Patent No. 6767895

; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; APPLICANT: Cognetix, Inc.  
 ; APPLICANT: Walker, Craig S.  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Jimenez, Elsie C.  
 ; APPLICANT: McIntosh, J. Michael  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: Watkins, Maren  
 ; APPLICANT: Jones, Robert M.  
 ; APPLICANT: Shen, Greg S.  
 ; TITLE OF INVENTION: I-Superfamily Conotoxins  
 ; FILE REFERENCE: 2314-238  
 ; CURRENT APPLICATION NUMBER: US/09/894,882  
 ; CURRENT FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: US 60/  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: US 60/243,410  
 ; PRIOR FILING DATE: 2000-10-27  
 ; PRIOR APPLICATION NUMBER: US 60/246,581  
 ; PRIOR FILING DATE: 2000-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/247,714  
 ; PRIOR FILING DATE: 2000-11-14  
 ; PRIOR APPLICATION NUMBER: US 60/264,256  
 ; PRIOR FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS: 506  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 36  
 ; TYPE: PPT  
 ; ORGANISM: Hadronyche versuta  
 ; US-09-894-882-4

Query Match 43.2%; Score 80; DB 4; Length 36;  
 Best Local Similarity 50.0%; Pred. No. 0.009;  
 Matches 17; Conservative 1; Mismatches 14; Indels 2; Gaps 1;

Qy 2 XICTPAGVKCPAALPCCGLCIGGVNNKV--CR 33  
 :||| | | | | | | | | | | | | | | | | | | | |  
 Db 1 TICTGADRPCAACCCPCGTCGQPEPNGVSYCR 34

RESULT 3  
 US-08-682-485A-7  
 ; Sequence 7, Application US/08682485A  
 ; Patent No. 5763568  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ATKINSON, RONALD K  
 ; APPLICANT: HOWDEN, MERLIN E.H.  
 ; APPLICANT: TYLER, MARGARET I  
 ; APPLICANT: VONARX, EDWARD J  
 ; TITLE OF INVENTION: Insecticidal Toxins Derived From  
 ; TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)  
 ; NUMBER OF SEQUENCES: 26  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Zeneca, Inc.  
 ; STREET: 1200 South 47th Street  
 ; CITY: Richmond  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/682,485A  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/682,485  
 ; FILING DATE: 17-JULY-1996

; APPLICATION NUMBER: US/08/256,933  
 ; FILING DATE: 27-JULY-1994  
 ; APPLICATION NUMBER: WO 93/15108  
 ; FILING DATE: 29-JAN-1993  
 ; APPLICATION NUMBER: AU PL0722  
 ; FILING DATE: 31-JAN-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Shaw, Melissa A.  
 ; REGISTRATION NUMBER: 38,301  
 ; REFERENCE/DOCKET NUMBER: PPD 5099/D1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 510-231-1542  
 ; TELEFAX: 510-231-1112  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 36 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Atrax formidabilis  
 ; US-08-682-485A-7

Query Match 41.1%; Score 76; DB 1; Length 36;  
 Best Local Similarity 45.7%; Pred. No. 0.026;  
 Matches 16; Conservative 2; Mismatches 15; Indels 2; Gaps 1;

Qy 1 XXICTPAGVKCPAALPCCGLCIGGVNNKV--CR 33  
 :||| | | | | | | | | | | | | | | | | | | | |  
 Db 1 SPTCTGADRPCAACCCPCGTCGQPEPNGVSYCR 35

RESULT 4  
 US-08-933-314-7  
 ; Sequence 7, Application US/08933314  
 ; Patent No. 5959182  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ATKINSON, RONALD K  
 ; APPLICANT: HOWDEN, MERLIN E.H.  
 ; APPLICANT: TYLER, MARGARET I  
 ; APPLICANT: VONARX, EDWARD J  
 ; TITLE OF INVENTION: Insecticidal Toxins Derived From  
 ; TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)  
 ; NUMBER OF SEQUENCES: 26  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Zeneca, Inc.  
 ; STREET: 1200 South 47th Street  
 ; CITY: Richmond  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/933,314  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/682,485  
 ; FILING DATE: 17-JULY-1996  
 ; APPLICATION NUMBER: US/08/256,933  
 ; FILING DATE: 27-JULY-1994  
 ; APPLICATION NUMBER: WO 93/15108  
 ; FILING DATE: 29-JAN-1993  
 ; APPLICATION NUMBER: AU PL0722  
 ; FILING DATE: 31-JAN-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Shaw, Melissa A.

REGISTRATION NUMBER: 38,301  
REFERENCE/DOCKET NUMBER: PPD 5099/D1  
TELEPHONE: 510-231-1542  
TELEFAX: 510-231-1112  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Atrax formidabilis

US-08-933-314-7  
Query Match 41.1%; Score 76; DB 2; Length 36;  
Best Local Similarity 45.7%; Pred. No. 0.026;  
Matches 16; Conservative 2; Mismatches 15; Indels 2; Gaps 1;  
QY 1 XXICTPAGVKCPAALPCCPGLRCIGGVNNKV--CR 33  
DB 1 SPTCTGADRPACACCCPCGTCCKGPEPNGVSYCR 35

RESULT 5  
US-08-682-485A-6  
Sequence 6, Application US/08682485A  
Patent No. 5763568  
GENERAL INFORMATION:  
APPLICANT: ATKINSON, RONALD K  
APPLICANT: HOWDEN, MERLIN E.H.  
APPLICANT: TYLER, MARGARET J  
APPLICANT: VONARX, EDWARD J  
TITLE OF INVENTION: Insecticidal Toxins Derived From  
Funnel Web (Atrax or Hadronyche Spiders)  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zeneca, Inc.  
STREET: 1200 South 47th Street  
CITY: Richmond  
STATE: California  
COUNTRY: USA  
ZIP: 94804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/682,485A  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/682,485  
FILING DATE: 17-JULY-1996  
APPLICATION NUMBER: US/08/256,933  
FILING DATE: 27-JULY-1994  
APPLICATION NUMBER: WO 93/15108  
FILING DATE: 29-JAN-1993  
APPLICATION NUMBER: AU PL0722  
FILING DATE: 31-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Shaw, Melissa A.  
REGISTRATION NUMBER: 38,301  
REFERENCE/DOCKET NUMBER: PPD 5099/D1  
TELEPHONE: 510-231-1542  
TELEFAX: 510-231-1112  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Atrax formidabilis  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 37  
OTHER INFORMATION: /label= a  
OTHER INFORMATION: /note= "this site may be amidated without loss  
of biological activity"  
US-08-682-485A-6

Query Match 41.1%; Score 76; DB 1; Length 37;  
Best Local Similarity 45.7%; Pred. No. 0.027;  
Matches 16; Conservative 2; Mismatches 15; Indels 2; Gaps 1;  
QY 1 XXICTPAGVKCPAALPCCPGLRCIGGVNNKV--CR 33  
DB 1 SPTCTGADRPACACCCPCGTCCKGPEPNGVSYCR 35

RESULT 6  
US-08-933-314-6  
Sequence 6, Application US/08933314  
Patent No. 5959182  
GENERAL INFORMATION:  
APPLICANT: ATKINSON, RONALD K  
APPLICANT: HOWDEN, MERLIN E.H.  
APPLICANT: TYLER, MARGARET J  
APPLICANT: VONARX, EDWARD J  
TITLE OF INVENTION: Insecticidal Toxins Derived From  
Funnel Web (Atrax or Hadronyche Spiders)  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zeneca, Inc.  
STREET: 1200 South 47th Street  
CITY: Richmond  
STATE: California  
COUNTRY: USA  
ZIP: 94804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,314  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/682,485  
FILING DATE: 17-JULY-1996  
APPLICATION NUMBER: US/08/256,933  
FILING DATE: 27-JULY-1994  
APPLICATION NUMBER: WO 93/15108  
FILING DATE: 29-JAN-1993  
APPLICATION NUMBER: AU PL0722  
FILING DATE: 31-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Shaw, Melissa A.  
REGISTRATION NUMBER: 38,301  
REFERENCE/DOCKET NUMBER: PPD 5099/D1  
TELEPHONE: 510-231-1542  
TELEFAX: 510-231-1112  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

; MOLECULE TYPE: protein  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Atrax formidabilis  
 ; FEATURE:  
 ; NAME/KEY: Modified-site  
 ; LOCATION: 37  
 ; OTHER INFORMATION: /label= a  
 ; OTHER INFORMATION: /notes "this site may be amidated without loss  
 ; OTHER INFORMATION: of biological activity"  
 US-08-933-314-6

Query Match 41.1%; Score 76; DB 2; Length 37;  
 Best Local Similarity 45.7%; Pred. No. 0.027;  
 Matches 16; Conservative 2; Mismatches 15; Indels 2; Gaps 1;

QY 1 XXICTPAGVKCPAALPCCPGLCIGGVNNKV--CR 33  
 DB 1 SPTCTGADRPCAACCPCCPGTSCKGPEPNGVSYCR 35

## RESULT 7

US-09-894-882-5  
 ; Sequence 5, Application US/09894882  
 ; Patent No. 6767895  
 ; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation  
 ; APPLICANT: Cognetix, Inc.  
 ; APPLICANT: Walker, Craig S.  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Jimenez, Elsie C.  
 ; APPLICANT: McIntosh, J. Michael  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: Watkins, Maren  
 ; APPLICANT: Jones, Robert M.  
 ; APPLICANT: Shen, Greg S.

; TITLE OF INVENTION: I-Superfamily Conotoxins  
 ; FILE REFERENCE: 2314-238  
 ; CURRENT APPLICATION NUMBER: US/09/894,882  
 ; CURRENT FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: US 60/  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: US 60/243,410  
 ; PRIOR FILING DATE: 2000-10-27  
 ; PRIOR APPLICATION NUMBER: US 60/246,581  
 ; PRIOR FILING DATE: 2000-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/247,714  
 ; PRIOR FILING DATE: 2000-11-14  
 ; PRIOR APPLICATION NUMBER: US 60/264,256  
 ; PRIOR FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS: 506  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 5  
 ; LENGTH: 37  
 ; TYPE: PRT  
 ; ORGANISM: Hadronyche versuta  
 US-09-894-882-5

Query Match 39.7%; Score 73.5; DB 4; Length 37;  
 Best Local Similarity 45.5%; Pred. No. 0.052;  
 Matches 15; Conservative 1; Mismatches 16; Indels 1; Gaps 1;

QY 2 XICTPAGVKCPAALPCCPGLCIGGVNN-KVCR 33  
 DB 1 AICTGADRPCAACCPCCPGTSCKAESNGVSYCR 33

## RESULT 8

US-09-894-882-461  
 ; Sequence 461, Application US/09894882  
 ; Patent No. 6767895  
 ; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation  
 ; APPLICANT: Cognetix, Inc.  
 ; APPLICANT: Walker, Craig S.  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Jimenez, Elsie C.  
 ; APPLICANT: McIntosh, J. Michael  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: Watkins, Maren  
 ; APPLICANT: Jones, Robert M.  
 ; APPLICANT: Shen, Greg S.  
 ; TITLE OF INVENTION: I-Superfamily Conotoxins  
 ; FILE REFERENCE: 2314-238  
 ; CURRENT APPLICATION NUMBER: US/09/894,882  
 ; CURRENT FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: US 60/  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: US 60/243,410  
 ; PRIOR FILING DATE: 2000-10-27  
 ; PRIOR APPLICATION NUMBER: US 60/246,581  
 ; PRIOR FILING DATE: 2000-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/247,714  
 ; PRIOR FILING DATE: 2000-11-14  
 ; PRIOR APPLICATION NUMBER: US 60/264,256  
 ; PRIOR FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS: 506  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 461  
 ; LENGTH: 31  
 ; TYPE: PRT  
 ; ORGANISM: Conus emaciatus  
 US-09-894-882-461

Query Match 37.3%; Score 69; DB 4; Length 31;  
 Best Local Similarity 44.8%; Pred. No. 0.14;  
 Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGLCIGGVNNKVC 32  
 DB 1 CFPFGIVCTPLPCCWGICC-GTCRNV 27

## RESULT 9

US-09-894-882-497  
 ; Sequence 497, Application US/09894882  
 ; Patent No. 6767895  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; APPLICANT: Cognetix, Inc.  
 ; APPLICANT: Walker, Craig S.  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Jimenez, Elsie C.  
 ; APPLICANT: McIntosh, J. Michael  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: Watkins, Maren  
 ; APPLICANT: Jones, Robert M.  
 ; APPLICANT: Shen, Greg S.  
 ; TITLE OF INVENTION: I-Superfamily Conotoxins  
 ; FILE REFERENCE: 2314-238  
 ; CURRENT APPLICATION NUMBER: US/09/894,882  
 ; CURRENT FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: US 60/  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: US 60/243,410  
 ; PRIOR FILING DATE: 2000-10-27  
 ; PRIOR APPLICATION NUMBER: US 60/246,581  
 ; PRIOR FILING DATE: 2000-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/247,714  
 ; PRIOR FILING DATE: 2000-11-14  
 ; PRIOR APPLICATION NUMBER: US 60/264,256  
 ; PRIOR FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS: 506  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 497



```
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

Query Match      37.3%; Score 69; DB 4; Length 39;
Best Local Similarity 44.8%; Pred. No. 0.18;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY      4 CTPAGVKCPAALPCCGRLRCIGVNNKVC 32
      |||||:|||||:|||||:
Db      1 CRPPGIYCTPYLPCCWGICC--GTCRNVC 27

RESULT 10
US-09-894-882-247
; Sequence 247, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-247

Query Match      37.3%; Score 69; DB 4; Length 67;
Best Local Similarity 44.8%; Pred. No. 0.29;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY      4 CTPAGVKCPAALPCCGRLRCIGVNNKVC 32
      |||||:|||||:|||||:
Db      29 CRPPGIYCTPYLPCCWGICC--GTCRNVC 55

RESULT 11
US-09-894-882-470
; Sequence 470, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-247

Query Match      37.3%; Score 69; DB 4; Length 67;
Best Local Similarity 44.8%; Pred. No. 0.29;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY      4 CTPAGVKCPAALPCCGRLRCIGVNNKVC 32
      |||||:|||||:|||||:
Db      29 CRPPGIYCTPYLPCCWGICC--GTCRNVC 55

RESULT 12
US-09-894-882-498
; Sequence 498, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 498
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-498

Query Match      36.2%; Score 67; DB 4; Length 40;
Best Local Similarity 50.0%; Pred. No. 0.31;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
```



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2005, 20:40:40 ; Search time 69 Seconds  
(without alignments)  
184.972 Million cell updates/sec

Title: US-10-019-823B-1

Perfect score: 185

Sequence: 1 XXICTPAGVKCPAALPCCPLRCIGGVNNKVR 33

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

*Search of Seq1 was run  
using "BLOSUM62DX" matrix -  
this allows an X in the  
query sequence to match  
any amino acid in the  
database sequence.*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	185	100.0	33	4	AAB66899 Insectici
2	185	100.0	33	4	AAB66900 Insectici
3	185	100.0	33	6	AAB66283 Paecilomy
4	185	100.0	34	6	AAB66261 Insectici
5	185	100.0	34	6	AAB66295 Insectici
6	185	100.0	34	6	AAB66260 Insectici
7	185	100.0	34	6	AAB66294 Insectici
8	185	100.0	34	6	AAB66259 Insectici
9	185	100.0	34	6	AAB66290 Insectici
10	185	100.0	34	6	AAB66292 Insectici
11	185	100.0	34	6	AAB66287 Insectici
12	185	100.0	34	6	AAB66289 Insectici
13	185	100.0	34	6	AAB66263 Insectici
14	185	100.0	34	6	AAB66284 Insectici
15	185	100.0	34	6	AAB66288 Insectici
16	185	100.0	34	6	AAB66296 Insectici
17	185	100.0	34	6	AAB66286 Insectici
18	185	100.0	34	6	AAB66291 Insectici
19	185	100.0	34	6	AAB66264 Insectici
20	185	100.0	34	6	AAB66285 Insectici
21	185	100.0	34	6	AAB66262 Insectici
22	185	100.0	34	6	AAB66297 Insectici
23	185	100.0	34	6	AAB66298 Insectici
24	185	100.0	34	6	AAB66293 Insectici
25	185	100.0	35	4	AAB66901 Insectici

ALIGNMENTS

RESULT 1

AAB66899

ID AAB66899 standard; peptide; 33 AA.

AC AAB66899;

XX 12-APR-2001 (first entry)

DT Insecticidal protein #1.

XX Insecticide; transgenic plant; insect-resistance.

DE Paecilomyces sp.

XX WO200100841-A1.

PN 04-JAN-2001.

PD 23-JUN-2000; 2000WO-GB002457.

XX 29-JUN-1999; 99GB-00015215.

PR 23-DEC-1999; 99GB-00030536.

XX (ZENE ) ZENECA LTD.

PA Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;

XX Vincent JL, Lee MD;

XX WPI; 2001-123015/13.

PT Novel insecticidal protein obtained from species of Paecilomyces for

PT controlling insects, and for insect-resistant transgenic plant

XX production.

XX Claim 1; Page 30; 72pp; English.

PS The present invention relates to novel insecticidal proteins obtained

CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The

CC insecticidal proteins can be used to produce transgenic plants, which are

CC insect-resistant. Also, the insecticidal proteins are useful for

CC controlling insects by providing them at a locus where insects feed

XX Sequence 33 AA;

XX Query Match 100.0%; Score 185; DB 4; Length 33;

XX Best Local Similarity 100.0%; Pred. No. 9.2e-14; Indels 0; Gaps 0;

XX Matches 33; Conservative 0; Mismatches 0;

XX

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XX

QY	1	XXICTPAGVKCPAALPCCPGLRCIGGVNNKVC	33
DB	1	XXICTPAGVKCPAALPCCPGLRCIGGVNNKVC	33
RESULT 2			
ID	AAB66900 standard; peptide; 33 AA.		
XX	AC		
XX	AAB66900;		
DT	12-APR-2001 (first entry)		
XX	Insecticidal protein #2.		
DE	Insecticide; transgenic plant; insect-resistance.		
XX	Paecilomyces sp.		
OS	WO200100841-A1.		
XX	04-JAN-2001.		
XX	23-JUN-2000; 2000WO-GB002457.		
PF	29-JUN-1999; 99GB-00015215.		
PR	23-DEC-1999; 99GB-00030536.		
XX	(ZENE ) ZENECA LTD.		
PA	Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;		
PI	Vincent JL, Lee MD;		
XX	WPI; 2001-123015/13.		
XX	Novel insecticidal protein obtained from species of Paecilomyces for		
PT	controlling insects, and for insect-resistant transgenic plant		
PT	production.		
XX	Claim 3; Page 30; 72pp; English.		
XX	The present invention relates to novel insecticidal proteins obtained		
CC	from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The		
CC	insecticidal proteins can be used to produce transgenic plants, which are		
CC	insect-resistant. Also, the insecticidal proteins are useful for		
CC	controlling insects by providing them at a locus where insects feed		
XX	Sequence 33 AA;		
SQ	Query Match 100.0%; Score 185; DB 4; Length 33;		
	Best Local Similarity 93.9%; Pred. No. 9.2e-14;		
	Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	XXICTPAGVKCPAALPCCPGLRCIGGVNNKVC	33
DB	1	XXICTPAGVKCPAALPCCPGLRCIGGVNNKVC	33
RESULT 3			
AAE36283	standard; peptide; 33 AA.		
ID	AAE36283		
XX	AC		
XX	AAE36283;		
DT	26-JUN-2003 (first entry)		
XX	Paecilomyces farinosus insecticidal protein.		
DE	Insecticidal protein; pesticide.		
XX	Paecilomyces farinosus.		
OS	WO200298911-A2.		
XX	PN		
RESULT 4			
AAE36261	standard; peptide; 34 AA.		
ID	AAE36261		
XX	AC		
XX	AAE36261;		
DT	26-JUN-2003 (first entry)		
XX	Insecticidal protein #3.		
DE	Insecticidal protein; pesticide.		
XX	Unidentified.		
OS	WO200298911-A2.		
XX	PN		
XX	12-DEC-2002.		
XX	30-MAY-2002; 2002WO-GB002666.		
XX	07-JUN-2001; 2001GB-00013900.		
XX	(SYGN ) SYNGENTA LTD.		
PA	Vincent JL, Viner R;		
XX	WPI; 2003-175137/17.		
XX	New insecticidal protein comprising an X-glycine motif at the amino-		
PT	terminus, useful as an active ingredient of a pesticide.		
PT	Claim 6; Page 23; 67pp; English.		
XX	The invention relates to insecticidal protein comprising an X-glycine		
CC	motif at the amino-terminus. Polynucleotide or DNA constructs of the		

RESULT 6  
AAE36260

```

PA (SYGN ) SYNGENTA LTD.
PI Vincent JL, Viner R;
XX WPI; 2003-175137/17.
XX New insecticidal protein comprising an X-glycine motif at the amino-
PT terminus, useful as an active ingredient of a pesticide.
XX Example 1; Page 66; 67pp; English.
XX The invention relates to insecticidal protein comprising an X-glycine
CC motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC invention are useful for producing plants or plant parts that are
CC resistant to insects. The protein or synergistic combination is useful as
CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify
CC other proteins with insecticidal activity. The present sequence is
CC insecticidal protein
XX Sequence 34 AA;
SQ
Query Match 100.0%; Score 185; DB 6; Length 34;
Best Local Similarity 93.9%; Pred. No. 9.4e-14;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 XXICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33
DB 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 34
:::|||||
RESULT 8
AAE36259
ID AAE36259 standard; peptide; 34 AA.
XX AC
XX 26-JUN-2003 (first entry)
XX Insecticidal protein #1.
XX Insecticidal protein; pesticide.
XX Unidentified.
XX Key Location/Qualifiers
FH Misc-difference 1 /note= "Xaa = any amino acid"
FT
XX WO200298911-A2.
XX 12-DEC-2002.
XX 30-MAY-2002; 2002WO-GB002666.
XX 07-JUN-2001; 2001GB-00013900.
XX (SYGN ) SYNGENTA LTD.
XX Vincent JL, Viner R;
XX WPI; 2003-175137/17.
XX New insecticidal protein comprising an X-glycine motif at the amino-
PT terminus, useful as an active ingredient of a pesticide.
XX Claim 1; Page 23; 67pp; English.
XX The invention relates to insecticidal protein comprising an X-glycine
CC motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC invention are useful for producing plants or plant parts that are
CC resistant to insects. The protein or synergistic combination is useful as
CC an active ingredient of a pesticide or for controlling insects.
CC

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CC Antibodies raised to the insecticidal proteins can be used to identify
CC other proteins with insecticidal activity. The present sequence is
CC insecticidal protein
XX Sequence 34 AA;
SQ
Query Match 100.0%; Score 185; DB 6; Length 34;
Best Local Similarity 93.9%; Pred. No. 9.4e-14;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 XXICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33
DB 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 34
:::|||||
RESULT 9
AAE36290
ID AAE36290 standard; peptide; 34 AA.
XX AC
XX 26-JUN-2003 (first entry)
XX Insecticidal protein #20.
XX Insecticidal protein; pesticide.
XX Unidentified.
XX OS
XX WO200298911-A2.
XX PN
XX 12-DEC-2002.
XX PD
XX 30-MAY-2002; 2002WO-GB002666.
XX PF
XX 07-JUN-2001; 2001GB-00013900.
XX PR
XX (SYGN ) SYNGENTA LTD.
XX Vincent JL, Viner R;
XX WPI; 2003-175137/17.
XX New insecticidal protein comprising an X-glycine motif at the amino-
PT terminus, useful as an active ingredient of a pesticide.
XX Example 1; Page 64; 67pp; English.
XX The invention relates to insecticidal protein comprising an X-glycine
CC motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC invention are useful for producing plants or plant parts that are
CC resistant to insects. The protein or synergistic combination is useful as
CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify
CC other proteins with insecticidal activity. The present sequence is
CC insecticidal protein
XX Sequence 34 AA;
SQ
Query Match 100.0%; Score 185; DB 6; Length 34;
Best Local Similarity 93.9%; Pred. No. 9.4e-14;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 XXICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33
DB 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 34
:::|||||
RESULT 10
AAE36292
ID AAE36292 standard; peptide; 34 AA.
XX AC
XX AAE36292;

```

XX	26-JUN-2003 (first entry)
DT	Insecticidal protein #22.
DE	Insecticidal protein; pesticide.
KW	Unidentified.
OS	WO200298911-A2.
XX	12-DEC-2002.
PD	30-MAY-2002; 2002WO-GB002666.
PF	07-JUN-2001; 2001GB-00013900.
PR	(SYGN ) SYNGENTA LTD.
PA	Vincent JL, Viner R;
XX	WPI; 2003-175137/17.
DR	New insecticidal protein comprising an X-glycine motif at the amino-
PT	terminus, useful as an active ingredient of a pesticide.
XX	Example 1; Page 65; 67pp; English.
PS	The invention relates to insecticidal protein comprising an X-glycine
CC	motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC	invention are useful for producing plants or plant parts that are
CC	resistant to insects. The protein or synergistic combination is useful as
CC	an active ingredient of a pesticide or for controlling insects.
CC	Antibodies raised to the insecticidal proteins can be used to identify
CC	other proteins with insecticidal activity. The present sequence is
CC	insecticidal protein
XX	Sequence 34 AA;
SQ	
Query Match	100.0%; Score 185; DB 6; Length 34;
Best Local Similarity	93.9%; Pred. No. 9.4e-14;
Matches	31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY	1 XXICTPAGVKCPAALPCCGGLRCIGGVNNKVC 33
DB	2 GKICTPAGVKCPAALPCCGGLRCIGGVNNKVC 34
RESULT 12	
AEE36289	ID AAE36289 standard; peptide; 34 AA.
XX	AC AAE36289;
XX	26-JUN-2003 (first entry)
DT	Insecticidal protein #19.
DE	Insecticidal protein; pesticide.
KW	Unidentified.
OS	WO200298911-A2.
PN	12-DEC-2002.
PD	30-MAY-2002; 2002WO-GB002666.
PF	07-JUN-2001; 2001GB-00013900.
PR	(SYGN ) SYNGENTA LTD.
PA	Vincent JL, Viner R;
PI	WPI; 2003-175137/17.
DR	New insecticidal protein comprising an X-glycine motif at the amino-
PT	terminus, useful as an active ingredient of a pesticide.
XX	Example 1; Page 64; 67pp; English.
PS	The invention relates to insecticidal protein comprising an X-glycine
CC	motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC	invention are useful for producing plants or plant parts that are
CC	resistant to insects. The protein or synergistic combination is useful as
CC	an active ingredient of a pesticide or for controlling insects.
CC	Antibodies raised to the insecticidal proteins can be used to identify
CC	other proteins with insecticidal activity. The present sequence is
CC	insecticidal protein
XX	Sequence 34 AA;
SQ	
Query Match	100.0%; Score 185; DB 6; Length 34;
Best Local Similarity	93.9%; Pred. No. 9.4e-14;
Matches	31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY	1 XXICTPAGVKCPAALPCCGGLRCIGGVNNKVC 33
DB	2 GKICTPAGVKCPAALPCCGGLRCIGGVNNKVC 34
RESULT 11	
AEE36287	ID AAE36287 standard; peptide; 34 AA.
XX	AC AAE36287;
XX	26-JUN-2003 (first entry)
DT	Insecticidal protein #17.
DE	Insecticidal protein; pesticide.
KW	Unidentified.
OS	WO200298911-A2.
PN	12-DEC-2002.
PD	30-MAY-2002; 2002WO-GB002666.
PF	07-JUN-2001; 2001GB-00013900.
PR	(SYGN ) SYNGENTA LTD.
PA	Vincent JL, Viner R;
PI	WPI; 2003-175137/17.
DR	New insecticidal protein comprising an X-glycine motif at the amino-
PT	terminus, useful as an active ingredient of a pesticide.
XX	Example 1; Page 63; 67pp; English.
PS	The invention relates to insecticidal protein comprising an X-glycine
CC	motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC	invention are useful for producing plants or plant parts that are
CC	resistant to insects. The protein or synergistic combination is useful as
CC	an active ingredient of a pesticide or for controlling insects.
CC	Antibodies raised to the insecticidal proteins can be used to identify
CC	other proteins with insecticidal activity. The present sequence is
CC	insecticidal protein
XX	Sequence 34 AA;
SQ	
Query Match	100.0%; Score 185; DB 6; Length 34;
Best Local Similarity	93.9%; Pred. No. 9.4e-14;
Matches	31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY	1 XXICTPAGVKCPAALPCCGGLRCIGGVNNKVC 33
DB	2 GKICTPAGVKCPAALPCCGGLRCIGGVNNKVC 34
RESULT 11	
AEE36287	ID AAE36287 standard; peptide; 34 AA.
XX	AC AAE36287;
XX	26-JUN-2003 (first entry)
DT	Insecticidal protein #17.
DE	Insecticidal protein; pesticide.
KW	Unidentified.
OS	WO200298911-A2.
PN	12-DEC-2002.
PD	30-MAY-2002; 2002WO-GB002666.
PF	07-JUN-2001; 2001GB-00013900.
PR	(SYGN ) SYNGENTA LTD.
PA	Vincent JL, Viner R;
PI	WPI; 2003-175137/17.
DR	New insecticidal protein comprising an X-glycine motif at the amino-
PT	terminus, useful as an active ingredient of a pesticide.
XX	Example 1; Page 63; 67pp; English.
PS	The invention relates to insecticidal protein comprising an X-glycine
CC	motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC	invention are useful for producing plants or plant parts that are
CC	resistant to insects. The protein or synergistic combination is useful as
CC	an active ingredient of a pesticide or for controlling insects.
CC	Antibodies raised to the insecticidal proteins can be used to identify
CC	other proteins with insecticidal activity. The present sequence is
CC	insecticidal protein
XX	Sequence 34 AA;
SQ	
Query Match	100.0%; Score 185; DB 6; Length 34;
Best Local Similarity	93.9%; Pred. No. 9.4e-14;
Matches	31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY	1 XXICTPAGVKCPAALPCCGGLRCIGGVNNKVC 33
DB	2 GKICTPAGVKCPAALPCCGGLRCIGGVNNKVC 34
RESULT 11	
AEE36287	ID AAE36287 standard; peptide; 34 AA.
XX	AC AAE36287;
XX	26-JUN-2003 (first entry)
DT	Insecticidal protein #17.
DE	Insecticidal protein; pesticide.
KW	Unidentified.
OS	WO200298911-A2.
PN	12-DEC-2002.
PD	30-MAY-2002; 2002WO-GB002666.
PF	07-JUN-2001; 2001GB-00013900.
PR	(SYGN ) SYNGENTA LTD.
PA	Vincent JL, Viner R;
PI	WPI; 2003-175137/17.
DR	New insecticidal protein comprising an X-glycine motif at the amino-
PT	terminus, useful as an active ingredient of a pesticide.
XX	Example 1; Page 63; 67pp; English.
PS	The invention relates

```

Best Local Similarity 93.9%; Pred. No. 9.4e-14;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33
   :|||||
DB 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 34

RESULT 13
AAE36263
ID AAE36263 standard; peptide; 34 AA.
XX
AC AAE36263;
XX
DT 26-JUN-2003 (first entry)
XX
DE Insecticidal protein #5.
XX
KW Insecticidal protein; pesticide.
XX
OS Unidentified.
XX
FN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
XX 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN ) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-
PT terminus, useful as an active ingredient of a pesticide.
XX
PS Example 1; Page 62; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine
CC motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC invention are useful for producing plants or plant parts that are
CC resistant to insects. The protein or synergistic combination is useful as
CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify
CC other proteins with insecticidal activity. The present sequence is
CC insecticidal protein
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 185; DB 6; Length 34;
Best Local Similarity 93.9%; Pred. No. 9.4e-14;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33
   :|||||
DB 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVC 34

RESULT 15
AAE36288
ID AAE36288 standard; peptide; 34 AA.
XX
AC AAE36288;
XX
DT 26-JUN-2003 (first entry)
XX
DE Insecticidal protein #18.
XX
KW Insecticidal protein; pesticide.
XX
OS Unidentified.
XX
PN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
XX 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN ) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-
PT terminus, useful as an active ingredient of a pesticide.
XX
PS Example 1; Page 64; 67pp; English.

```



XX The invention relates to insecticidal protein comprising an X-glycine  
CC motif at the amino-terminus. Polynucleotide or DNA constructs of the  
CC invention are useful for producing plants or plant parts that are  
CC resistant to insects. The protein or synergistic combination is useful as  
CC an active ingredient of a pesticide or for controlling insects.  
CC Antibodies raised to the insecticidal proteins can be used to identify  
CC other proteins with insecticidal activity. The present sequence is  
CC insecticidal protein  
XX  
SQ Sequence 34 AA;  
Query Match 100.0%; Score 185; DB 6; Length 34;  
Best Local Similarity 93.9%; Pred. No. 9.4e-14;  
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 XXICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 33  
Db ::|||||||||||||||||||||||||||||  
2 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 34  
Search completed: February 14, 2005, 21:01:56  
Job time : 70 secs

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	82	42.3	36	4	US-09-894-882-3	Sequence 3, Appli
2	79	40.7	36	4	US-09-894-882-4	Sequence 4, Appli
3	75	38.7	36	1	US-08-682-485A-7	Sequence 7, Appli
4	75	38.7	36	2	US-08-933-314-7	Sequence 7, Appli
5	75	38.7	37	2	US-08-682-485A-6	Sequence 6, Appli
6	75	38.7	37	2	US-08-933-314-6	Sequence 6, Appli
7	72.5	37.4	37	4	US-09-894-882-5	Sequence 5, Appli
8	69	35.6	31	4	US-09-894-882-5	Sequence 5, Appli
9	69	35.6	39	4	US-09-894-882-4	Sequence 461, App
10	69	35.6	67	4	US-09-894-882-4	Sequence 497, App
11	67	34.5	32	4	US-09-894-882-247	Sequence 247, App
12	67	34.5	40	4	US-09-894-882-498	Sequence 470, App
13	67	34.5	68	4	US-09-894-882-274	Sequence 498, App
14	59	30.4	155	4	US-09-894-882-274	Sequence 274, App
15	59	30.4	211	4	US-09-252-991A-28474	Sequence 28474, A
16	59	30.4	2471	1	US-09-902-540-15694	Sequence 15694, A
17	59	30.4	2471	1	US-08-185-432-16	Sequence 16, Appl
18	59	30.4	2471	3	US-08-083-590A-19	Sequence 19, Appl
19	59	30.4	2471	4	US-08-532-384-19	Sequence 19, Appl
20	59	30.4	2471	4	US-08-899-232-1	Sequence 1, Appli
21	58.5	30.2	34	1	US-08-121-457-1	Sequence 1, Appli
22	58.5	30.2	34	1	US-08-117-080-5	Sequence 5, Appli
23	58.5	30.2	34	2	US-08-471-329-5	Sequence 5, Appli
24	58.5	30.2	34	2	US-08-915-142-5	Sequence 5, Appli
25	58	29.9	908	4	US-08-714-741-44	Sequence 44, Appl
26	57.5	29.6	180	4	US-09-894-882-248	Sequence 248, App
27	57.5	29.6	281	4	US-09-510-238A-286	Sequence 286, App
28	57.5	29.6	281	4	US-09-253-991A-23962	Sequence 23962, A

```

; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma C.
; APPLICANT: Jimenez, Eisie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Hadronyche versuta
; US-09-894-882-4

Query Match          40.7%; Score 79; DB 4; Length 36;
Best Local Similarity 51.5%; Pred No. 0.0058;
Matches 17; Conservative 0; Mismatches 14; Indels 2; Gaps 1;

QY 3 ICTPAGVKCPAALPCCPGRLCIGGVNKKV--CR 33
DB 2 ICTGADRFCAACCCPGTSCQGPENGVS YCR 34

RESULT 3
US-08-682-485A-7
; Sequence 7, Application US/08682485A
; Patent No. 5763568
; GENERAL INFORMATION:
; APPLICANT: ATKINSON, RONALD K
; APPLICANT: HOWDEN, MERLIN E.H.
; APPLICANT: TYLER, MARGARET I
; APPLICANT: VONARX, EDWARD J
; TITLE OF INVENTION: Insecticidal Toxins Derived From
; TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zeneca, Inc.
; STREET: 1200 South 47th Street
; CITY: Richmond
; STATE: California
; COUNTRY: USA
; ZIP: 94804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,485A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,485
; FILING DATE: 17-JULY-1996

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; APPLICATION NUMBER: US/08/256,933
; FILING DATE: 27-JULY-1994
; APPLICATION NUMBER: WO 93/15108
; FILING DATE: 29-JAN-1993
; APPLICATION NUMBER: AU PL0722
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Shaw, Melissa A.
; REGISTRATION NUMBER: 38,301
; REFERENCE/DOCKET NUMBER: PPD 5099/D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-231-1542
; TELEFAX: 510-231-1112
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Atrax formidabilis
; US-08-682-485A-7

Query Match          38.7%; Score 75; DB 1; Length 36;
Best Local Similarity 50.0%; Pred. No. 0.029;
Matches 16; Conservative 0; Mismatches 14; Indels 2; Gaps 1;

QY 4 CTTPAGVKCPAALPCCPGRLCIGGVNKKV--CR 33
DB 4 CTGADRFCAACCCPGTSCQGPENGVS YCR 35

RESULT 4
US-08-933-314-7
; Sequence 7, Application US/08933314
; Patent No. 5959182
; GENERAL INFORMATION:
; APPLICANT: ATKINSON, RONALD K
; APPLICANT: HOWDEN, MERLIN E.H.
; APPLICANT: TYLER, MARGARET I
; APPLICANT: VONARX, EDWARD J
; TITLE OF INVENTION: Insecticidal Toxins Derived From
; TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zeneca, Inc.
; STREET: 1200 South 47th Street
; CITY: Richmond
; STATE: California
; COUNTRY: USA
; ZIP: 94804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,314
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,485
; FILING DATE: 17-JULY-1996
; APPLICATION NUMBER: US/08/256,933
; FILING DATE: 27-JULY-1994
; APPLICATION NUMBER: WO 93/15108
; FILING DATE: 29-JAN-1993
; APPLICATION NUMBER: AU PL0722
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Shaw, Melissa A.

```

PRIOR APPLICATION DATA: US/08/682,485  
 APPLICATION NUMBER: US/08/682,485  
 FILING DATE: 17-JULY-1996  
 APPLICATION NUMBER: US/08/256,933  
 FILING DATE: 27-JULY-1994  
 APPLICATION NUMBER: WO 93/15108  
 FILING DATE: 29-JAN-1993  
 APPLICATION NUMBER: AU PL0722  
 FILING DATE: 31-JAN-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Shaw, Melissa A.  
 REGISTRATION NUMBER: 38,301  
 REFERENCE/DOCKET NUMBER: PPD 5099/D1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 510-231-1542  
 TELEFAX: 510-231-1112  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 37 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

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; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Atrax formidabilis
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 37
; OTHER INFORMATION: /label= a
; OTHER INFORMATION: /note= "this site may be amidated without loss
; OTHER INFORMATION: of biological activity"
US-08-933-314-6

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08-933-314-6

Query Match	38.7%	Score	75;	DB	2;	Length	37;
Best Local Similarity	50.0%	Pred. NO.	0.029;				
Matches	16;	Conservative	0;	Mismatches	14;	Indels	2;
Gaps	1;						

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/ APPLICANT: University of Utah Research Foundation
/ APPLICANT: Cognetix, Inc.
/ APPLICANT: Walker, Craig S.
/ APPLICANT: Shetty, Reshma
/ APPLICANT: Jimenez, Elsie C.
/ APPLICANT: McIntosh, J. Michael
/ APPLICANT: Olivera, Baldomero M.
/ APPLICANT: Watkins, Maren M.
/ APPLICANT: Jones, Robert M.
/ APPLICANT: Shen, Greg S.
/ TITLE OF INVENTION: I-Superfamily Conotoxins
/ FILE REFERENCE: 2314-238
/ CURRENT APPLICATION NUMBER: US/09/894,882
/ CURRENT FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: US 60/
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 60/243,410
/ PRIOR FILING DATE: 2000-10-27
/ PRIOR APPLICATION NUMBER: US 60/246,581
/ PRIOR FILING DATE: 2000-11-08
/ PRIOR APPLICATION NUMBER: US 60/247,714
/ PRIOR FILING DATE: 2000-11-14
/ PRIOR APPLICATION NUMBER: US 60/264,256
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 506
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 461
/ LENGTH: 31
/ TYPE: PRT
/ ORGANISM: Conus emaciatus
/ US-09-894-882-461

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; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

Query Match      35.6%; Score 69; DB 4; Length 39;
Best Local Similarity 44.8%; Pred. No. 0.15;
Matches 13; Conservative 2; Mismatches 12; Indels 1; Gaps 1;

Qy      4 CTPAGVKCPAALPCCPGRLCTGGVNNKYC 32
      |||||:|||||:|||||:
Db      1 CFPFGIYCTPYLPCGWGICC--GTCRNV 27

RESULT 10
US-09-894-882-247
; Sequence 247, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma C.
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-247

Query Match      35.6%; Score 69; DB 4; Length 67;
Best Local Similarity 44.8%; Pred. No. 0.25;
Matches 13; Conservative 2; Mismatches 12; Indels 1; Gaps 1;

Qy      4 CTPAGVKCPAALPCCPGRLCTGGVNNKYC 32
      |||||:|||||:|||||:
Db      29 CFPFGIYCTPYLPCGWGICC--GTCRNV 55

RESULT 11
US-09-894-882-470
; Sequence 470, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma C.
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren

; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-247

Query Match      35.6%; Score 69; DB 4; Length 67;
Best Local Similarity 44.8%; Pred. No. 0.25;
Matches 13; Conservative 2; Mismatches 12; Indels 1; Gaps 1;

Qy      4 CTPAGVKCPAALPCCPGRLCTGGVNNKYC 32
      |||||:|||||:|||||:
Db      29 CFPFGIYCTPYLPCGWGICC--GTCRNV 55

RESULT 12
US-09-894-882-498
; Sequence 498, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma C.
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 498
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-498

Query Match      34.5%; Score 67; DB 4; Length 40;
Best Local Similarity 50.0%; Pred. No. 0.27;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
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Qy 4 CTPAGVKCPAALPCCPGLRCIG 25  
Db 1 CFPLGTGFCRSRYLPCCSGMCCSG 22

RESULT 13

US-09-894-882-274  
; Sequence 274, Application US/09894882  
; Patent No. 6767895  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Rashna  
; APPLICANT: Jimenez, Elsie C.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: Watkins, Marten  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Shen, Greg S.  
; TITLE OF INVENTION: I-Superfamily Conotoxins  
; FILE REFERENCE: 2314-238  
; CURRENT APPLICATION NUMBER: US/09/894,882  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/243,410  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/246,581  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: US 60/247,714  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/264,256  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 274  
; LENGTH: 68  
; TYPE: PRT  
; ORGANISM: Conus virgo  
US-09-894-882-274

Query Match 34.5%; Score 67; DB 4; Length 68;  
Best Local Similarity 50.0%; Pred. No. 0.44;  
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 4 CTPAGVKCPAALPCCPGLRCIG 25  
Db 29 CFPLGTGFCRSRYLPCCSGMCCSG 50

RESULT 14

US-09-252-991A-28474  
; Sequence 28474, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 28474  
; LENGTH: 155  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-28474

Query Match 30.4%; Score 59; DB 4; Length 155;  
Best Local Similarity 52.6%; Pred. No. 8;  
Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 5 TPAGVKCPAALPCCPGLRC 23  
Db 7 TPASRRPSTAWCCPGRR 25

RESULT 15

US-09-902-540-15694  
; Sequence 15694, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 15694  
; LENGTH: 211  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-15694

Query Match 30.4%; Score 59; DB 4; Length 211;  
Best Local Similarity 42.9%; Pred. No. 11;  
Matches 9; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 3 ICTPAGVKCPAALPCCPGLRC 23  
Db 180 VCAPIGEACGESAACCLGLMC 200

Search completed: March 9, 2005, 17:27:35  
Job time : 2.06257 secs



Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	82	42.3	36	9	US-09-894-882-3		Sequence 3, Appli
2	79	40.7	36	9	US-09-894-882-4		Sequence 4, Appli
3	73	37.6	35	14	US-10-072-602B-571		Sequence 571, Ap
4	73	37.6	82	14	US-10-072-602B-140		Sequence 140, Ap
5	72.5	37.4	37	9	US-09-894-882-5		Sequence 5, Appli
6	69.5	35.8	30	14	US-10-072-602B-570		Sequence 570, Ap
7	69.5	35.8	77	14	US-10-072-602B-137		Sequence 137, Ap
8	69	35.6	31	9	US-09-894-882-461		Sequence 461, App
9	69	35.6	39	9	US-09-894-882-497		Sequence 497, App
10	69	35.6	67	9	US-09-894-882-247		Sequence 247, App
11	68	35.1	3501	14	US-10-123-155-37		Sequence 37, App
12	68	35.1	3501	14	US-10-146-731-37		Sequence 37, App
13	68	35.1	3501	14	US-10-140-472-37		Sequence 37, App

```

Query Match          42.3%; Score 82; DB 9; Length 36;
Best Local Similarity 51.5%; Pred. No. 0.022; Indels
Matches 17; Conservative 1; Mismatches 13; Gaps 1;

QY      3  ICTPAGVKCPAALPCCPGLCIGGVNNKV--CR 33
      |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      2  ICTGADRPCAACCCPGTSCQGPESNGVYCR 34
      |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 2
US-09-894-882-4
; Sequence 4, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Hadronyche versuta
US-09-894-882-4

Query Match          40.7%; Score 79; DB 9; Length 36;
Best Local Similarity 51.5%; Pred. No. 0.049;
Matches 17; Conservative 0; Mismatches 14; Indels 2; Gaps 1;

QY      3  ICTPAGVKCPAALPCCPGLCIGGVNNKV--CR 33
      |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      2  ICTGADRPCAACCCPGTSCQGPNGVYCR 34
      |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 3
US-10-072-602B-571
; Sequence 571, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.

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; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Hadronyche versuta
US-09-894-882-5

Query Match      37.4%; Score 72.5; DB 9; Length 37;
Best Local Similarity 46.9%; Pred. No. 0.27;
Matches 15; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

Qy 3 ICTGAGVCPAALPCCPGRLCIGGVNN-KVCR 33
Db 2 ICTGADRPAAACCCPGCTCKAESNGVSYCR 33

RESULT 6
US-10-072-602B-570
; Sequence 570, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 570
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Conus lividus
US-10-072-602B-570

Query Match      35.8%; Score 69.5; DB 14; Length 30;
Best Local Similarity 44.8%; Pred. No. 0.5;
Matches 13; Conservative 2; Mismatches 13; Indels 1; Gaps 1;

Qy 4 CTPAGVKCPAALPCCPGRLCIGGVNNKVC 32
Db 4 CTPAGVKCPAALPCCPGRLCIGGVNNKVC 32

RESULT 7
US-10-072-602B-137
; Sequence 137, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 137
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Conus lividus
US-10-072-602B-137

Query Match      35.8%; Score 69.5; DB 14; Length 77;
Best Local Similarity 44.8%; Pred. No. 1.1;
Matches 13; Conservative 2; Mismatches 13; Indels 1; Gaps 1;

Qy 4 CTPAGVKCPAALPCCPGRLCIGGVNNKVC 32
Db 49 CGHSGAGC-YTRPCPGHLHCSGGQAGGLC 76

RESULT 8
US-09-894-882-461
; Sequence 461, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
```

; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 461  
; LENGTH: 31  
; TYPE: PRT  
; ORGANISM: Conus emaciatus  
US-09-894-882-461

Query Match 35.6%; Score 69; DB 9; Length 31;  
Best Local Similarity 44.8%; Pred. No. 0.59;  
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

Qy 4 CTPAGVKCPAALPCCGRLGIGGVNNKVC 32  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 CFPFGIYCTPYLPCCWGICC--GTCRNVC 27

RESULT 9  
US-09-894-882-497  
; Sequence 497, Application US/09894882  
; Patent No. US20020102607A1

; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jimenez, Elsie C.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: Watkins, Maren  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Shen, Greg S.

; TITLE OF INVENTION: I-Superfamily Conotoxins  
; FILE REFERENCE: 2314-238

; CURRENT APPLICATION NUMBER: US/09/894,882  
; CURRENT FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: US 60/

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 60/243,410

; PRIOR FILING DATE: 2000-10-27

; PRIOR APPLICATION NUMBER: US 60/246,581

; PRIOR FILING DATE: 2000-11-08

; PRIOR APPLICATION NUMBER: US 60/247,714

; PRIOR FILING DATE: 2000-11-14

; PRIOR APPLICATION NUMBER: US 60/264,256

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 506

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 497

; LENGTH: 39

; TYPE: PRT

; ORGANISM: Conus emaciatus

US-09-894-882-497

Query Match 35.6%; Score 69; DB 9; Length 39;  
Best Local Similarity 44.8%; Pred. No. 0.71;  
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

Qy 4 CTPAGVKCPAALPCCGRLGIGGVNNKVC 32  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 CFPFGIYCTPYLPCCWGICC--GTCRNVC 27

RESULT 10  
US-09-894-882-247  
; Sequence 247, Application US/09894882  
; Patent No. US20020102607A1

; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jimenez, Elsie C.  
; APPLICANT: McIntosh, J. Michael

; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: Watkins, Maren  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Shen, Greg S.  
; TITLE OF INVENTION: I-Superfamily Conotoxins  
; FILE REFERENCE: 2314-238  
; CURRENT APPLICATION NUMBER: US/09/894,882  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/243,410  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/246,581  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: US 60/247,714  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/264,256  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 247  
; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Conus emaciatus  
US-09-894-882-247

Query Match 35.6%; Score 69; DB 9; Length 67;  
Best Local Similarity 44.8%; Pred. No. 1.2;  
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

Qy 4 CTPAGVKCPAALPCCGRLGIGGVNNKVC 32  
| | | | | | | | | | | | | | | | | | | | | |  
Db 29 CFPFGIYCTPYLPCCWGICC--GTCRNVC 55

RESULT 11

US-10-123-155-37

; Sequence 37, Application US/10123155

; Publication No. US20030068794A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Geritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C30

; CURRENT APPLICATION NUMBER: US/10/123,155

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 37

; LENGTH: 3501

; TYPE: DNA

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 2762, 2778

; OTHER INFORMATION: unknown base

US-10-123-155-37

Query Match 35.1%; Score 68; DB 14; Length 3501;  
Best Local Similarity 46.2%; Pred. No. 51;  
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 GKICTPAGVKCPAALPCCPGRLRCIGG 26  
Db 888 GACCAAGTACCAAGCCTGTGCTGG 913

## RESULT 12

US-10-146-731-37  
; Sequence 37, Application US/10146731  
; Publication No. US20030129692A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C323  
; CURRENT APPLICATION NUMBER: US/10/146,731  
; CURRENT FILING DATE: 2002-05-15

; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 37

; LENGTH: 3501  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 2762, 2778  
; OTHER INFORMATION: unknown base  
US-10-146-731-37

Query Match 35.1%; Score 68; DB 14; Length 3501;  
Best Local Similarity 46.2%; Pred. No. 51;  
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 GKICTPAGVKCPAALPCCPGRLRCIGG 26  
Db 888 GACCAAGTACCAAGCCTGTGCTGG 913

## RESULT 13

US-10-140-472-37  
; Sequence 37, Application US/10140472  
; Publication No. US20030138888A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C168  
; CURRENT APPLICATION NUMBER: US/10/140,472  
; CURRENT FILING DATE: 2002-05-06

; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 37  
; LENGTH: 3501  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 2762, 2778  
; OTHER INFORMATION: unknown base  
US-10-140-472-37

Query Match 35.1%; Score 68; DB 14; Length 3501;  
Best Local Similarity 46.2%; Pred. No. 51;  
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 GKICTPAGVKCPAALPCCPGRLRCIGG 26  
Db 888 GACCAAGTACCAAGCCTGTGCTGG 913

## RESULT 14

US-10-141-761-37  
; Sequence 37, Application US/10141761  
; Publication No. US20030148432A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C198  
; CURRENT APPLICATION NUMBER: US/10/141,761  
; CURRENT FILING DATE: 2002-05-08

; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 37  
; LENGTH: 3501  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 2762, 2778  
; OTHER INFORMATION: unknown base  
US-10-141-761-37

Query Match 35.1%; Score 68; DB 14; Length 3501;

Best Local Similarity 46.2%; Pred. No. 51;  
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
QY 1 GKICTPAGVKCPAALPCCPGRLRCIGG 26  
Db 888 GACCAAGTACCAAGCCTGTGCTGG 913

RESULT 15  
US-10-142-885-37  
; Sequence 37, Application US/10142885  
; Publication No. US20030157604A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C248  
; CURRENT APPLICATION NUMBER: US/10/142,885  
; CURRENT FILING DATE: 2002-05-10  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 37  
; LENGTH: 3501  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 2762, 2778  
; OTHER INFORMATION: unknown base  
US-10-142-885-37

Query Match 35.1%; Score 68; DB 14; Length 3501;  
Best Local Similarity 46.2%; Pred. No. 51;  
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
QY 1 GKICTPAGVKCPAALPCCPGRLRCIGG 26  
Db 888 GACCAAGTACCAAGCCTGTGCTGG 913

Search completed: March 9, 2005, 18:08:03  
Job time : 4.24047 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2005, 20:32:21 ; Search time 0.761133 Seconds  
(without alignments)  
4171.616 Million cell updates/sec

Title: US-10-019-823B-2

Perfect score: 194

Sequence: 1 GKICTPAGVKCPAALPCCPLRCIGGVNNKVC 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	33.0	1064	2 A40136	fibropellin Ia - s
2	60	30.9	422	2 S48564	probable membrane
3	60	30.9	570	2 A48936	fibropellin C prec
4	58.5	30.2	34	2 A31043	mu-conotoxin GS -
5	58	29.9	37	2 E44007	apoptoxin III - tr
6	57.5	29.6	417	2 T08724	hypothetical prote
7	57	29.4	1221	2 T23472	hypothetical prote
8	56.5	29.1	585	2 S43572	C0585.5 protein (c
9	56.5	29.1	585	2 E88571	protein C0585.5 [i
10	56.5	29.1	1390	2 T30346	insulin receptor -
11	56	28.9	197	2 T10081	sperm mitochondria
12	56	28.9	238	2 T04166	thauatin-like pro
13	56	28.9	2352	2 T30201	Notch homolog prot
14	56	28.9	2531	2 S18188	notch protein homo
15	56	28.9	2531	2 A46019	notch-1 protein -
16	55	28.4	132	2 H75335	hypothetical prote
17	54.5	28.1	218	2 T03287	osmotin protein ho
18	54.5	28.1	601	2 T22025	hypothetical prote
19	54.5	28.1	601	2 D89711	protein F40E10.4 [
20	54.5	28.1	768	2 A87722	protein ZC123.1 [i
21	54.5	28.1	1207	1 EGHU	epidermal growth f
22	54.5	28.1	4543	1 A53102	alpha-2-macroglobu
23	54	27.8	73	2 H43019	platelet aggregati
24	54	27.8	74	2 S25773	testis-specific pr
25	54	27.8	269	2 T26957	hypothetical prote
26	54	27.8	283	2 E88597	protein Y47D38.6 [
27	54	27.8	2338	2 S45306	notch 3 protein -
28	54	27.8	2321	2 S78549	notch3 protein - h
29	53	27.3	375	2 A41428	CEF-10 protein pre

#### ALIGNMENTS

##### RESULT 1

A40136  
fibropellin Ia - sea urchin (Strongylocentrotus purpuratus)  
N;Alternate names: epidermal growth factor homolog precursor  
N;Contains: alternatively spliced fibropellin Ib (EGFI)  
C;Species: Strongylocentrotus purpuratus (purple urchin)  
C;Date: 13-May-1992 #sequence revision 17-Sep-1997 #text\_change 09-Jul-2004  
C;Accession: A40136; B40136; C40136; A29316; A43131  
R;Belgadillo-Reynoso, M.G.; Rollo, D.R.; Hursh, D.A.; Raff, R.A.  
J. Mol. Evol. 29, 314-327, 1989  
A;Title: Structural analysis of the uEGF gene in the sea urchin Strongylocentrotus purpuratus  
A;Reference number: A40136; MUID:90112459; PMID:2514273  
A;Accession: A40136  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-114 <DEL>  
A;Cross-references: UNIPROT:P10079; GB:X17530; NID:g10225; PID:g667061  
A;Accession: B40136  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 181-251,329-370,'R',372-408,'RA',411-441 <DE2>  
A;Accession: C40136  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 'K',747-821,898-978 <DE3>  
R;Hursh, D.A.; Andrews, M.E.; Raff, R.A.  
Science 237, 1487-1490, 1987  
A;Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.  
A;Reference number: A29316; MUID:87319677; PMID:3498216  
A;Accession: A29316  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 'S',280-481,786-1064 <HUR>  
A;Cross-references: GB:M17421; NID:g161474; PIDN:AAA30050.1; PID:g552260  
R;Hunt, L.T.; Barker, W.C.  
FASEB J. 3, 1760-1764, 1989  
A;Title: Avidin-like domain in an epidermal growth factor homolog from a sea urchin.  
A;Reference number: A43131; MUID:89196806; PMID:2784773  
A;Content: annotation  
C;Comment: EGF homology repeats 10-17 are spliced out in the short form (fibropellin Ib)  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-1064/Product: fibropellin I #status predicted <FIB>  
F;23-54/Domain: EGF homology <EG01>  
F;57-175/Domain: C1r/C1s repeat homology <C1r>  
F;180-211/Domain: EGF homology <EG02>  
F;218-249/Domain: EGF homology <EG03>  
F;256-287/Domain: EGF homology <EG04>  
F;294-325/Domain: EGF homology <EG05>  
F;332-363/Domain: EGF homology <EG06>  
F;370-401/Domain: EGF homology <EG07>  
F;408-439/Domain: EGF homology <EG08>  
F;446-477/Domain: EGF homology <EG09>

protein C (activat  
Delta-4 protein - f  
crumbs protein - f  
Xotch protein - Af  
hypothetical prote  
alpha-2-macroglobu  
alpha-2-macroglobu  
metallothionein A  
platelet aggregati  
conserved hypothet  
Motch B protein -  
E2 glycoprotein pr  
transmembrane prot  
pathogenesis-relat  
osmotin-like prote  
osmotin-like prote

30 53 27.3 456 1 KXBO  
31 53 27.3 686 2 JC7569  
32 53 27.3 2139 2 A35672  
33 53 27.3 2524 2 A35844  
34 52.5 27.1 596 2 T26950  
35 52.5 27.1 4544 1 S02392  
36 52.5 27.1 4545 1 S25111  
37 52 26.8 64 2 A25775  
38 52 26.8 71 2 G43019  
39 52 26.8 134 2 AD0652  
40 52 26.8 1203 2 A49175  
41 52 26.8 1449 2 S47423  
42 52 26.8 2437 2 S42612  
43 51.5 26.5 233 2 S31829  
44 51.5 26.5 238 2 S28001  
45 51.5 26.5 246 2 S30144

F:484-515/Domain: EGF homology <EG10>  
F:522-533/Domain: EGF homology <EG11>  
F:560-591/Domain: EGF homology <EG12>  
F:598-629/Domain: EGF homology <EG13>  
F:636-667/Domain: EGF homology <EG14>  
F:674-705/Domain: EGF homology <EG15>  
F:712-743/Domain: EGF homology <EG16>  
F:750-781/Domain: EGF homology <EG17>  
F:788-819/Domain: EGF homology <EG18>  
F:826-857/Domain: EGF homology <EG19>  
F:864-895/Domain: EGF homology <EG20>  
F:902-933/Domain: EGF homology <EG21>  
F:936-1064/Region: avidin-like  
F:23-34,28-43,45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-27  
S:7,451-466,468-477,484-495/disulfide bonds: #status predicted  
F:489-504,506-515,522-533,527-542,544-553,560-571,565-580,582-591,598-609,603-618,620-62  
08,810-819,826-837,831-846,848-857,864-875,869-884,886-895,902-913,907-922,924-933/disul

Query Match 33.0%; Score 64; DB 2; Length 1064;  
Best Local Similarity 39.5%; Pred. No. 6.7;  
Matches 15; Conservative 3; Mismatches 12; Indels 8; Gaps 2;  
Qy 3 ICTPA--GVKCP-----AALPCCPGLRCIGGVNNKVC 32  
Db 429 ICAPGFDGLNCNNIDECASRPCQNGAVCDGVNGFVC 466

RESULT 2  
S48564  
probable membrane protein YLR213c - yeast (Saccharomyces cerevisiae)  
N:Alternate names: hypothetical protein L8167.22  
C:Species: Saccharomyces cerevisiae  
C>Date: 02-Dec-1994 #sequence\_revision 02-Dec-1994 #text\_change 09-Jul-2004  
C:Accession: S48564  
R:Pauley, A.  
A:Submitted to the EMBL Data Library, September 1994  
A:Description: The sequence of S. cerevisiae cosmid 8167.  
A:Reference number: S48545  
A:Accession: S48564  
A:Molecule type: DNA  
A:Residues: 1-422 <PAU>  
A:Cross-references: UNIPROT:Q05790; EMBL:U14913; NID:G544497; PID:G544518; GSPDB:GN00012  
C:Genetics:  
A:Gene: SGD:CRRI; MIPS:YLR213C  
A:Cross-references: SGD:S0004203  
A:Map position: 12R  
C:Keywords: transmembrane protein  
F:3-19/Domain: transmembrane #status predicted <TMM>  
Query Match 30.9%; Score 60; DB 2; Length 422;  
Best Local Similarity 40.6%; Pred. No. 9.3;  
Matches 13; Conservative 2; Mismatches 9; Indels 8; Gaps 2;  
Qy 4 CTPAGVKCPAALPCC-----PGLRCIGGVN 28  
Db 31 CSPNN-PCPAEWPCSPYNECGAGPTCVGGCN 61

RESULT 3  
A48836  
fibropellin C precursor - sea urchin (Strongylocentrotus purpuratus)  
N:Alternate names: EGF repeat-containing protein; epidermal growth factor-related protei  
C:Species: Strongylocentrotus purpuratus (purple urchin)  
C>Date: 01-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A48836  
R:Biggrove, B.W.; Raff, R.A.  
Dev. Biol. 157, 526-538, 1993  
A:Title: The SpEGF III gene encodes a member of the fibropellins: EGF repeat-containing  
A:Reference number: A48836; MUID:93273088; PMID:8500658  
A:Accession: A48836  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-570 <BIS>

A:Cross-references: UNIPROT:P49013; GB:L07045; NID:G310659; PID:G310660  
A>Note: sequence extracted from NCBI backbone (NCBIN:132724, NCBIP:132725)  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-570/Product: fibropellin C #status predicted <FIB>  
F:19-54/Domain: EGF homology <EG1>  
F:57-175/Domain: Ctr/Cis repeat homology <Clr>  
F:176-211/Domain: EGF homology <EG2>  
F:214-249/Domain: EGF homology <EG3>  
F:252-287/Domain: EGF homology <EG4>  
F:290-325/Domain: EGF homology <EG5>  
F:328-363/Domain: EGF homology <EG6>  
F:366-401/Domain: EGF homology <EG7>  
F:404-439/Domain: EGF homology <EG8>  
F:442-570/Region: avidin-like  
F:23-34,28-43,45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-27  
fide bonds: #status predicted

Query Match 30.9%; Score 60; DB 2; Length 570;  
Best Local Similarity 35.1%; Pred. No. 12;  
Matches 13; Conservative 4; Mismatches 12; Indels 8; Gaps 2;  
Qy 4 CTPA--GVKCP-----AALPCCPGLRCIGGVNNKVC 32  
Db 240 CIPFGVNCENNINECASIPCLNGICVDGINQFAC 276

RESULT 4  
A31043  
mu-conotoxin GS - cone shell (Conus geographus)  
C:Species: Conus geographus (geography cone)  
C>Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 09-Jul-2004  
C:Accession: A31043  
R:Yanagawa, Y.; Abe, T.; Satake, M.; Odani, S.; Suzuki, J.; Ishikawa, K.  
Biochemistry 27, 6256-6262, 1988  
A:Title: A novel sodium channel inhibitor from Conus geographus: purification, structure  
A:Reference number: A31043; MUID:89118210; PMID:2851318  
A:Accession: A31043  
A:Molecule type: protein  
A:Residues: 1-34 <YAN>  
A:Cross-references: UNIPROT:PI5472  
A>Note: there are three disulfide bonds  
A:Superfamily: unassigned conotoxins  
C:Keywords: carboxyglutamic acid; hydroxyproline; myotoxin; sodium channel inhibitor; ver  
F:10,11/Modified site: 4-hydroxyproline (Pro) #status experimental  
F:32/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental  
F:34/Modified site: amidated carboxyl end (Val) #status absent

Query Match 30.2%; Score 58.5; DB 2; Length 34;  
Best Local Similarity 44.8%; Pred. No. 1.9;  
Matches 13; Conservative 3; Mismatches 10; Indels 3; Gaps 2;  
Qy 4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32  
Db 2 CSGRGRSCLPP--QCCMGLRC-GRGNPKC 27

RESULT 5  
E44007  
aptotoxin III - trap-door spider (Aptostichus schlingeri)  
N:Alternate names: insecticidal peptide Aps III  
C:Species: Aptostichus schlingeri  
C>Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C:Accession: E44007  
R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Quistad, G.B.  
Toxicol 30, 1043-1050, 1992  
A:Title: Identification of insecticidal peptides from venom of the trap-door spider, Apt  
A:Reference number: A44007; MUID:93069259; PMID:1440641  
A:Accession: E44007  
A:Molecule type: protein  
A:Residues: 1-37 <SKI>  
A:Cross-references: UNIPROT:P49268; PIDN:AAB24051.1; PID:G259281  
A>Note: sequence extracted from NCBI backbone (NCBIP:119526)  
C:Keywords: disulfide bond; toxin; venom



Query Match 29.9%; Score 58; DB 2; Length 37;  
Best Local Similarity 37.1%; Pred. No. 2.3;  
Matches 13; Conservative 1; Mismatches 15; Indels 6; Gaps 1;

QY 4 CTPAGVKCPAALPCCPG-----LRICIGGVNNKVC 32  
DB 1 CNSKGTCTNADECCGKGCAYNVWNCICGGGCKTC 35

RESULT 6  
T08724  
hypothetical protein DKFZp566D213.1 - human  
C;Species: Homo sapiens (man)  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C;Accession: T08724  
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, May 1999  
A;Reference number: Z16468  
A;Accession: T08724  
A;Molecule type: mRNA  
A;Residues: 1-417 <KOE>  
A;Cross-references: UNIPROT:Q9Y409; EMBL:AL050275  
A;Experimental source: fetal kidney; clone DKFZp566D213  
C;Genetics:  
A;Note: DKFZp566D213.1

Query Match 29.6%; Score 57.5; DB 2; Length 417;  
Best Local Similarity 31.1%; Pred. No. 18;  
Matches 14; Conservative 4; Mismatches 14; Indels 13; Gaps 1;

QY 2 KICTPAGVKCPAALPC-----CPGLRCIGGVNNKVC 33  
DB 140 KLCCPAGTFGSCLPFCGTERPCGYGQCEGTRGGSGHCDQC 184

RESULT 7  
T23472  
hypothetical protein K08E7.5 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T23472  
R;Smyle, R.  
submitted to the EMBL Data Library, July 1996  
A;Reference number: Z19745  
A;Accession: T23472  
A;Status: preliminary; translated from GE/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1221 <WIL>  
A;Cross-references: UNIPROT:Q21344; EMBL:Z77666; PIDN:CA801228.1; GSPDB:GN00022; CESP:K08E7  
A;Experimental source: clone K08E7  
C;Genetics:  
A;Gene: CESP:K08E7.5  
A;Map position: 4  
A;Introns: 26/1; 103/1; 170/1; 640/1; 802/2; 831/1; 864/3; 891/3; 908/1; 938/2; 980/1; 1

Query Match 29.4%; Score 57; DB 2; Length 1221;  
Best Local Similarity 34.5%; Pred. No. 49;  
Matches 10; Conservative 3; Mismatches 14; Indels 2; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGLRICIGGVNNKVC 32  
DB 971 CAPPAPCLPTIFCCPIPC--POPIC 997

RESULT 8  
S43572  
C05B5.5 protein (clone C05B5) - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 07-Sep-1994 #sequence\_revision 10-Nov-1995 #text\_change 10-Nov-1995  
C;Accession: S43572  
R;Mortimore, B.  
submitted to the EMBL Data Library, April 1994

## RESULT 11

T10081  
sperm mitochondrial capsule selenoprotein - mouse  
A:Accession: T30201  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
C:Date: 16-Jul-1999 #sequence\_revision 04-Mar-2000 #text\_change 09-Jul-2004  
C:Accession: T10081; A37199  
R:Kleene, K.C.; Smith, J.; Bozorgzadeh, A.; Harris, M.; Hahn, L.; Karimpour, I.; Gerstel  
Dev. Biol. 137, 395-402, 1990  
A:Title: Sequence and developmental expression of the mRNA encoding the seleno-protein c  
A:Reference number: A37199; MUID:90152148; PMID:2303168  
A:Accession: T10081  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-6, 'X', 18-33, 'X', 35-197 <KLE1>  
A:Cross-references: UNIPROT:P15265; EMBL:M29603; NID:g199088; PIDN:AAAS3045.1; PID:g5672  
A:Experimental source: strain CD-1  
A:Note: in Genbank entry MUSMCS, release 113.0, PIDN:AAAS3045.1, the selenocysteine UGA  
A:Accession: A37199  
A:Molecule type: mRNA  
A:Residues: 55-197 <KLE2>  
A:Cross-references: GB:M29603; NID:g199088  
A:Note: the authors translated the codon TGT for residue 112 as Pro  
C:Genetics:  
A:Gene: MCS  
A:Genome: nuclear  
A:Keywords: mitochondrion; selenocysteine; sperm  
F:7,17,34/Modified site: selenocysteine #status predicted

Query Match 28.9%; Score 56; DB 2; Length 197;  
Best Local Similarity 45.0%; Pred. No. 15;  
Matches 9; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 4 CTPAGVKCPALPCCPGRLC 23  
DB 87 CCFKSPCCPKSPCCPPKPC 106

RESULT 12  
T04166  
thaumatin-like protein - rice  
A:Species: Oryza sativa (rice)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T04166  
R:Cole, K.C.; Velazhahan, R.; Anuratha, C.S.; Muchukrishnan, S.  
submitted to the EMBL Data Library, November 1996  
A:Description: Induction of thaumatin-like proteins (TLPs) in Rhizoctonia solani- infect  
A:Reference number: Z15250  
A:Accession: T04166  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-238 <COL>  
A:Cross-references: UNIPROT:O04364; EMBL:U77657; NID:g2062388; PIDN:AAAS3368.1; PID:g206  
C:Superfamily: thaumatin I

Query Match 28.9%; Score 56; DB 2; Length 238;  
Best Local Similarity 45.2%; Pred. No. 17;  
Matches 14; Conservative 2; Mismatches 13; Indels 2; Gaps 2;  
QY 1 GKICTPAGVKCPALPCCPGRLCIGGVNN 29  
DB 146 GAGCPKGGPRCATITPQCFSELAPGGCN 176

RESULT 13  
T30201  
Notch homolog protein - sea squirt (Halocynthia roretzi)  
A:Species: Halocynthia roretzi  
C:Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 08-Sep-2002  
C:Accession: T30201  
R:Hori, S.; Saichoh, T.; Matsumoto, M.; Makabe, K.W.; Nishida, H.  
Dev. Genes Evol. 207, 371-380, 1997  
A:Title: Notch homologue from Halocynthia roretzi is preferentially expressed in the cen

A:Reference number: Z20775

A:Accession: T30201

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-2352 <HOR>

A:Cross-references: EMBL:AB001327; NID:d1204472; PID:d1026501; PIDN:BAAS5571.1

C:Genetics:

A:Gene: Notch

C:Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 28.9%; Score 56; DB 2; Length 2352;

Best Local Similarity 36.8%; Pred. No. 1.1e+02;

Matches 14; Conservative 2; Mismatches 14; Indels 8; Gaps 2;

QY 4 CTP--AGVKCPALPCCPGRLCIGGVNNKVC 33

DB 593 CTPGYTGEHCDTDINECDNFCNGATCQNEVNNFVC 630

## RESULT 14

S18188

notch protein homolog - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 02-Aug-2002

C:Accession: S18188

R:Weinmaster, G.; Roberts, V.J.; Lemke, G.

Development 113, 199-205, 1991

A:Title: A homolog of Drosophila Notch expressed during mammalian development.

A:Reference number: S18188; MUID:92111383; PMID:1764995

A:Accession: S18188

A:Molecule type: mRNA

A:Residues: 1-2531 <WEI>

A:Cross-references: EMBL:X57405; NID:g57634; PID:g57635

C:Superfamily: notch protein; ankyrin repeat homology; EGF homology

F:987-1018/Domain: EGF homology <EGF1>

F:1025-1056/Domain: EGF homology <EGF2>

F:1233-1264/Domain: EGF homology <EGF2>

F:1917-1949/Domain: ankyrin repeat homology <AN1>

F:1950-1982/Domain: ankyrin repeat homology <AN2>

F:1984-2016/Domain: ankyrin repeat homology <AN3>

F:2017-2049/Domain: ankyrin repeat homology <AN4>

F:2050-2082/Domain: ankyrin repeat homology <AN5>

Query Match 28.9%; Score 56; DB 2; Length 2531;

Best Local Similarity 36.8%; Pred. No. 1.1e+02;

Matches 14; Conservative 2; Mismatches 14; Indels 8; Gaps 2;

QY 4 CTP--AGVKCPALPCCPGRLC-----CIGGVNNKVC 33

DB 245 CLPGFAGQCNENVDPCGNCKNGACVDGVNTYNC 282

## RESULT 15

A46019

notch-1 protein - mouse

N:Alternate names: notch protein

C:Species: Mus musculus (house mouse)

C:Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 16-Aug-2004

C:Accession: A46019; S25144; C49175; B46438; A46438; PH1569; S32109

R:del Amo, F. F.; Gendron-Maguire, M.; Swiatek, P. J.; Jenkins, N. A.; Copeland, N. G.; Gridi

Genomics 15, 259-264, 1993

A:Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of

A:Reference number: A46019; MUID:93194170; PMID:8449489

A:Accession: A46019

A:Status: not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-2531 <DEL>

A:Cross-references: UNIPROT:Q01705; GB:Z11886; GB:S47228; NID:g288502; PIDN:CAA77941.1;

A:Note: sequence extracted from NCBI backbone (NCBIP:127318)

R:Franco del Amo, F.; Smith, D. E.; Swiatek, P. J.; Gendron-Maguire, M.; Greenspan, R. J.; N

submitted to the EMBL Data Library, April 1992

A:Description: Expression pattern of Notch, a mouse homolog of Drosophila Notch, suggest

A:Reference number: S25144

A;Accession: S25144  
 A;Molecule type: mRNA  
 A;Residues: 1551-2108,'Q',2110-2114,'ALP',2118-2170 <FRA>  
 A;Cross-references: EMBL:Z11886  
 R;Lardelli, M.; Lendahl, U.  
 Exp. Cell Res. 204, 364-372, 1993  
 A;Title: Notch A and Notch B-two mouse Notch homologues coexpressed in a wide variety of  
 A;Reference number: A49175; MUID:93178563; PMID:8440332  
 A;Accession: C49175  
 A;Status: preliminary; nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1161-1547 <LAP>  
 A;Cross-references: EMBL:X68278; NID:9287987; PIDN:CAA48339.1; PID:9287988  
 A;Experimental source: embryo  
 A;Note: sequence extracted from NCBI backbone (NCBIP:126159)  
 R;Kopan, R.; Weintraub, H.  
 J. Cell Biol. 121, 631-641, 1993  
 A;Title: Mouse notch: expression in hair follicles correlates with cell fate determination  
 A;Reference number: A46438; MUID:93252998; PMID:8486742  
 A;Accession: B46438  
 A;Status: preliminary  
 A;Molecule type: nucleic acid  
 A;Residues: 1865-1932,'RR',1935-1937,'L',1938-1967,'I',1969-2044,'IE',2047-2052,'S',2054  
 A;Experimental source: embryo  
 A;Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBIP:131247)  
 C;Comment: This protein has many EGF repeats and lin-12[1172]/Notch repeats.  
 C;Comment: This protein is one of the neurogenic proteins controlling the decision between  
 C;Genetics:  
 A;Gene: notch-1  
 A;Map position: 2  
 A;Note: proximal region of chromosome 2  
 C;Superfamily: Notch protein; ankyrin repeat homology; EGF homology  
 F;106-138/Domain: EGF homology <EGF1>  
 F;144-175/Domain: EGF homology <EG01>  
 F;222-254/Domain: EGF homology <EGF2>  
 F;261-292/Domain: EGF homology <EG02>  
 F;339-370/Domain: EGF homology <EG03>  
 F;416-449/Domain: EGF homology <EGF3>  
 F;456-487/Domain: EGF homology <EG04>  
 F;494-525/Domain: EGF homology <EG05>  
 F;532-563/Domain: EGF homology <EG06>  
 F;607-638/Domain: EGF homology <EG07>  
 F;682-713/Domain: EGF homology <EG08>  
 F;757-788/Domain: EGF homology <EG09>  
 F;795-826/Domain: EGF homology <EG10>  
 F;873-904/Domain: EGF homology <EG11>  
 F;911-942/Domain: EGF homology <EG12>  
 F;949-980/Domain: EGF homology <EG13>  
 F;987-1018/Domain: EGF homology <EG14>  
 F;1025-1056/Domain: EGF homology <EG15>  
 F;1063-1094/Domain: EGF homology <EG16>  
 F;1149-1180/Domain: EGF homology <EG17>  
 F;1187-1218/Domain: EGF homology <EG18>  
 F;1233-1264/Domain: EGF homology <EGF4>  
 F;1352-1383/Domain: EGF homology <EG19>  
 F;1391-1425/Domain: EGF homology <EGF>  
 F;1917-1948/Domain: ankyrin repeat homology <AN1>  
 F;1949-1981/Domain: ankyrin repeat homology <AN2>  
 F;1983-2015/Domain: ankyrin repeat homology <AN3>  
 F;2016-2048/Domain: ankyrin repeat homology <AN4>  
 F;2049-2081/Domain: ankyrin repeat homology <AN5>

Query Match 28.9%; Score 56; DB 2; Length 2531;  
 Best Local Similarity 36.8%; Pred. No. 1.le+02;  
 Matches 14; Conservative 2; Mismatches 14; Indels 8; Gaps 2;

Qy 4 CTP--AGVKCPALPCPGRLR-----CIGGVNKKVR 33  
 Db 245 CLPFGAGNCEENVDCPGNNCKNGGACVDGVNTYCR 282

Search completed: February 14, 2005, 21:00:42  
 Job time : 0.761133 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:11:42 ; Search time 3.72277 Seconds  
(without alignments)  
4539.261 Million cell updates/sec

Title: US-10-019-823B-2

Perfect score: 194

Sequence: 1 GXICTPAGVKCPAALPCCPLGRLCIGGVNNKVC 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	42.3	36	1 TXJJA HADVE	P82227 hadronyche
2	79	40.7	36	1 TXJB HADVE	P82226 hadronyche
3	73	37.6	72	2 Q9TVN1	Q9tvn1 conus livid
4	73	37.6	72	2 Q9UAA2	Q9uaa2 conus livid
5	73	37.6	72	2 Q9UAA4	Q9uaa4 conus livid
6	73	37.6	72	2 Q9UAA7	Q9uaa7 conus livid
7	73	37.6	72	2 Q9UAB0	Q9uab0 conus livid
8	73	37.6	72	2 Q9UAB1	Q9uab1 conus livid
9	72.5	37.4	37	1 TXJC HADVE	P82228 hadronyche
10	72	37.1	72	2 Q9UAA3	Q9uaa3 conus livid
11	72	37.1	72	2 Q9UAA5	Q9uaa5 conus livid
12	72	37.1	2524	2 Q9GPA5	Q9gpa5 branchiosto
13	70.5	36.3	33	1 TXC5 PHONI	P84015 phoneutria
14	69.5	35.8	3775	2 Q7PMF9	Q7pmf9 anophelies
15	69	35.6	67	1 CKK CONVR	Q7y2s9 conus virgo
16	68	35.1	71	2 Q9UAA9	Q9uaa9 conus livid
17	66	34.0	71	2 Q9UAB3	Q9uab3 conus livid
18	65	33.5	71	2 Q9TW08	Q9tw08 conus livid
19	65	33.5	71	2 Q9UAA0	Q9uaa0 conus livid
20	65	33.5	71	2 Q9UAA1	Q9uaa1 conus livid
21	65	33.5	71	2 Q9UAA6	Q9uaa6 conus livid
22	65	33.5	71	2 Q9UAA8	Q9uaa8 conus livid
23	65	33.5	71	2 Q9UAB2	Q9uab2 conus livid
24	64.5	33.2	76	2 Q9BFP3	Q9bfp3 conus ventr
25	64	33.0	1064	1 FBPI STRPU	P10079 strongyloce
26	63	32.5	233	2 Q946Y8	Q946y8 hordeum vul
27	62.5	32.2	80	2 Q9BPF5	Q9bpf5 conus arena
28	62	32.0	77	2 Q75WH6	Q75wh6 macrothale
29	61.5	31.7	77	2 Q75WH3	Q75wh3 macrothale
30	61.5	31.7	494	2 Q6FNU8	Q6fnu8 candida gla
31	61.5	31.7	496	2 Q6CL87	Q6cl87 kluyveromyc

32 60.5 31.2 406 2 Q25059 heliocidari  
33 60 30.9 328 2 Q6TVP0 Q6tvp0 orf virus.  
34 60 30.9 422 2 Q05790 Q05790 saccharomyc  
35 60 30.9 570 1 FBPI STRPU P49013 strongyloce  
36 59 30.4 419 2 Q8T0I9 Q8t0i9 drosophila  
37 59 30.4 419 2 Q9U3W8 Q9u3w8 drosophila  
38 59 30.4 1060 2 Q968S4 Q968s4 drosophila  
39 59 30.4 1060 2 Q9VM97 Q9vm97 drosophila  
40 59 30.4 1317 2 Q6IQ50 Q6iq50 homo sapien  
41 59 30.4 1529 2 Q7XLQ7 Q7xlg7 oryza sativ  
42 59 30.4 2471 1 NTC2 HUMAN Q04371 homo sapien  
43 58.5 30.2 34 1 CXGS-CONGE P15472 conus geogr  
44 58.5 30.2 72 2 Q9BFP5 Q9bfp5 conus ventr  
45 58.5 30.2 75 2 Q9BFP4 Q9bfp4 conus ventr

#### ALIGNMENTS

##### RESULT 1

TXJJA HADVE  
ID TXJJA HADVE STANDARD; PRT; 36 AA.  
AC P82227;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Janus-atracotoxin-Hv1a (J-ActX-Hv1a).  
OS Hadronyche versuta (Blue mountains funnel-web spider) (Attrax versutus).  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
OC Mygalomorphae; Hexathelidae; Hadronyche.  
OX NCBI\_TaxID=6904;  
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TXJJB HADVE  
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DT 30-MAY-2000 (Rel. 39, Created)  
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DE Janus-atracotoxin-Hv1b (J-ActX-Hv1b).  
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AC P82226;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Janus-atracotoxin-Hv1b (J-ActX-Hv1b).  
OS Hadronyche versuta (Blue mountains funnel-web spider) (Attrax versutus).  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
OC Mygalomorphae; Hexathelidae; Hadronyche.  
OX NCBI\_TaxID=6904;  
RN [1]  
RP SEQUENCE.

EMBL; AF089930;	AAD48185.1;	-
EMBL; AF089931;	AAD48186.1;	-
EMBL; AF089932;	AAD48187.1;	-
EMBL; AF089933;	AAD48188.1;	-
EMBL; AF089941;	AAD48196.1;	-
EMBL; AF089942;	AAD48197.1;	-
EMBL; AF089943;	AAD48198.1;	-
EMBL; AF089944;	AAD48199.1;	-
EMBL; AF089945;	AAD48200.1;	-
EMBL; AF089946;	AAD48201.1;	-
EMBL; AF089947;	AAD48202.1;	-
EMBL; AF089948;	AAD48203.1;	-
EMBL; AF089949;	AAD48204.1;	-
EMBL; AF089950;	AAD48205.1;	-
EMBL; AF089951;	AAD48206.1;	-
EMBL; AF089953;	AAD48208.1;	-
EMBL; AF089954;	AAD48209.1;	-
GO; GO:0005576;	C:extracellular;	IEA.
GO; GO:0008200;	F:ion channel inhibitor activity;	IEA.
GO; GO:0009405;	P:pathogenesis;	IEA.
InterPro; IPR004214;	Conotoxin.	
Pfam; PF02950;	Conotoxin; 1.	
NON TER	1	
SEQUENCE	72 AA; 7984 MW; B2057DDC87553B8D CRC64;	

Query Match                      37.6%; Score 73; DB 2; Length 72;  
 Best Local Similarity        46.4%; Pred. No. 0.18;  
 Matches     13; Conservative     4; Mismatches     9; Indels     2; Gaps     1;

2 KICTPAGVKCPAALPCCPGLRC--IGGV 27  
   | | | | : | | | : | | | : | | |  
 42 RTCSPAGEVCTSKSPCCCTGFLCSHIGGM 69

RESULT 4			
Q9UAA2	PRELIMINARY;	PRT;	72 AA.
ID			
Q9UAA2;			
AC			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DC	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Four-loop conotoxin LVWIA (Fragment).		
OS	Conus lividus.		
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;		
OC	Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;		
OC	Neogastropoda; Conoidea; Conidae; Conus.		
OX	NCBI_TaxID=89426;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99289555; PubMed=10359796; DOI=10.1073/pnas.96.12.6820;		
FT	Duda T.F. Jr., Palumbi S.R.;		
RA	"Molecular genetics of ecological diversification: duplication and		
RT	rapid evolution of toxin genes of the venomous gastropod Conus.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).		
DR	EMBL; AF089959; AAD48214.1;		
DR	GO; GO:0005576; C:extracellular;		
DR	GO; GO:0008200; F:ion channel inhibitor activity;		
DR	GO; GO:0009405; P:pathogenesis;		
DR	InterPro; IPR004214; Conotoxin.		
DR	Pfam; PF02950; Conotoxin; 1.		
FT	NON TER		
SQ	SEQUENCE        72 AA; 7924 MW; 74762D9C9193EB8B CRC64;		

Query Match                      37.6%; Score 73; DB 2; Length 72;  
 Best Local Similarity        46.4%; Pred. No. 0.18;  
 Matches     13; Conservative     4; Mismatches     9; Indels     2; Gaps     1;

2 KICTPAGVKCPAALPCCPGLRC--IGGV 27  
   | | | | : | | | : | | | : | | |  
 42 RTCSPAGEVCTSKSPCCCTGFLCSHIGGM 69

Q9UAA4	PRELIMINARY;	PRT;	72 AA.		
ID Q9UAA4					
AC Q9UAA4					
DT 01-MAY-2000	(TrEMBLrel. 13, Created)				
DT 01-MAY-2000	(TrEMBLrel. 13, Last sequence update)				
DT 01-OCT-2003	(TrEMBLrel. 25, Last annotation update)				
DE Four-loop conotoxin LVVIA (Fragment).					
DS Conus lividus.					
OS Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;					
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;					
OC Neogastropoda; Conoidea; Conidae; Conus.					
OX NCBI_TaxID=89426;					
RN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=99289555; PubMed=10359796; DOI=10.1073/pnas.96.12.6820;					
RA Duda T.F. Jr., Palumbi S.R.;					
RT "Molecular genetics of ecological diversification: duplication and					
RT rapid evolution of toxin genes of the venomous gastropod Conus.";					
RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823 (1999).					
DR EMBL; AF089912; AAD48210.1;					
DR GO; GO:0005576; C:extracellular; IEA.					
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.					
DR GO; GO:0009405; P:pathogenesis; IEA.					
DR InterPro; IPR004214; Conotoxin.					
DR Pfam; PF02950; Conotoxin; 1.					
PT NON TER	1				
SQ SEQUENCE	72 AA; 7998 MW; B4DE7DDC87553B8D CRC64;				
Query Match	37.6%; Score 73; DB 2; Length 72;				
Best Local Similarity	46.4%; Pred. No. 0.18;				
Matches	13; Conservative 4; Mismatches 9; Indels 2; Gaps 1;				
Qy	2 KICTPAGVKCPAALPCCPGLRG--IGGV 27				
Db	42 RTCSPAGEVCTSKEPCCTGFLCHTIGGM 69				
RESULT 6					
Q9UAA7	PRELIMINARY;	PRT;	72 AA.		
ID Q9UAA7					
AC Q9UAA7					
DT 01-MAY-2000	(TrEMBLrel. 13, Created)				
DT 01-MAY-2000	(TrEMBLrel. 13, Last sequence update)				
DT 01-OCT-2003	(TrEMBLrel. 25, Last annotation update)				
DE Four-loop conotoxin LVVIA (Fragment).					
DS Conus lividus.					
OS Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;					
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;					
OC Neogastropoda; Conoidea; Conidae; Conus.					
OX NCBI_TaxID=89426;					
RN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=99289555; PubMed=10359796; DOI=10.1073/pnas.96.12.6820;					
RA Duda T.F. Jr., Palumbi S.R.;					
RT "Molecular genetics of ecological diversification: duplication and					
RT rapid evolution of toxin genes of the venomous gastropod Conus.";					
RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823 (1999).					
DR EMBL; AF089912; AAD48167.1;					
DR GO; GO:0005576; C:extracellular; IEA.					
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.					
DR GO; GO:0009405; P:pathogenesis; IEA.					
DR InterPro; IPR004214; Conotoxin.					
DR Pfam; PF02950; Conotoxin; 1.					
PT NON TER	1				
SQ SEQUENCE	72 AA; 7970 MW; B7A0DDDC875533D8D CRC64;				
Query Match	37.6%; Score 73; DB 2; Length 72;				
Best Local Similarity	46.4%; Pred. No. 0.18;				
Matches	13; Conservative 4; Mismatches 9; Indels 2; Gaps 1;				
Qy	2 KICTPAGVKCPAALPCCPGLRG--IGGV 27				
Db	42 RTCSPAGEVCTSKEPCCTGFLCHTIGGM 69				

QY	2	KICTPAGVKCPAALPCCGPLRC--IGSV	27
	:	: ::   :	:
Db	42	RTCSPAGEVCTSKSPCTGFLCLSHIGM	69
	:	: ::   :	:
RESULT 9			
ID	-TXJC	HADVE	STANDARD; PRT; 37 AA.
AC	P82228;		
DT	30-MAY-2000	(Rel. 39, Created)	
DT	30-MAY-2000	(Rel. 39, Last sequence update)	
DT	25-OCT-2004	(Rel. 45, Last annotation update)	
DE	Janus-atracotoxin-Hv1c (J-ACTX-Hv1c).		
OS	Hadronyche versuta (Blue mountains funnel-web spider) (Atrax versutus),		
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;		
OC	Mygalomorphae; Hexathelidae; Hadronyche.		
OX	NCHI_TaxID=6904;		
[1]			
RN	SEQUENCE, FUNCTION, AND STRUCTURE BY NMR.		
RC	TISSUE=Venom;		
EX	MEDLINE=20343014; PubMed=10881200; DOI=10.1038/75921;		
RA	Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H.,		
RA	Nicholson G.M., Christie M.J., King G.F.;		
RT	"Discovery and characterization of a family of insecticidal		
RT	neurotoxins with a rare vicinal disulfide bridge.";		
RL	Nat. Struct. Biol. 7:505-513(2000).		
CC	- FUNCTION: Insecticidal neurotoxin.		
CC	- SUBCELLULAR LOCATION: Secreted.		
CC	- TISSUE SPECIFICITY: Expressed by the venom gland.		
DR	PDB; 1DL0; NMR; A=1-37.		
KW	3D-structure; Direct protein sequencing; Neurotoxin; Toxin.		
FT	DISULFID 3 17		
FT	DISULFID 10 22		
FT	DISULFID 13 14		
FT	DISULFID 16 32		
FT	-TURN 6 7		
FT	STRAND 9 9		
FT	TURN 18 19		
FT	STRAND 20 24		
FT	TURN 26 27		
FT	STRAND 30 34		
SQ	SEQUENCE 37 AA; 3768 MW; E4DDF046CC750FFC CRC64;		
	Query Match 37.4%; Score 72.5; DB 1; Length 37;		
	Best Local Similarity 46.9%; Pred. No. 0.11;		
	Matches 15; Conservative 0; Mismatches 16; Indels 1; Gaps 1;		
QY	3	ICTPAGVKCPAALPCCGPLRCIGGVNN-KVCR	33
	:	: ::   :	:
Db	2	ICTGDPRCAACGCCPGTSCAESNGVS YCR	33
	:	: ::   :	:
RESULT 10			
Q9UAA3			
ID	Q9UAA3	PRELIMINARY; PRT; 72 AA.	
AC	Q9UAA3;		
DT	01-MAY-2000	(TrEMBLrel. 13, Created)	
DT	01-MAY-2000	(TrEMBLrel. 13, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Four-loop conotoxin LVIVA (fragment).		
OS	Conus lividus.		
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;		
OC	Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypso gastropoda;		
OC	Neogastropoda; Conoidea; Conidae; Conus.		
OX	NCHI_TaxID=89426;		
[1]			
RN	SEQUENCE FROM N.A.		
RP	MEDLINE=99289555; PubMed=10359796; DOI=10.1073/pnas.96.12.6820;		
RA	Duda T.F. Jr., Palumbi S.R.;		
RT	"Molecular genetics of ecological diversification: duplication and		
RT	rapid evolution of toxin genes of the venomous gastropod Conus.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).		



RA Abi-Rached L., Pontarotti P., Lardelli M.;  
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole larvae;  
 RA Lardelli M.T.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Y12539; CAC19873.1; -;  
 DR HSP; P07207; IOT8.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0030154; P:cell differentiation; IEA.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
 DR InterPro; IPR008985; ConA like lec\_gl.  
 DR InterPro; IPR000345; CytC\_heme\_BS.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001438; EGF\_II.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR000800; Notch\_region.  
 DR Pfam; PF00023; Ank; 6.  
 DR Pfam; PF00008; EGF; 34.  
 DR Pfam; PF07645; EGF\_Ca; 2.  
 DR Pfam; PF00086; Notch; 3.  
 DR PRINTS; PR01415; ANKYRIN.  
 DR PRINTS; PR01452; NOTCH.  
 DR SMART; SM00248; ANK; 6.  
 DR SMART; SM00179; EGF\_Ca; 21.  
 DR SMART; SM00004; NL; 3.  
 DR PROSITE; PS50088; ANK\_REPEAT; 4.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 23.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; 34.  
 DR PROSITE; PS01186; EGF\_2; 28.  
 DR PROSITE; PS50026; EGF\_3; 36.  
 DR PROSITE; PS01187; EGF\_Ca; 22.  
 KW ANK repeat; EGF-like domain; Receptor.  
 SQ SEQUENCE 2524 AA; 270970 MW; C3CA57E306D23EC9 CRC64;

Query Match 37.1%; Score 72; DB 2; Length 2524;  
 Best Local Similarity 45.9%; Pred. No. 5.4;  
 Matches 17; Conservative 2; Mismatches 10; Indels 8; Gaps 2;  
 QY 4 CTPA-GVKCP-----AALPCCPGLCIGGVNKKVC 32  
 DB 768 CLPGYGVNCDINTDECA5NCPQNGRCCLDGVNYYVC 804

RESULT 13  
 TXCS\_PHONI STANDARD; PRT; 33 AA.  
 AC P84015;  
 DT 25-OCT-2004 (Rel. 45, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DE 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Venom protein PH10C5.  
 OS Phoneutria nigriventer (Brazilian armed spider).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
 OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.  
 OX NCBI\_TaxID=6918;  
 RN [1]  
 RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS  
 RC SPECTROMETRY.  
 RC TISSUE=Venom;  
 RA Richardson M., Pimenta A.M.C., Bemquerer M.P., Santoro M.M.,  
 RA Figueiredo S.G., Cordeiro M.N.;  
 RT "New peptide PH10C5 from venom of Brazilian armed spider Phoneutria  
 RT nigriventer has sequence similarities with snake disintegrins,  
 RT vasotocin-neurophysins and other spider toxins.";

RL Submitted (JUN-2004) to Swiss-Prot.  
 CC -!- FUNCTION: Non-toxic to mice.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.  
 CC -!- MASS SPECTROMETRY: MW=3672.7; METHOD=Electrospray; RANGE=1-33;  
 CC NOTE=Ref.1.  
 KW Direct protein sequencing.  
 SQ SEQUENCE 33 AA; 3679 MW; 77F1127D4785D6E1 CRC64;  
 Query Match 36.3%; Score 70.5; DB 1; Length 33;  
 Best Local Similarity 40.0%; Pred. No. 0.18;  
 Matches 12; Conservative 6; Mismatches 11; Indels 1; Gaps 1;  
 QY 4 CTPAGVKCPAALPCCPGLCIGGVNKKVC 33  
 DB 3 CAQKGKIC-HDIHCTNLKCVREGSNRVCR 31

RESULT 14  
 Q7PMF9 PRELIMINARY; PRT; 3775 AA.  
 ID Q7PMF9  
 AC Q7PMF9;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DE ENSANGP00000011881 (Fragment).  
 GN Name=ENSANGG00000009392;  
 OS Anopheles gambiae str. PEST.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.  
 OX NCBI\_TaxID=180454;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PEST;  
 RA Anopheles Genome Sequencing Consortium;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC EMBL; AAB01008980; EAA13897.2; -;  
 DR HSP; P16109; 1FSB.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
 DR InterPro; IPR000345; CytC\_heme\_BS.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR Pfam; PF00008; EGF; 3.  
 DR Pfam; PF07645; EGF\_Ca; 16.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 17.  
 DR PROSITE; PS00615; CYTOCHROME\_C; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 25.  
 DR PROSITE; PS50026; EGF\_3; 25.  
 DR PROSITE; PS01187; EGF\_Ca; 16.  
 KW EGF-like domain.  
 FT NON\_TER 1  
 FT NON\_TER 3775  
 SQ SEQUENCE 3775 AA; 396198 MW; 51C4106F6E9908F4 CRC64;

Query Match 35.8%; Score 69.5; DB 2; Length 3775;  
 Best Local Similarity 41.9%; Pred. No. 16;  
 Matches 13; Conservative 5; Mismatches 12; Indels 1; Gaps 1;  
 QY 3 ICT-PAGVKCPAALPCCPGLCIGGVNKKVC 32  
 DB 1353 VCTNPRQCQCGANMQCPGVCVGVGNLC 1383  
 RESULT 15  
 CXX\_CONV

```

ID  CKX CONVR  STANDARD;  PRT;  67 AA.
AC  Q7YZS9;
DT  29-MAR-2004 (Rel. 43, Created)
DT  29-MAR-2004 (Rel. 43, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Kappa-conotoxin VITx precursor.
GN  Name=VITX;
OS  Conus virgo (Virgin cone).
OC  Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC  Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC  Neogastropoda; Conoidea; Conidae; Conus.
OX  NCBI_TaxID=89427;
RN  [1]
RP  SEQUENCE FROM N.A., SEQUENCE OF 27-53, SYNTHESIS OF 27-60, AND MASS
RP  SPECTROMETRY.
RC  TISSUE=Venom, and Venom duct;
RX  PubMed=1289360; DOI=10.1016/S0041-0101(03)00099-0;
RA  Kaferstein S., Huys I., Lamthanh H., Stocklin R., Sotto F., Menez A.,
RA  Tytgat J., Mebs D.;
RT  "A novel conotoxin inhibiting vertebrate voltage-sensitive potassium
RT  channels.";
RL  Toxicon 42:43-52(2003).
RN  [2]
RP  SEQUENCE FROM N.A.
RP  TISSUE=Venom duct;
RC  Kaferstein S.;
RL  Theis (2001), University of Darmstadt, Germany.
CC  -!- FUNCTION: Kappa-conotoxins bind and inhibit voltage-sensitive
CC  potassium channels. This toxin inhibits the vertebrate potassium
CC  channels Kv1.1 and Kv1.3, but not Kv1.2. It has no effect on HERG-
CC  type channels, sodium hH1 channels and Kir-type channels (IRK1).
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC  -!- PTM: Contains four disulfide bonds.
CC  -!- MASS SPECTROMETRY: MW=3933.3; METHOD=Electrospray; RANGE=27-60;
CC  NOTE=Ref.1.
CC  -!- SIMILARITY: Belongs to the conotoxin O-superfamily. Kappa-type
CC  family.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AJ560778; CAD90965.1; -.
KW  Direct protein sequencing; Signal; Toxin.
FT  SIGNAL 1 26
FT  CHAIN 27 60 Kappa-conotoxin VITx.
FT  PROPEP 61 67
FT  CONFLICT 38 38 P -> S (in Ref. 1).
FT  CONFLICT 49 49 G -> S (in Ref. 1).
SQ  SEQUENCE 67 AA; 7599 MW; 46671D012446F62D CRC64;

Query Match 35.6%; Score 69; DB 1; Length 67;
Best Local Similarity 44.8%; Pred. No. 0.51;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY 4 CTPAGVKCPALPCCPGLRCITGGVNNKVC 32
DB 29 CFPFGIYCTPYLPCCWGICC--GTCRNVC 55

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Search completed: February 14, 2005, 20:40:16  
 Job time : 4.72277 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:22:09 ; Search time 2.75816 Seconds  
(without alignments)  
3909.384 Million cell updates/sec

Title: US-10-019-823B-2

Perfect score: 194

Sequence: 1 GKICTPAGVKCPAALPCCPLRCIGGVNNKVC 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA.\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
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- 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
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- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
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- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	42.3	36	9 US-09-894-882-3	Sequence 3, Appli
2	79	40.7	36	9 US-09-894-882-4	Sequence 4, Appli
3	73	37.6	35	14 US-10-072-602B-571	Sequence 571, App
4	73	37.6	82	14 US-10-072-602B-140	Sequence 140, App
5	72.5	37.4	37	9 US-09-894-882-5	Sequence 5, Appli
6	69.5	35.8	30	14 US-10-072-602B-570	Sequence 570, App
7	69.5	35.8	77	14 US-10-072-602B-137	Sequence 137, App
8	69	35.6	31	9 US-09-894-882-461	Sequence 461, App
9	69	35.6	39	9 US-09-894-882-497	Sequence 497, App
10	69	35.6	67	9 US-09-894-882-247	Sequence 247, App
11	68	35.1	3501	14 US-10-123-155-37	Sequence 37, Appl
12	68	35.1	3501	14 US-10-146-731-37	Sequence 37, Appl
13	68	35.1	3501	14 US-10-140-472-37	Sequence 37, Appl

14	35.1	3501	14	US-10-141-761-37	Sequence 37, Appl
15	35.1	3501	14	US-10-142-885-37	Sequence 37, Appl
16	35.1	3501	14	US-10-158-790-37	Sequence 37, Appl
17	35.1	3501	15	US-10-137-871-37	Sequence 37, Appl
18	35.1	3501	15	US-10-140-923-37	Sequence 37, Appl
19	35.1	3501	15	US-10-141-756-37	Sequence 37, Appl
20	35.1	3501	15	US-10-141-759-37	Sequence 37, Appl
21	35.1	3501	15	US-10-140-805-37	Sequence 37, Appl
22	35.1	3501	15	US-10-140-864-37	Sequence 37, Appl
23	35.1	3501	15	US-10-142-426-37	Sequence 37, Appl
24	35.1	32	9	US-09-894-882-470	Sequence 470, App
25	34.5	32	14	US-10-072-602B-581	Sequence 581, App
26	34.5	40	9	US-09-894-882-498	Sequence 498, App
27	34.5	68	9	US-09-894-882-274	Sequence 274, App
28	34.5	79	14	US-10-072-602B-255	Sequence 255, App
29	33.5	77	14	US-10-072-602B-191	Sequence 191, App
30	33.5	2292	14	US-10-184-644-493	Sequence 493, App
31	33.5	2292	14	US-10-184-634-493	Sequence 493, App
32	64.5	86	15	US-10-424-599-240605	Sequence 240605, App
33	64	33.0	30	14 US-10-072-602B-576	Sequence 576, App
34	64	33.0	566	10 US-09-900-449A-6	Sequence 6, Appli
35	64	33.0	572	10 US-09-900-449A-7	Sequence 7, Appli
36	64	33.0	601	10 US-09-900-449A-5	Sequence 5, Appli
37	64	33.0	639	10 US-09-900-449A-4	Sequence 4, Appli
38	64	33.0	1064	14 US-10-173-461-5	Sequence 5, Appli
39	63	32.5	1971	14 US-10-123-155-139	Sequence 139, App
40	63	32.5	1971	14 US-10-146-731-139	Sequence 139, App
41	63	32.5	1971	14 US-10-140-472-139	Sequence 139, App
42	63	32.5	1971	14 US-10-141-761-139	Sequence 139, App
43	63	32.5	1971	14 US-10-142-885-139	Sequence 139, App
44	63	32.5	1971	14 US-10-158-790-139	Sequence 139, App
45	63	32.5	1971	15 US-10-137-871-139	Sequence 139, App

#### ALIGNMENTS

RESULT 1  
US-09-894-882-3  
; Sequence 3, Application US/09894882  
; Patent No. US20020102607A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jimenez, Elsie C.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: Watkins, Maren  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Shen, Greg S.  
; TITLE OF INVENTION: I-Superfamily Conotoxins  
; FILE REFERENCE: 2314-238  
; CURRENT APPLICATION NUMBER: US/09/894,882  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/243,410  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/246,581  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: US 60/247,714  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/264,256  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Hadronyche versuta  
US-09-894-882-3



; APPLICANT: McIntosh, J. Michael  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: Watkins, Maren  
 ; APPLICANT: Jones, Robert M.  
 ; APPLICANT: Shen, Greg S.  
 ; TITLE OF INVENTION: I-Superfamily Conotoxins  
 ; FILE REFERENCE: 2314-238  
 ; CURRENT APPLICATION NUMBER: US/09/894,882  
 ; CURRENT FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: US 60/  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: US 60/243,410  
 ; PRIOR FILING DATE: 2000-10-27  
 ; PRIOR APPLICATION NUMBER: US 60/246,581  
 ; PRIOR FILING DATE: 2000-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/247,714  
 ; PRIOR FILING DATE: 2000-11-14  
 ; PRIOR APPLICATION NUMBER: US 60/264,256  
 ; PRIOR FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS: 506  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 5  
 ; LENGTH: 37  
 ; TYPE: PRT  
 ; ORGANISM: Hadronyche versuta  
 ; US-09-894-882-5  
 Query Match 37.4%; Score 72.5; DB 9; Length 37;  
 Best Local Similarity 46.9%; Pred. No. 0.27;  
 Matches 15; Conservative 0; Mismatches 16; Indels 1; Gaps 1;  
 QY 3 ICTPAGVKCPAALPCCPGRLRCIGGVNN-KVCR 33  
 DB 2 ICTGADRPCAACCCPCPGTCKAESNGVGYCR 33  
 RESULT 6  
 US-10-072-602B-570  
 ; Sequence 570, Application US/10072602B  
 ; Publication No. US20030109670A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; APPLICANT: Cognetix, Inc.  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: McIntosh, J. Michael  
 ; APPLICANT: Watkins, Maren  
 ; APPLICANT: Garrett, James E.  
 ; APPLICANT: Cruz, Lourdes J.  
 ; APPLICANT: Grilley, Michelle  
 ; APPLICANT: Schoenfeld, Robert M.  
 ; APPLICANT: Walker, Craig  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Jones, Robert M.  
 ; TITLE OF INVENTION: Cone Snail Peptides  
 ; FILE REFERENCE: 2314-249  
 ; CURRENT APPLICATION NUMBER: US/10/072,602B  
 ; CURRENT FILING DATE: 2002-02-11  
 ; PRIOR APPLICATION NUMBER: US 60/267,408  
 ; PRIOR FILING DATE: 2001-02-09  
 ; NUMBER OF SEQ ID NOS: 638  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 570  
 ; LENGTH: 30  
 ; TYPE: PRT  
 ; ORGANISM: Conus lividus  
 ; US-10-072-602B-570  
 Query Match 35.8%; Score 69.5; DB 14; Length 30;  
 Best Local Similarity 44.8%; Pred. No. 0.49;  
 Matches 13; Conservative 2; Mismatches 13; Indels 1; Gaps 1;  
 QY 4 CTPAGVKCPAALPCCPGRLRCIGGVNNKYC 32  
 DB 4 CTPAGVKCPAALPCCPGRLRCIGGVNNKYC 32  
 RESULT 7  
 US-10-072-602B-137  
 ; Sequence 137, Application US/10072602B  
 ; Publication No. US20030109670A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; APPLICANT: Cognetix, Inc.  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: McIntosh, J. Michael  
 ; APPLICANT: Watkins, Maren  
 ; APPLICANT: Garrett, James E.  
 ; APPLICANT: Cruz, Lourdes J.  
 ; APPLICANT: Grilley, Michelle  
 ; APPLICANT: Schoenfeld, Robert M.  
 ; APPLICANT: Walker, Craig  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Jones, Robert M.  
 ; TITLE OF INVENTION: Cone Snail Peptides  
 ; FILE REFERENCE: 2314-249  
 ; CURRENT APPLICATION NUMBER: US/10/072,602B  
 ; CURRENT FILING DATE: 2002-02-11  
 ; PRIOR APPLICATION NUMBER: US 60/267,408  
 ; PRIOR FILING DATE: 2001-02-09  
 ; NUMBER OF SEQ ID NOS: 638  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 137  
 ; LENGTH: 77  
 ; TYPE: PRT  
 ; ORGANISM: Conus lividus  
 ; US-10-072-602B-137  
 Query Match 35.8%; Score 69.5; DB 14; Length 77;  
 Best Local Similarity 44.8%; Pred. No. 1.1;  
 Matches 13; Conservative 2; Mismatches 13; Indels 1; Gaps 1;  
 QY 4 CTPAGVKCPAALPCCPGRLRCIGGVNNKYC 32  
 DB 49 CCHSGAGC-YTRPCPGHLHCSGGGAGGLC 76  
 RESULT 8  
 US-09-894-882-461  
 ; Sequence 461, Application US/09894882  
 ; Patent No. US20020102607A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; APPLICANT: Cognetix, Inc.  
 ; APPLICANT: Walker, Craig S.  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Jimenez, Elsie C.  
 ; APPLICANT: McIntosh, J. Michael  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: Watkins, Maren  
 ; APPLICANT: Jones, Robert M.  
 ; APPLICANT: Shen, Greg S.  
 ; TITLE OF INVENTION: I-Superfamily Conotoxins  
 ; FILE REFERENCE: 2314-238  
 ; CURRENT APPLICATION NUMBER: US/09/894,882  
 ; CURRENT FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: US 60/  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: US 60/243,410  
 ; PRIOR FILING DATE: 2000-10-27  
 ; PRIOR APPLICATION NUMBER: US 60/246,581  
 ; PRIOR FILING DATE: 2000-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/247,714  
 ; PRIOR FILING DATE: 2000-11-14  
 ; PRIOR APPLICATION NUMBER: US 60/264,256  
 ; PRIOR FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS: 506

; APPLICANT: McIntosh, J. Michael  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: Watkins, Maren  
 ; APPLICANT: Jones, Robert M.  
 ; APPLICANT: Shen, Greg S.  
 ; TITLE OF INVENTION: I-Superfamily Conotoxins  
 ; FILE REFERENCE: 2314-238  
 ; CURRENT APPLICATION NUMBER: US/09/894,882  
 ; CURRENT FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: US 60/  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: US 60/243,410  
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 ; PRIOR APPLICATION NUMBER: US 60/246,581  
 ; PRIOR FILING DATE: 2000-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/247,714  
 ; PRIOR FILING DATE: 2000-11-14  
 ; PRIOR APPLICATION NUMBER: US 60/264,256  
 ; PRIOR FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS: 506  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 5  
 ; LENGTH: 37  
 ; TYPE: PRT  
 ; ORGANISM: Hadronyche versuta  
 ; US-09-894-882-5  
 Query Match 37.4%; Score 72.5; DB 9; Length 37;  
 Best Local Similarity 46.9%; Pred. No. 0.27;  
 Matches 15; Conservative 0; Mismatches 16; Indels 1; Gaps 1;  
 QY 3 ICTPAGVKCPAALPCCPGRLRCIGGVNN-KVCR 33  
 DB 2 ICTGADRPACCAACCPCCPGTCKAESNGVGYCR 33  
 RESULT 6  
 US-10-072-602B-570  
 ; Sequence 570, Application US/10072602B  
 ; Publication No. US20030109670A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; APPLICANT: Cognetix, Inc.  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: McIntosh, J. Michael  
 ; APPLICANT: Watkins, Maren  
 ; APPLICANT: Garrett, James E.  
 ; APPLICANT: Cruz, Lourdes J.  
 ; APPLICANT: Grille, Michelle  
 ; APPLICANT: Schoenfeld, Robert M.  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Jones, Robert M.  
 ; TITLE OF INVENTION: Cone Snail Peptides  
 ; FILE REFERENCE: 2314-249  
 ; CURRENT APPLICATION NUMBER: US/10/072,602B  
 ; CURRENT FILING DATE: 2002-02-11  
 ; PRIOR APPLICATION NUMBER: US 60/267,408  
 ; PRIOR FILING DATE: 2001-02-09  
 ; NUMBER OF SEQ ID NOS: 638  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 570  
 ; LENGTH: 30  
 ; TYPE: PRT  
 ; ORGANISM: Conus lividus  
 ; US-10-072-602B-570  
 Query Match 35.8%; Score 69.5; DB 14; Length 30;  
 Best Local Similarity 44.8%; Pred. No. 0.49;  
 Matches 13; Conservative 2; Mismatches 13; Indels 1; Gaps 1;  
 QY 4 CTPAGVKCPAALPCCPGRLRCIGGVNNKYC 32  
 DB 4 CTPAGVKCPAALPCCPGRLRCIGGVNNKYC 32  
 RESULT 7  
 US-10-072-602B-137  
 ; Sequence 137, Application US/10072602B  
 ; Publication No. US20030109670A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; APPLICANT: Cognetix, Inc.  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: McIntosh, J. Michael  
 ; APPLICANT: Watkins, Maren  
 ; APPLICANT: Garrett, James E.  
 ; APPLICANT: Cruz, Lourdes J.  
 ; APPLICANT: Grille, Michelle  
 ; APPLICANT: Schoenfeld, Robert M.  
 ; APPLICANT: Walker, Craig  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Jones, Robert M.  
 ; TITLE OF INVENTION: Cone Snail Peptides  
 ; FILE REFERENCE: 2314-249  
 ; CURRENT APPLICATION NUMBER: US/10/072,602B  
 ; CURRENT FILING DATE: 2002-02-11  
 ; PRIOR APPLICATION NUMBER: US 60/267,408  
 ; PRIOR FILING DATE: 2001-02-09  
 ; NUMBER OF SEQ ID NOS: 638  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 137  
 ; LENGTH: 77  
 ; TYPE: PRT  
 ; ORGANISM: Conus lividus  
 ; US-10-072-602B-137  
 Query Match 35.8%; Score 69.5; DB 14; Length 77;  
 Best Local Similarity 44.8%; Pred. No. 1.1;  
 Matches 13; Conservative 2; Mismatches 13; Indels 1; Gaps 1;  
 QY 4 CTPAGVKCPAALPCCPGRLRCIGGVNNKYC 32  
 DB 49 CCHSGAGC-YTRPCPGHLHCSGGAGGLC 76  
 RESULT 8  
 US-09-894-882-461  
 ; Sequence 461, Application US/09894882  
 ; Patent No. US20020102607A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; APPLICANT: Cognetix, Inc.  
 ; APPLICANT: Walker, Craig S.  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Jimenez, Elsie C.  
 ; APPLICANT: McIntosh, J. Michael  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: Watkins, Maren  
 ; APPLICANT: Jones, Robert M.  
 ; APPLICANT: Shen, Greg S.  
 ; TITLE OF INVENTION: I-Superfamily Conotoxins  
 ; FILE REFERENCE: 2314-238  
 ; CURRENT APPLICATION NUMBER: US/09/894,882  
 ; CURRENT FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: US 60/  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: US 60/243,410  
 ; PRIOR FILING DATE: 2000-10-27  
 ; PRIOR APPLICATION NUMBER: US 60/246,581  
 ; PRIOR FILING DATE: 2000-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/247,714  
 ; PRIOR FILING DATE: 2000-11-14  
 ; PRIOR APPLICATION NUMBER: US 60/264,256  
 ; PRIOR FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS: 506

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 461
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-461

Query Match      35.6%; Score 69; DB 9; Length 31;
Best Local Similarity 44.8%; Pred. No. 0.57;
Matches 13; Conservative 2; Mismatches 12; Indels 1; Gaps 1;

QY      4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
Db      1 CFPFGIYCTPYLPCCGWICG--GTCRNV 27

RESULT 9
US-09-894-882-497
; Sequence 497, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reehma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Robert M.
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

Query Match      35.6%; Score 69; DB 9; Length 39;
Best Local Similarity 44.8%; Pred. No. 0.7;
Matches 13; Conservative 2; Mismatches 12; Indels 1; Gaps 1;

QY      4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
Db      1 CFPFGIYCTPYLPCCGWICG--GTCRNV 27

RESULT 10
US-09-894-882-247
; Sequence 247, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reehma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

Query Match      35.6%; Score 69; DB 9; Length 39;
Best Local Similarity 44.8%; Pred. No. 0.7;
Matches 13; Conservative 2; Mismatches 12; Indels 1; Gaps 1;

QY      4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
Db      1 CFPFGIYCTPYLPCCGWICG--GTCRNV 27

RESULT 11
US-10-123-155-37
; Sequence 37, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 37
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2762, 2778
; OTHER INFORMATION: unknown base
US-10-123-155-37

; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-247

Query Match      35.6%; Score 69; DB 9; Length 67;
Best Local Similarity 44.8%; Pred. No. 1.1;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY      4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32
Db      29 CFPFGIYCTPYLPCCGWICG--GTCRNV 55
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Query Match 35.1%; Score 68; DB 14; Length 3501;  
Best Local Similarity 46.2%; Pred. No. 50;  
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCGRLRCIGG 26  
DB 888 GACCAAAGTACCAAGCCTGTGCTGG 913

## RESULT 12

US-10-146-731-37

; Sequence 37, Application US/10146731

; Publication No. US20030129692A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330R1C323

; CURRENT APPLICATION NUMBER: US/10/146,731

; CURRENT FILING DATE: 2002-05-15

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 37

; LENGTH: 3501

; TYPE: DNA

; ORGANISM: Homo Sapien

; NAME/KEY: unsure

; LOCATION: 2762, 2778

; OTHER INFORMATION: unknown base

US-10-146-731-37

Query Match 35.1%; Score 68; DB 14; Length 3501;  
Best Local Similarity 46.2%; Pred. No. 50;  
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCGRLRCIGG 26  
DB 888 GACCAAAGTACCAAGCCTGTGCTGG 913

## RESULT 13

US-10-140-472-37

; Sequence 37, Application US/10140472

; Publication No. US20030138888A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C168  
; CURRENT APPLICATION NUMBER: US/10/140,472  
; CURRENT FILING DATE: 2002-05-06  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 37  
; LENGTH: 3501  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; NAME/KEY: unsure  
; LOCATION: 2762, 2778  
; OTHER INFORMATION: unknown base  
US-10-140-472-37

Query Match 35.1%; Score 68; DB 14; Length 3501;  
Best Local Similarity 46.2%; Pred. No. 50;  
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCGRLRCIGG 26  
DB 888 GACCAAAGTACCAAGCCTGTGCTGG 913

## RESULT 14

US-10-141-761-37

; Sequence 37, Application US/10141761

; Publication No. US20030148432A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330R1C198

; CURRENT APPLICATION NUMBER: US/10/141,761

; CURRENT FILING DATE: 2002-05-08

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 37

; LENGTH: 3501

; TYPE: DNA

; ORGANISM: Homo Sapien

; NAME/KEY: unsure

; LOCATION: 2762, 2778

; OTHER INFORMATION: unknown base  
US-10-141-761-37

Query Match 35.1%; Score 68; DB 14; Length 3501;

Best Local Similarity 46.2%; Pred. No. 50;  
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCGRLRCIGG 26  
DB 888 GACCAAGTACCCAAAGCCTGTGCTGG 913

RESULT 15  
US-10-142-885-37  
; Sequence 37, Application US/10142885  
; Publication No. US20030157604A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C248  
; CURRENT APPLICATION NUMBER: US/10/142,885  
; CURRENT FILING DATE: 2002-05-10  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 37  
; LENGTH: 3501  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 2762, 2778  
; OTHER INFORMATION: unknown base  
US-10-142-885-37

Query Match 35.1%; Score 68; DB 14; Length 3501;  
Best Local Similarity 46.2%; Pred. No. 50;  
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCGRLRCIGG 26  
DB 888 GACCAAGTACCCAAAGCCTGTGCTGG 913

Search completed: February 14, 2005, 20:56:33  
Job time : 3.75816 secs



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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:24:54 ; Search time 1.02489 Seconds  
(without alignments)  
2403.590 Million cell updates/sec

Title: US-10-019-823B-2  
Perfect score: 194  
Sequence: 1 GK1CTPAGVKCPAALPCCPGLRCIGGVNNKVC 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	42.3	36	4	US-09-894-882-3
2	79	40.7	36	4	US-09-894-882-4
3	75	38.7	36	1	US-08-682-485A-7
4	75	38.7	36	2	US-08-933-314-7
5	75	38.7	37	1	US-08-682-485A-6
6	75	38.7	37	2	US-08-933-314-6
7	72.5	37.4	37	4	US-09-894-882-5
8	69	35.6	31	4	US-09-894-882-461
9	69	35.6	39	4	US-09-894-882-497
10	69	35.6	67	4	US-09-894-882-247
11	67	34.5	32	4	US-09-894-882-470
12	67	34.5	40	4	US-09-894-882-498
13	67	34.5	68	4	US-09-894-882-274
14	59	30.4	155	4	US-09-252-991A-28474
15	59	30.4	211	4	US-09-902-540-15694
16	59	30.4	2471	1	US-08-185-432-16
17	59	30.4	2471	1	US-08-083-590A-19
18	59	30.4	2471	3	US-08-532-384-19
19	59	30.4	2471	4	US-08-899-232-1
20	59	30.4	2471	4	US-09-121-457-1
21	58.5	30.2	34	1	US-08-117-080-5
22	58.5	30.2	34	1	US-08-471-329-5
23	58.5	30.2	34	2	US-08-915-142-5
24	58.5	30.2	908	4	US-08-714-741-44
25	58	29.9	39	4	US-09-894-882-248
26	57.5	29.6	180	4	US-09-510-238A-286
27	57.5	29.6	281	4	US-09-252-991A-23962

28 57.5 29.6 420 4 US-09-907-794A-109 Sequence 109, App  
29 57.5 29.6 420 4 US-09-905-125A-109 Sequence 109, App  
30 57.5 29.6 420 4 US-09-902-775A-109 Sequence 109, App  
31 57.5 29.6 420 4 US-09-906-700-109 Sequence 109, App  
32 57.5 29.6 420 4 US-09-903-603A-109 Sequence 109, App  
33 57.5 29.6 420 4 US-09-904-920A-109 Sequence 109, App  
34 57.5 29.6 420 4 US-09-909-064-109 Sequence 109, App  
35 57.5 29.6 420 4 US-09-905-381A-109 Sequence 109, App  
36 57.5 29.6 420 4 US-09-906-618-109 Sequence 109, App  
37 57 29.4 259 3 US-09-161-241-11 Sequence 11, Appl  
38 57 29.4 493 4 US-09-252-991A-16925 Sequence 16925, A  
39 56.5 29.1 30 4 US-09-894-882-474 Sequence 474, App  
40 56.5 29.1 44 4 US-09-894-882-296 Sequence 296, App  
41 56.5 29.1 44 4 US-09-894-882-502 Sequence 502, App  
42 56.5 29.1 70 4 US-09-894-882-295 Sequence 295, App  
43 56 28.9 642 3 US-08-872-855-10 Sequence 10, Appl  
44 56 28.9 2732 4 US-09-086-436-30 Sequence 30, Appl  
45 55.5 28.6 161 4 US-10-293-622-4 Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-09-894-882-3  
; Sequence 3, Application US/09894882  
; Patent No. 6767895

GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jimenez, Elsie C.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: Watkins, Maren  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Shen, Greg S.  
; TITLE OF INVENTION: I-Superfamily Conotoxins  
; FILE REFERENCE: 2314-238  
; CURRENT APPLICATION NUMBER: US/09/894,882  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/243,410  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/246,581  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: US 60/247,714  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/264,256  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Hadronyche versuta

US-09-894-882-3  
Query Match 42.3%; Score 82; DB 4; Length 36;  
Best Local Similarity 51.5%; Pred. No. 0.0044;  
Matches 17; Conservative 1; Mismatches 13; Indels 2; Gaps 1;

QY 3 ICTPAGVKCPAALPCCPGLRCIGGVNNKV--CR 33  
DB 2 ICTGDRPCAACCPCPGTSCQGPESNGVYCR 34

RESULT 2  
US-09-894-882-4  
; Sequence 4, Application US/09894882  
; Patent No. 6767895

Query Match 38.7%; Score 75; DB 1; Length 36;  
Best Local Similarity 50.0%; Pred. No. 0.029;  
Matches 16: Conservative 0; Mismatches 14; Indels

US-09-894-882-4

Query Match 38.7%; Score 75; DB 1; Length 36;  
Best Local Similarity 50.0%; Pred. No. 0.029;  
Matches 16: Conservative 0; Mismatches 14; Indels

Qy	4	CTPAGVKCPAALPCCPLRCITGGVNNKV--CR	33
Db	4	CTGADRPCCAACCPCCPGTSCKGPEPNGVSYCR	35

RESULT 4  
US-08-933-314-7  
; Sequence 7, Application US/08933314  
; Patent No. 5959182  
; GENERAL INFORMATION:  
; APPLICANT: ATKINSON, RONALD K  
; APPLICANT: HOWDEN, MERLIN E.H.  
; APPLICANT: TYLER, MARGARET I  
; APPLICANT: VONARX, EDWARD J  
; TITLE OF INVENTION: Insecticidal Toxins Derived From  
; TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Zeneca, Inc.  
; STREET: 1200 South 47th Street  
; CITY: Richmond  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/933,314  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/682,485  
; FILING DATE: 17-JULY-1995  
; APPLICATION NUMBER: US/08/256,933  
; FILING DATE: 27-JULY-1994  
; APPLICATION NUMBER: WO 93/15108  
; FILING DATE: 29-JAN-1993  
; APPLICATION NUMBER: AU PL0722  
; FILING DATE: 31-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Shaw, Melissa A.

REGISTRATION NUMBER: 38,301  
REFERENCE/DOCKET NUMBER: PPD 5099/D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-231-1542  
TELEFAX: 510-231-1112  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Atrax formidabilis  
US-08-933-314-7

Query Match 38.7%; Score 75; DB 2; Length 36;  
Best Local Similarity 50.0%; Pred. No. 0.029;  
Matches 16; Conservative 0; Mismatches 14; Indels 2; Gaps 1;  
QY 4 CTGAGVCKPAALPCCPGLCIGGVNNKV--CR 33  
DB 4 CTGADRPCAACCCPGTSCCKGPEPNGSVYCR 35

RESULT 5  
US-08-682-485A-6  
Sequence 6, Application US/08682485A  
Patent No. 5763568  
GENERAL INFORMATION:  
APPLICANT: ATKINSON, RONALD K  
APPLICANT: HOWDEN, MERLIN E.H.  
APPLICANT: TYLER, MARGARET I  
APPLICANT: VONARX, EDWARD J  
TITLE OF INVENTION: Insecticidal Toxins Derived From  
FUNNEL WEB (ATRAX OR HADRONYCHE SPIDERS)  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zeneca, Inc.  
STREET: 1200 South 47th Street  
CITY: Richmond  
STATE: California  
COUNTRY: USA  
ZIP: 94804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/682,485A  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/682,485  
FILING DATE: 17-JULY-1996  
APPLICATION NUMBER: US/08/256,933  
FILING DATE: 27-JULY-1994  
APPLICATION NUMBER: WO 93/15108  
FILING DATE: 29-JAN-1993  
APPLICATION NUMBER: AU PL0722  
FILING DATE: 31-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Shaw, Melissa A.  
REGISTRATION NUMBER: 38,301  
REFERENCE/DOCKET NUMBER: PPD 5099/D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-231-1542  
TELEFAX: 510-231-1112  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Atrax formidabilis  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 37  
OTHER INFORMATION: /label=a  
OTHER INFORMATION: /note="this site may be amidated without loss  
of biological activity"  
US-08-682-485A-6

Query Match 38.7%; Score 75; DB 1; Length 37;  
Best Local Similarity 50.0%; Pred. No. 0.029;  
Matches 16; Conservative 0; Mismatches 14; Indels 2; Gaps 1;  
QY 4 CTGAGVCKPAALPCCPGLCIGGVNNKV--CR 33  
DB 4 CTGADRPCAACCCPGTSCCKGPEPNGSVYCR 35

RESULT 6  
US-08-933-314-6  
Sequence 6, Application US/08933314  
Patent No. 5959182  
GENERAL INFORMATION:  
APPLICANT: ATKINSON, RONALD K  
APPLICANT: HOWDEN, MERLIN E.H.  
APPLICANT: TYLER, MARGARET I  
APPLICANT: VONARX, EDWARD J  
TITLE OF INVENTION: Insecticidal Toxins Derived From  
FUNNEL WEB (ATRAX OR HADRONYCHE SPIDERS)  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zeneca, Inc.  
STREET: 1200 South 47th Street  
CITY: Richmond  
STATE: California  
COUNTRY: USA  
ZIP: 94804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,314  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/682,485  
FILING DATE: 17-JULY-1996  
APPLICATION NUMBER: US/08/256,933  
FILING DATE: 27-JULY-1994  
APPLICATION NUMBER: WO 93/15108  
FILING DATE: 29-JAN-1993  
APPLICATION NUMBER: AU PL0722  
FILING DATE: 31-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Shaw, Melissa A.  
REGISTRATION NUMBER: 38,301  
REFERENCE/DOCKET NUMBER: PPD 5099/D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-231-1542  
TELEFAX: 510-231-1112  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Atrax formidabilis  
FEATURE: Modified-site  
LOCATION: 37  
OTHER INFORMATION: /label= a  
OTHER INFORMATION: /note= "this site may be amidated without loss  
of biological activity"  
US-08-933-314-6

Query Match 38.7%; Score 75; DB 2; Length 37;  
Best Local Similarity 50.0%; Pred. No. 0.029;  
Matches 16; Conservative 0; Mismatches 14; Indels 2; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGRLRCIGGVNKKV--CR 33  
DB 4 CTGADRPCAACCCPGTSCGKPGPENGVS YCR 35

RESULT 7  
US-09-894-882-5  
Sequence 5, Application US/09894882  
Patent No. 6767895  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Walker, Craig S.  
APPLICANT: Shetty, Reshma  
APPLICANT: Jimenez, Elsie C.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Watkins, Maren  
APPLICANT: Jones, Robert M.  
APPLICANT: Shen, Greg S.  
TITLE OF INVENTION: I-Superfamily Conotoxins  
FILE REFERENCE: 2314-238  
CURRENT APPLICATION NUMBER: US/09/894,882  
CURRENT FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: US 60/  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 60/243,410  
PRIOR FILING DATE: 2000-10-27  
PRIOR APPLICATION NUMBER: US 60/246,581  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: US 60/247,714  
PRIOR FILING DATE: 2000-11-14  
PRIOR APPLICATION NUMBER: US 60/264,256  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 5  
LENGTH: 37  
TYPE: PRT  
ORGANISM: Hadronyche versuta  
US-09-894-882-5

Query Match 37.4%; Score 72.5; DB 4; Length 37;  
Best Local Similarity 46.9%; Pred. No. 0.057;  
Matches 15; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 3 ICTPAGVKCPAALPCCPGRLRCIGGVN--KVCR 33  
DB 2 ICTGADRPCAACCCPGTSCGKPGPENGVS YCR 33

RESULT 8  
US-09-894-882-461  
Sequence 461, Application US/09894882  
Patent No. 6767895  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Walker, Craig S.  
APPLICANT: Shetty, Reshma  
APPLICANT: Jimenez, Elsie C.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Watkins, Maren  
APPLICANT: Jones, Robert M.  
APPLICANT: Shen, Greg S.  
TITLE OF INVENTION: I-Superfamily Conotoxins  
FILE REFERENCE: 2314-238  
CURRENT APPLICATION NUMBER: US/09/894,882  
CURRENT FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: US 60/  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 60/243,410  
PRIOR FILING DATE: 2000-10-27  
PRIOR APPLICATION NUMBER: US 60/246,581  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: US 60/247,714  
PRIOR FILING DATE: 2000-11-14  
PRIOR APPLICATION NUMBER: US 60/264,256  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 5  
LENGTH: 37  
TYPE: PRT  
ORGANISM: Hadronyche versuta  
US-09-894-882-5

APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Walker, Craig S.  
APPLICANT: Shetty, Reshma  
APPLICANT: Jimenez, Elsie C.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Watkins, Maren  
APPLICANT: Jones, Robert M.  
APPLICANT: Shen, Greg S.  
TITLE OF INVENTION: I-Superfamily Conotoxins  
FILE REFERENCE: 2314-238  
CURRENT APPLICATION NUMBER: US/09/894,882  
CURRENT FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: US 60/  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 60/243,410  
PRIOR FILING DATE: 2000-10-27  
PRIOR APPLICATION NUMBER: US 60/246,581  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: US 60/247,714  
PRIOR FILING DATE: 2000-11-14  
PRIOR APPLICATION NUMBER: US 60/264,256  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 461  
LENGTH: 31  
TYPE: PRT  
ORGANISM: Conus emaciatus  
US-09-894-882-461

Query Match 35.6%; Score 69; DB 4; Length 31;  
Best Local Similarity 44.8%; Pred. No. 0.12;  
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGRLRCIGGVNKKV 32  
DB 1 CFPFGIYCTPYLPCCWGICC--GTCRNVC 27

RESULT 9  
US-09-894-882-497  
Sequence 497, Application US/09894882  
Patent No. 6767895  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Walker, Craig S.  
APPLICANT: Shetty, Reshma  
APPLICANT: Jimenez, Elsie C.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Watkins, Maren  
APPLICANT: Jones, Robert M.  
APPLICANT: Shen, Greg S.  
TITLE OF INVENTION: I-Superfamily Conotoxins  
FILE REFERENCE: 2314-238  
CURRENT APPLICATION NUMBER: US/09/894,882  
CURRENT FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: US 60/  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 60/243,410  
PRIOR FILING DATE: 2000-10-27  
PRIOR APPLICATION NUMBER: US 60/246,581  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: US 60/247,714  
PRIOR FILING DATE: 2000-11-14  
PRIOR APPLICATION NUMBER: US 60/264,256  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 497

Query Match 37.4%; Score 72.5; DB 4; Length 37;  
Best Local Similarity 46.9%; Pred. No. 0.057;  
Matches 15; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 3 ICTPAGVKCPAALPCCPGRLRCIGGVN--KVCR 33  
DB 2 ICTGADRPCAACCCPGTSCGKPGPENGVS YCR 33

```
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

Query Match          35.6%; Score 69; DB 4; Length 39;
Best Local Similarity 44.8%; Pred. No. 0.15;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGLCIGVNNKVC 32
   |||||:|||||:|||||:
Db 1 CRPPGIYCTPLPCCWGICC--GTCRNV 27
   |||||:|||||:|||||:

RESULT 10
US-09-894-882-247
; Sequence 247, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-247

Query Match          35.6%; Score 69; DB 4; Length 67;
Best Local Similarity 44.8%; Pred. No. 0.25;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGLCIGVNNKVC 32
   |||||:|||||:|||||:
Db 29 CRPPGIYCTPLPCCWGICC--GTCRNV 55
   |||||:|||||:|||||:

RESULT 11
US-09-894-882-470
; Sequence 470, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-247

Query Match          34.5%; Score 67; DB 4; Length 32;
Best Local Similarity 50.0%; Pred. No. 0.22;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 4 CTPAGVKCPAALPCCPGLCIG 25
   |||||:|||||:|||||:
Db 1 CFPGLTFCRSYLPCCGMCCSG 22
   |||||:|||||:|||||:

RESULT 12
US-09-894-882-498
; Sequence 498, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 498
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-498

Query Match          34.5%; Score 67; DB 4; Length 40;
Best Local Similarity 50.0%; Pred. No. 0.27;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
```

```

RESULT 14
US-09-252-991A-28474
; Sequence 28474, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28474
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28474

```

Search completed: February 14, 2005, 20:58:55  
Job time : 1.02489 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:20:21 ; Search time 4.51404 Seconds  
(without alignments)  
2827.419 Million cell updates/sec

Title: US-10-019-823B-2

Perfect score: 194

Sequence: 1 GKICTPAGVKCPAALPCCPGLRCIGGVNKKVCR 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	194	100.0	33	4	AAB66900 Insectici
2	194	100.0	33	6	AAB66900 Insectici
3	194	100.0	34	6	AAB66900 Insectici
4	194	100.0	34	6	AAB66900 Insectici
5	194	100.0	34	6	AAB66900 Insectici
6	194	100.0	34	6	AAB66900 Insectici
7	194	100.0	34	6	AAB66900 Insectici
8	194	100.0	34	6	AAB66900 Insectici
9	194	100.0	34	6	AAB66900 Insectici
10	194	100.0	34	6	AAB66900 Insectici
11	194	100.0	34	6	AAB66900 Insectici
12	194	100.0	34	6	AAB66900 Insectici
13	194	100.0	34	6	AAB66900 Insectici
14	194	100.0	34	6	AAB66900 Insectici
15	194	100.0	34	6	AAB66900 Insectici
16	194	100.0	34	6	AAB66900 Insectici
17	194	100.0	34	6	AAB66900 Insectici
18	194	100.0	34	6	AAB66900 Insectici
19	194	100.0	34	6	AAB66900 Insectici
20	194	100.0	34	6	AAB66900 Insectici
21	194	100.0	34	6	AAB66900 Insectici
22	194	100.0	34	6	AAB66900 Insectici
23	194	100.0	34	6	AAB66900 Insectici
24	194	100.0	35	4	AAB66900 Insectici
25	194	100.0	35	6	AAB66900 Insectici

26	194	100.0	35	6	AAB66900 Insectici
27	194	100.0	35	6	AAB66900 Insectici
28	183	94.3	33	4	AAB66900 Insectici
29	82	42.3	36	5	ABB88548 Janus fac
30	79	40.7	36	5	ABB88549 Janus fac
31	75	38.7	36	2	AAB66900 Insectici
32	75	38.7	37	2	AAB66900 Insectici
33	73	37.6	35	5	ABG99786 Conus sp
34	73	37.6	82	5	ABG99454 Conus sp
35	72.5	37.4	37	5	ABB88550 Janus fac
36	72.5	37.4	37	7	ADL11907 Atracotox
37	72	37.1	33	7	ADL11905 Raventoxi
38	69.5	35.8	30	5	ABG99785 Conus sp
39	69.5	35.8	77	5	ABG99452 Conus sp
40	69	35.6	31	5	ABB88889 Conus ema
41	69	35.6	39	5	ABB88925 Conus ema
42	69	35.6	67	5	ABB88713 Conus ema
43	69	35.6	2020	8	ADP31056 Human sec
44	67	34.5	32	5	ABB88898 Conus vir
45	67	34.5	32	5	ABG99796 Conus sp

ALIGNMENTS

RESULT 1  
AAB66900  
ID AAB66900 standard; peptide; 33 AA.  
XX  
AC AAB66900;  
XX  
DT 12-APR-2001 (first entry)  
XX  
DE Insecticidal protein #2.  
XX  
KW Insecticide; transgenic plant; insect-resistance.  
XX  
OS Paecilomyces sp.  
XX  
PN WO200100841-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-GB002457.  
XX  
PR 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX  
DR WPI; 2001-123015/13.  
XX  
PT Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
production.  
XX  
PS Claim 3; Page 30; 72pp; English.  
XX  
CC The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66900 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX  
SQ Sequence 33 AA;

Query Match 100.0%; Score 194; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1e-14;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33
Db 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33

RESULT 2
AAE36283
ID AAE36283 standard; peptide; 33 AA.
XX
AC AAE36283;
XX
DT 26-JUN-2003 (first entry)
XX
DE Paecilomyces farinosus insecticidal protein.
XX
KW Insecticidal protein; pesticide.
XX
OS Paecilomyces farinosus.
XX
PN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN ) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-
terminus, useful as an active ingredient of a pesticide.
XX
PS Claim 6; Page 23; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine
motif at the amino-terminus. Polynucleotide or DNA constructs of the
invention are useful for producing plants or plant parts that are
resistant to insects. The protein or synergistic combination is useful as
an active ingredient of a pesticide or for controlling insects.
Antibodies raised to the insecticidal proteins can be used to identify
other proteins with insecticidal activity. The present sequence is
insecticidal protein
XX
SQ Sequence 34 AA;
Query Match 100.0%; Score 194; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33
Db 2 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 34

RESULT 4
AAE36295
ID AAE36295 standard; peptide; 34 AA.
XX
AC AAE36295;
XX
DT 26-JUN-2003 (first entry)
XX
DE Insecticidal protein #25.
XX
KW Insecticidal protein; pesticide.
XX
OS Unidentified.
XX
PN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN ) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-
terminus, useful as an active ingredient of a pesticide.
XX
PS Example 1; Page 66; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine
motif at the amino-terminus. Polynucleotide or DNA constructs of the
invention are useful for producing plants or plant parts that are
resistant to insects. The protein or synergistic combination is useful as
an active ingredient of a pesticide or for controlling insects.
Antibodies raised to the insecticidal proteins can be used to identify
other proteins with insecticidal activity. The present sequence is
insecticidal protein
XX
SQ Sequence 33 AA;
Query Match 100.0%; Score 194; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33
Db 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33

RESULT 3
AAE36261
ID AAE36261 standard; peptide; 34 AA.
XX
AC AAE36261;
XX
DT 26-JUN-2003 (first entry)
XX
DE Insecticidal protein #3.
XX
KW Insecticidal protein; pesticide.
XX
OS Unidentified.
XX
PN WO200298911-A2.
```



CC invention are useful for producing plants or plant parts that are  
CC resistant to insects. The protein or synergistic combination is useful as  
CC an active ingredient of a pesticide or for controlling insects.  
CC Antibodies raised to the insecticidal proteins can be used to identify  
CC other proteins with insecticidal activity. The present sequence is  
CC insecticidal protein  
XX  
SQ Sequence 34 AA;

Query Match 100.0%; Score 194; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 1e-14;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33  
DB 2 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 34

RESULT 5  
AAE36260  
ID AAE36260 standard; peptide; 34 AA.

AC AAE36260;

DT 26-JUN-2003 (first entry)

DE Insecticidal protein #2.

KW Insecticidal protein; pesticide.

XX Unidentified.

OS WO200298911-A2.

PN 12-DEC-2002.

PF 30-MAY-2002; 2002WO-GB002666.

PR 07-JUN-2001; 2001GB-00013900.

XX (SYGN ) SYNGENTA LTD.

PI Vincent JL, Viner R;

DR WPI; 2003-175137/17.

PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

PS Claim 5; Page 23; 67pp; English.

CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein  
XX  
SQ Sequence 34 AA;

Query Match 100.0%; Score 194; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 1e-14;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33  
DB 2 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 34

RESULT 6  
AAE36294

ID AAE36294 standard; peptide; 34 AA.

AC AAE36294;

DT 26-JUN-2003 (first entry)

DE Insecticidal protein #24.

KW Insecticidal protein; pesticide.

OS Unidentified.

PN WO200298911-A2.

PD 12-DEC-2002.

PF 30-MAY-2002; 2002WO-GB002666.

PR 07-JUN-2001; 2001GB-00013900.

XX (SYGN ) SYNGENTA LTD.

PI Vincent JL, Viner R;

DR WPI; 2003-175137/17.

PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

PS Example 1; Page 66; 67pp; English.

CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein  
XX  
SQ Sequence 34 AA;

Query Match 100.0%; Score 194; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 1e-14;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33  
DB 2 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 34

RESULT 7  
AAE36259  
ID AAE36259 standard; peptide; 34 AA.

AC AAE36259;

DT 26-JUN-2003 (first entry)

DE Insecticidal protein #1.

KW Insecticidal protein; pesticide.

OS Unidentified.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "Xaa = any amino acid"

PN WO200298911-A2.

XX 12-DEC-2002.

XX

```

PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN ) SYNGENTA LTD.
XX
XX Vincent JL, Viner R;
XX WPI; 2003-175137/17.
XX
DR New insecticidal protein comprising an X-glycine motif at the amino-
PT terminus, useful as an active ingredient of a pesticide.
XX
XX Claim 1; Page 23; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine
CC motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC invention are useful for producing plants or plant parts that are
CC resistant to insects. The protein or synergistic combination is useful as
CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify
CC other proteins with insecticidal activity. The present sequence is
CC insecticidal protein
XX
SQ Sequence 34 AA;
Query Match 100.0%; Score 194; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33
Db 2 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 34

RESULT 9
AAE36292
ID AAE36292 standard; peptide; 34 AA.
XX
AC AAE36292;
XX
DT 26-JUN-2003 (first entry)
XX
DE Insecticidal protein #22.
XX
XX Insecticidal protein; pesticide.
XX
XX Unidentified.
XX
FN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN ) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-
PT terminus, useful as an active ingredient of a pesticide.
XX
PS Example 1; Page 65; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine
CC motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC invention are useful for producing plants or plant parts that are
CC resistant to insects. The protein or synergistic combination is useful as
CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify
CC other proteins with insecticidal activity. The present sequence is
CC insecticidal protein
XX
SQ Sequence 34 AA;
Query Match 100.0%; Score 194; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33
Db 2 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 34

RESULT 10
AAE36287
ID AAE36287 standard; peptide; 34 AA.
XX
AC AAE36287;

```



```
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKCTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33
DB 2 GKCTPAGVKCPAALPCCPGRLRCIGGVNNKVC 34

RESULT 13
AAE36284
ID AAE36284 standard; peptide; 34 AA.
AC AAE36284;
DT 26-JUN-2003 (first entry)
DE Insecticidal protein #14.
KW Insecticidal protein; pesticide.
OS Unidentified.
PN WO200298911-A2.
PD 12-DEC-2002.
PF 30-MAY-2002; 2002WO-GB002666.
PR 07-JUN-2001; 2001GB-00013900.
PA (SYGN ) SYNGENTA LTD.
PI Vincent JL, Viner R;
DR WPI; 2003-175137/17.
XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX Example 1; Page 64; 67pp; English.
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.
XX Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein
XX Sequence 34 AA;
SQ Query Match 100.0%; Score 194; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKCTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33
DB 2 GKCTPAGVKCPAALPCCPGRLRCIGGVNNKVC 34

RESULT 15
AAE36296
ID AAE36296 standard; peptide; 34 AA.
AC AAE36296;
XX 26-JUN-2003 (first entry)
DT Insecticidal protein #26.
DE Insecticidal protein; pesticide.
KW Insecticidal protein; pesticide.
XX Unidentified.
OS WO200298911-A2.
PN 12-DEC-2002.
PD 30-MAY-2002; 2002WO-GB002666.
PR 07-JUN-2001; 2001GB-00013900.
PA (SYGN ) SYNGENTA LTD.
PI Vincent JL, Viner R;
DR WPI; 2003-175137/17.
XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX Example 1; Page 66; 67pp; English.

Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKCTPAGVKCPAALPCCPGRLRCIGGVNNKVC 33
DB 2 GKCTPAGVKCPAALPCCPGRLRCIGGVNNKVC 34

RESULT 14
AAE36288
ID AAE36288 standard; peptide; 34 AA.
AC AAE36288;
DT 26-JUN-2003 (first entry)
DE Insecticidal protein #18.
KW Insecticidal protein; pesticide.
XX
```

XX CC The invention relates to insecticidal protein comprising an X-glycine  
 CC motif at the amino-terminus. Polynucleotide or DNA constructs of the  
 CC invention are useful for producing plants or plant parts that are  
 CC resistant to insects. The protein or synergistic combination is useful as  
 CC an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify  
 CC other proteins with insecticidal activity. The present sequence is  
 CC insecticidal protein  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 194; DB 6; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 1e-14;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKICTPAGVKCPAALPCCPLRCIGGVNKKVCR 33  
 |||||  
 Db 2 GKICTPAGVKCPAALPCCPLRCIGGVNKKVCR 34  
 |||||

Search completed: February 14, 2005, 20:50:20  
 Job time : 4.51404 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:11:42 ; Search time 80.9984 Seconds  
(without alignments)  
4539.261 Million cell updates/sec

Title: US-10-019-823B-54  
Perfect score: 3749  
Sequence: 1\_MKLKNQKHQSFSNAKVDK.....KRELFEIVKYAKQLHIERNM 718

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3722.5	99.3	719	1 C1IA_BACTK	Q45752 bacillus th
2	3722.5	99.3	719	2 Q6X181	Q6X181 bacillus th
3	3717.5	99.2	719	2 Q93NJ5	Q85796 bacillus th
4	3716.5	99.1	719	2 Q85796	Q85796 bacillus th
5	3587.5	95.7	719	2 Q8XV61	Q8XV61 bacillus th
6	3513.5	93.7	719	2 Q9F0P8	Q9F0P8 bacillus th
7	3482.5	92.9	719	1 C1IB_BACTE	Q45709 bacillus th
8	3359.5	89.6	719	1 C1ID_BACTU	Q9XDL1 bacillus th
9	3358.5	89.6	719	1 C1IC_BACTU	Q87404 bacillus th
10	2415	64.4	1239	1 C1BE_BACTU	Q45739 bacillus th
11	2415	64.4	1233	1 C1BC_BACTM	Q45774 bacillus th
12	2249	60.0	1228	2 Q93T75	Q93C75 bacillus th
13	2248	60.0	1228	1 C1BA_BACTK	P05517 bacillus th
14	2240	59.7	1228	2 Q93NM5	Q93NM5 bacillus th
15	2165	57.7	849	2 Q6PYW8	Q6PYW8 bacillus th
16	2165	57.7	1227	1 C1BE_BACTU	O85805 bacillus th
17	2089	55.7	1231	2 Q8KNY2	Q8KNY2 bacillus th
18	2084	55.6	1231	1 C1BD_BACTZ	Q9ZAZ5 bacillus th
19	1974	52.7	1215	1 C1KA_BACTM	Q45715 bacillus th
20	1895	50.5	381	2 Q45740	Q45740 bacillus th
21	1652	44.1	1157	1 C8MA_BACUK	Q45704 bacillus th
22	1643.5	43.8	1144	2 Q8KZL7	Q8KZL7 bacillus th
23	1480.5	39.5	1157	1 C9CA_BACTO	Q45733 bacillus th
24	1473	39.3	1169	1 C8BA_BACUK	Q45705 bacillus th
25	1462	39.0	1166	1 C1GA_BACTU	Q45746 bacillus th
26	1461.5	39.0	1169	1 C1FB_BACTM	O66377 bacillus th
27	1456.5	38.9	1167	1 C1JA_BACTU	Q45738 bacillus th
28	1455.5	38.8	1174	2 Q45749	Q45749 bacillus th
29	1445.5	38.6	1118	2 Q9AM83	Q9AM83 bacillus th
30	1441.5	38.5	1155	1 C1AB_BACTK	P06578 bacillus th
31	1441.5	38.5	1155	2 Q7BE98	Q7BE98 bacillus th

32	1441.5	38.5	1155	2 Q9F296	Q9F296 bacillus th
33	1436.5	38.3	1156	2 Q6GUA7	Q6GUA7 bacillus th
34	1433	38.2	1180	2 Q9S5V8	Q9S5V8 bacillus th
35	1432	38.2	1176	2 Q7WZT9	Q7WZT9 bacillus th
36	1431.5	38.2	1177	2 Q6EIX3	Q6EIX3 bacillus th
37	1430	38.1	793	2 Q6FYW7	Q6FYW7 bacillus th
38	1429.5	38.1	1155	2 Q93T21	Q93C21 bacillus th
39	1426	38.0	1176	2 Q45736	Q45736 bacillus th
40	1424	38.0	1169	2 Q8GHE8	Q8GHE8 bacillus th
41	1424	38.0	1181	1 C1AE_BACTL	Q03748 bacillus th
42	1422	37.9	1176	1 C1AA_BACTK	P02965 bacillus th
43	1422	37.9	1176	2 Q9RC30	Q9RC30 bacillus th
44	1417	37.8	1169	1 C1GB_BACTZ	Q9ZAZ6 bacillus th
45	1400	37.3	1179	1 C1AD_BACTA	Q03744 bacillus th

ALIGNMENTS

RESULT 1  
C1IA\_BACTK  
ID C1IA\_BACTK STANDARD; PRT: 719 AA.  
AC Q45752; P71092; Q45750; Q45751; Q45756;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DE Pesticidal crystal protein cryIIa (insecticidal delta-endotoxin)  
DE CryII(a) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
GN Name=cryIIa; Synonyms=CGCryV, cryII(a), cryV, cryVI;  
OS Bacillus thuringiensis (subsp. kurstaki).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=29339;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSIR732;  
RA MEDLINE=93298009; PubMed=8517758;  
RA Gleave A.P., Williams R., Hedges R.J.;  
RT "Screening by polymerase chain reaction of Bacillus thuringiensis  
RT serotypes for the presence of cryV-like insecticidal protein genes and  
RT characterization of a cryV gene cloned from B. thuringiensis subsp.  
RT kurstaki".  
RL Appl. Environ. Microbiol. 59:1683-1687(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JHCC4835;  
RA MEDLINE=92269582; PubMed=1588820;  
RA Taylor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;  
RT "Identification and characterization of a novel Bacillus thuringiensis  
RT delta-endotoxin entomocidal to coleopteran and lepidopteran larvae".  
RL Mol. Microbiol. 6:1211-1217(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HD-1.  
RA MEDLINE=95314293; PubMed=7793960;  
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;  
RT "Distribution of cryV-type insecticidal protein genes in Bacillus  
RT thuringiensis and cloning of cryV-type genes from Bacillus  
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.  
RT entomocidus".  
RL Appl. Environ. Microbiol. 61:2402-2407(1995).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AB88;  
RA MEDLINE=96178985; PubMed=8606196;  
RA Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,  
RA Craig J.A., Koziel M.G., Estruch J.J.;  
RT "Cloning of a cryV-type insecticidal protein gene from Bacillus  
RT thuringiensis: the cryV-encoded protein is expressed early in  
RT stationary phase".  
RL J. Bacteriol. 178:2141-2144(1996).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=61;

RA Solvapatiyan A., Bhatnagar R.K.;  
RT "Isolation, cloning and expression of cryV gene.";  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
CC -|- FUNCTION: Promotes colloidotomic lysis by binding to the midgut  
CC epithelial cells of certain coleopter and lepidopteran species.  
CC Active on Plutella xylostella and Bombyx mori.  
CC -|- DEVELOPMENTAL STAGE: The crystal protein is produced during  
CC sporulation and is accumulated both as an inclusion and as part of  
CC the spore coat.  
CC -|- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
CC terminus.  
CC -|- SIMILARITY: Belongs to the delta endotoxin family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; M98544; AAA22354.1; -;  
CC EMBL; X62821; CAA44633.1; -;  
CC EMBL; L36338; AAC36999.1; -;  
CC EMBL; L49391; AAB00958.1; -;  
CC EMBL; Y08920; CAA70124.1; -;  
CC PIR; S13915; I39815.  
CC PIR; S25383; S25383.  
CC HSSP; P02965; 1C1Y.  
CC InterPro; IPR001178; Endotoxin.  
CC InterPro; IPR005638; endotoxin\_C.  
CC InterPro; IPR005639; endotoxin\_N.  
CC InterPro; IPR008979; Gal\_bind\_Like.  
CC Pfam; PF03944; Endotoxin\_C; 1.  
CC Pfam; PF00555; Endotoxin\_M; 1.  
CC Pfam; PF03945; Endotoxin\_N; 1.  
CC Sporulation; Toxin.  
KW VARIANT 159 159 K -> R (in strain 61).  
FT VARIANT 233 233 D -> Y (in strain JHCC4835 and strain HD-  
FT VARIANT 443 443 A -> V (in strain AB88).  
FT VARIANT 711 712 KQ -> NE (in strain HD-1 and strain 61).  
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;  
  
Query Match 99.3%; Score 3722.5; DB 1; Length 719;  
Best Local Similarity 99.4%; Pred. No. 2.4e-251;  
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
  
QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCIKMSYENVEPVSASTI 60  
DB 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCIKMSYENVEPVSASTI 60  
  
QY 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEIPEHVEEIIINOKISTYA 120  
DB 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEIPEHVEEIIINOKISTYA 120  
  
QY 121 RNKALTDLKGLDALAVYHDSLESVWGNNRNNTRARSVVKSVQYIALELMFVKLPSPFVSG 180  
DB 121 RNKALTDLKGLDALAVYHDSLESVWGNNRNNTRARSVVKSVQYIALELMFVKLPSPFVSG 180  
  
QY 181 BEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWYS 240  
DB 181 BEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWYS 240  
  
QY 241 TGLNLRGNAESWRYNQFRDMLTLMVLDLVALPSPYDTOMYPIKTTAQLTREVYTDAI 300  
DB 241 TGLNLRGNAESWRYNQFRDMLTLMVLDLVALPSPYDTOMYPIKTTAQLTREVYTDAI 300  
  
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360  
DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360  
  
QY 361 GGKLEFRTIGTGLNISTOGSNTSINPVLFTSRSRVRTESLAGLNLFLTQPVN-VPR 419

DB 361 GGKLEFRTIGTGLNISTOGSNTSINPVLFTSRSRVRTESLAGLNLFLTQPVN-VPR 420  
QY 420 VDFHFKVTHPTASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479  
DB 421 VDFHFKVTHPTASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
QY 480 ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539  
DB 481 ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
QY 540 TGTFGDIRVNIINPPFAQRYRVRIRVASTYDLOFHTSINGKAINQGNFSATMWRGEDLDYK 599  
DB 541 TGTFGDIRVNIINPPFAQRYRVRIRVASTYDLOFHTSINGKAINQGNFSATMWRGEDLDYK 600  
QY 600 TTXTVGTFTTSSLVDQSTFTTGANFSSGNEVTDRIEFVPEVTEYAEYDFEKAQEKV 659  
DB 601 TFRTVGTFTTSSLVDQSTFTTGANFSSGNEVTDRIEFVPEVTEYAEYDFEKAQEKV 660  
QY 660 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 718  
DB 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
  
RESULT 2  
Q6X181 PRELIMINARY; PRT; 719 AA.  
AC Q6X181, 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cry1I.  
GN Names=cry1I;  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY262167; AAP86782.1; -;  
DR GO; GO:0005102; F:receptor binding; IEA.  
DR GO; GO:0006952; P:defense response; IEA.  
DR GO; GO:0009405; P:pathogenesis; IEA.  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR008979; Gal\_bind\_Like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;  
  
Query Match 99.3%; Score 3722.5; DB 2; Length 719;  
Best Local Similarity 99.4%; Pred. No. 2.4e-251;  
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
  
QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCIKMSYENVEPVSASTI 60  
DB 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCIKMSYENVEPVSASTI 60  
  
QY 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEIPEHVEEIIINOKISTYA 120  
DB 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEIPEHVEEIIINOKISTYA 120  
  
QY 121 RNKALTDLKGLDALAVYHDSLESVWGNNRNNTRARSVVKSVQYIALELMFVKLPSPFVSG 180  
DB 121 RNKALTDLKGLDALAVYHDSLESVWGNNRNNTRARSVVKSVQYIALELMFVKLPSPFVSG 180  
  
QY 181 BEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWYS 240  
DB 181 BEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWYS 240



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QY 241 TGLNLRGNTNAESWVRYNQFRDMLTLMVLDLVALFSPSYDTQMPYPIKTTAQLTREVTDAI 300
Db 241 TGLNLRGNTNAESWVRYNQFRDMLTLMVLDLVALFSPSYDTQMPYPIKTTAQLTREVTDAI 300
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Db 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVITYSLLSRWSNTQYNNMW 360
QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLOTQPVN-VPR 419
Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLOTQPVN-VPR 420
QY 420 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479
Db 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 480 ASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDIILRTN 539
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QY 540 TGTGDIRVININPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 599
Db 541 TGTGDIRVININPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 600 TFXTVGFTTFFSLLDVQSTFTIGAMNPFSSGNEVYIDRIEFVPEVYEAEDPEKAQEKV 659
Db 601 TFRTVGFTTFFSLLDVQSTFTIGAMNPFSSGNEVYIDRIEFVPEVYEAEDPEKAQEKV 660
QY 660 TALFTSTNPRGLTKDVKHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
Db 661 TALFTSTNPRGLTKDVKHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 3
Q93NJ5 PRELIMINARY; PRT; 719 AA.
AC Q93NJ5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Crylla.
GN Name=CryIIa;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Song F., Zhang J., Gu A., Huang D., Li G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF373207; AAK66742.1; -.
DR HSSP; P02965; 1CIV.
DR GO; GO:0005102; F_receptor binding; IEA.
DR GO; GO:0006952; P_defense response; IEA.
DR GO; GO:0009405; P_pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;

Query Match 99.2%; Score 3717.5; DB 2; Length 719;
Best Local Similarity 99.3%; Pred. No. 5.5e-251;
Matches 714; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Db 1 MKLNQDKQKQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMEYENVEPFVSASTI 60
QY 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKQKQWEIFMBHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKQKQWEIFMBHVEEIIINQKISTYA 120
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Db 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKQKQWEIFMBHVEEIIINQKISTYA 120
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Db 121 RNKALTDLKGLGDALAVYHDSLESWGNRNNTARSVVKSQYIALELMFVKQLPSPFAVSG 180
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSYHCVKWKYS 240
Db 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSYHCVKWKYS 240
QY 241 TGLNLRGNTNAESWVRYNQFRDMLTLMVLDLVALFSPSYDTQMPYPIKTTAQLTREVTDAI 300
Db 241 TGLNLRGNTNAESWVRYNQFRDMLTLMVLDLVALFSPSYDTQMPYPIKTTAQLTREVTDAI 300
QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVITYSLLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVITYSLLSRWSNTQYNNMW 360
QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLOTQPVN-VPR 419
Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLOTQPVN-VPR 420
QY 420 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479
Db 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 480 ASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDIILRTN 539
Db 481 ASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDIILRTN 540
QY 540 TGTGDIRVININPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 599
Db 541 TGTGDIRVININPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 600 TFXTVGFTTFFSLLDVQSTFTIGAMNPFSSGNEVYIDRIEFVPEVYEAEDPEKAQEKV 659
Db 601 TFRTVGFTTFFSLLDVQSTFTIGAMNPFSSGNEVYIDRIEFVPEVYEAEDPEKAQEKV 660
QY 660 TALFTSTNPRGLTKDVKHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
Db 661 TALFTSTNPRGLTKDVKHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 4
O85796 PRELIMINARY; PRT; 719 AA.
AC O85796;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Insecticidal protein.
GN Name=cryVI01;
OS Bacillus thuringiensis (subsp. kurstaki).
OG Plasmid large plasmid.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SI01;
RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076953; AAC26910.1; -.
DR HSSP; P02965; 1CIV.
DR GO; GO:0005102; F_receptor binding; IEA.
DR GO; GO:0006952; P_defense response; IEA.
DR GO; GO:0009405; P_pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
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KW Plasmid. 719 AA; 81230 MW; 42746D478359BBA7 CRC64;  
SQ SEQUENCE 719 AA; 81230 MW; 42746D478359BBA7 CRC64;  
Query Match 99.1%; Score 3716.5; DB 2; Length 719;  
Best Local Similarity 99.3%; Pred. No. 6.4e-251;  
Matches 714; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
Qy 1 M K L N Q D K H Q S F S S N A K V D I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60  
Db 1 M K L N Q D K H Q S F S S N A K V D I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60  
Qy 61 Q T G I G I A G K I L G T L G V P F A G O V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120  
Db 61 Q T G I G I A G K I L G T L G V P F A G O V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120  
Qy 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N T R A S V V K S Q Y I A L E L M F V Q K L P S P A V S G 180  
Db 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N T R A S V V K S Q Y I A L E L M F V Q K L P S P A V S G 180  
Qy 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S H C V K W Y S 240  
Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S H C V K W Y S 240  
Qy 241 T G L N L R G T N A E S W R Y N Q P R D M T L M V L D L V A L F P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 300  
Db 241 T G L N L R G T N A E S W R Y N Q P R D M T L M V L D L V A L F P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 300  
Qy 301 G T V H P H S F T S T T W Y N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T O Y N M W 360  
Db 301 G T V H P H S F T S T T W Y N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T O Y N M W 360  
Qy 361 G G H K L E P R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N - V P R 419  
Db 361 G G H K L E P R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420  
Qy 420 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 479  
Db 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
Qy 480 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R T N 539  
Db 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R T N 540  
Qy 540 T G T F G D I R V N I N P P F A Q R Y R I R Y A S T T D I Q F H T S I N G K A I N Q G N F S A T N W R G E D L D Y K 599  
Db 541 T G T F G D I R V N I K P P F A Q R Y R I R Y A S T T D I Q F H T S I N G K A I N Q G N F S A T N W R G E D L D Y K 600  
Qy 600 T F X T V G F T T P F S L I D V Q S T F T I G A W N F S S G N E V Y D I R I E F V P V E V T Y E A E Y D F E K A Q E K V 659  
Db 601 T F R T V G F T T P F S F L D V Q S T F T I G A W N F S S G N E V Y D I R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
Qy 660 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 718  
Db 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719

RESULT 5  
Q8KY61 PRELIMINARY; PRT; 719 AA.  
AC Q8KY61  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Cry.  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_taxid=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Porcar M., Martinez C., Caballero P.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF278797; AAM73516.1; --  
DR FIR; B42459; B42459.

HSP; P02965; ICIY.  
DR GO; 0005102; F:receptor binding; IEA.  
DR GO; 0006952; P:defense response; IEA.  
DR GO; 0009405; P:pathogenesis; IEA.  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR008979; Gal\_bind\_like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
SQ SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;  
Query Match 95.7%; Score 3587.5; DB 2; Length 719;  
Best Local Similarity 95.7%; Pred. No. 6.6e-242;  
Matches 688; Conservative 12; Mismatches 18; Indels 1; Gaps 1;  
Qy 1 M K L N Q D K H Q S F S S N A K V D I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60  
Db 1 M K L N Q D K H Q S F S S N A K V D I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60  
Qy 61 Q T G I G I A G K I L G T L G V P F A G O V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120  
Db 61 Q T G I G I A G K I L G T L G V P F A G O V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120  
Qy 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N T R A S V V K S Q Y I A L E L M F V Q K L P S P A V S G 180  
Db 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N T R A S V V K S Q Y I A L E L M F V Q K L P S P A V S G 180  
Qy 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S H C V K W Y S 240  
Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S H C V K W Y S 240  
Qy 241 T G L N L R G T N A E S W R Y N Q P R D M T L M V L D L V A L F P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 300  
Db 241 T G L N L R G T N A E S W R Y N Q P R D M T L M V L D L V A L F P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 300  
Qy 301 G T V H P H S F T S T T W Y N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T O Y N M W 360  
Db 301 G T V H P N A S F A S T T W Y N N A P S F S T I E S A V V R N P H L L D F L E Q V T I Y S L L S R W S N T O Y N M W 360  
Qy 361 G G H K L E P R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N - V P R 419  
Db 361 G G H R L E P R T I G G M L N T S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420  
Qy 420 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 479  
Db 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480  
Qy 480 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R T N 539  
Db 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R T N 540  
Qy 540 T G T F G D I R V N I N P P F A Q R Y R I R Y A S T T D I Q F H T S I N G K A I N Q G N F S A T N W R G E D L D Y K 599  
Db 541 T G T F G D I R V N I N P P F A Q R Y R I R Y A S T T D I Q F H T S I N G K A I N Q G N F S A T N W R G E D L D Y K 600  
Qy 600 T F X T V G F T T P F S L I D V Q S T F T I G A W N F S S G N E V Y D I R I E F V P V E V T Y E A E Y D F E K A Q E K V 659  
Db 601 T F R T V G F T T P F S F D V Q S T F T I G A W N F S S G N E V Y D I R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
Qy 660 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 718  
Db 661 T A L F T S T N P G L K T N V T E Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H T G R N M 719

RESULT 6  
Q9F0P8 PRELIMINARY; PRT; 719 AA.  
ID Q9F0P8  
AC Q9F0P8;  
DT 01-MAR-2001 (TReMBLrel. 16, Created)  
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Name=crvII;  
GN Bacillus thuringiensis.  
OS Plasmid pBTC19.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BT007;  
RX MEDLINE=22837682; PubMed=12957903;  
RA DOI=10.1128/AEM.69.9.5207-5211.2003;  
RA Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,  
Hu Y., Li G., Huang D.;  
RT "Identification of cryII-type genes from Bacillus thuringiensis  
strains and characterization of a novel cryII-type gene.";  
RL Appl. Environ. Microbiol. 69:5207-5211(2003).  
DR EMBL; AF211139; AAC43526.1; --  
DR HSSP; P02965; 1CIY.  
DR GO; GO:0005102; F:receptor binding; IEA.  
DR GO; GO:0006952; P:defense response; IEA.  
DR GO; GO:0009405; P:pathogenesis; IEA.  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR008979; Gal\_bind\_like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
KW Plasmid.  
SQ SEQUENCE 719 AA; 81024 MW; 7E17481922C435E6 CRC64;  
  
Query Match 93.7%; Score 3513.5; DB 2; Length 719;  
Best Local Similarity 93.0%; Pred. No. 9.9e-237;  
Matches 669; Conservative 26; Mismatches 23; Indels 1; Gaps 1;  
  
QY 1 MCLKNODKQHSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFVSASTI 60  
DB 1 MCLKNPDKQHSNAKVDKIATDSLKNETDIELQNHEDFLRMSEHSIDPFVSASTI 60  
  
QY 61 QTGIGIAGKILGTLPVPAQVSLVSGFILGELWPKQKQWEIFMEHVEEINOKLSTVA 120  
DB 61 QTGIGIAGKILGTLPVPAQVSLVSGFILGELWPKQKQWEIFMEHVEEINOKLSTVA 120  
  
QY 121 RNKALTDLKGDLAVYHDSLESVGVNRRNTPARSVKSYQYIALBLMFVKQLPSFVSG 180  
DB 121 RNIALADLKGDLAVYHDSLESVGVNRRNTPARSVKSYQYIALBLMFVKQLPSFVSG 180  
  
QY 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSISTFYNRQVERAGDYSYHCVKWS 240  
DB 181 EEVPLPIYAQAANLHLLLRDASVFGKEWGLSSSISTFYNRQVERAGDYSYHCVKWS 240  
  
QY 241 TGLNNLRGTNAESWRYNPRDWTMLVLDLVALFPSTOMYPIKTATQLTREVVTDAI 300  
DB 241 TGLNNLRGTNAESWRYNPRDWTMLVLDLVALFPSTOMYPIKTATQLTREVVTDAI 300  
  
QY 301 GTVHPHPSFTSTWYNNAPFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQTMNMW 360  
DB 301 GTVHPNAPSTWYNNAPFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQTMNMW 360  
  
QY 361 GGHKLEFRITGTLNSTQGSTNTSINPVLPTSDVDVRTESLAGNLFLTPQVYV-VP 419  
DB 361 GGHKLEFRITGTLNSTQGSTNTSINPVLPTSDVDVRTESLAGNLFLTPQVNGVPR 420  
  
QY 420 VDFHWFVTHPTASDNFYYPGAGIGTQLQDSNELPPEATGPNVSEYSHRLSHGLLS 479  
DB 421 VDFHWFATLPASDNFYYPGAGIGTQLQDSNELPPEATGPNVSEYSHRLSHGLLS 480  
  
QY 480 ASHVKALVSWTHRSADRTNTIEPNSITQIPLKAFNLSSGAAVVRGPGFTGGDILRRTN 539  
DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
  
QY 540 TGTGDIRVNNPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMNGEDLDYK 599  
DB 1 MCLKNPDKQHSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFVSASTI 60  
DB 1 MCLKNPDKQHSFSSNAKVDKIATDSLKNETDIELQNHEDCLKMEYENVEPFVSASTI 60

Db 541 TGTGDIRVNNPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMNGEDLDYK 600  
QY 600 TFXTVGFTTFPSLLDVQSTFTTGAMNFSNGNEVYIDRIEFVPEVVEVYEAEDFEKQAEKV 659  
Db 601 TFRTVGFTTFPSFSDVQSTFTTGAMNFSNGNEVYIDRIEFVPEVVEVYEAEDFEKQAEKV 660  
QY 660 TALFTSTNPRGLTKDVKDYHIDQVSNLVESLSDEFYLDKRELFELVYKAKQHIERNM 718  
Db 661 TALFTSTNPRGLTKDVKDYHIDQVSNLVESLSDEFYLDKRELFELVYKAKQHIERNM 719

RESULT 7  
CLIB\_BACTE STANDARD; PRT; 719 AA.  
AC Q45709;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Pesticidal crystal protein cryIIb (insecticidal delta-endotoxin  
DE CryII(b)) (crystalline entomocidal protoxin) (81 kDa crystal protein).  
GN Name=cryIIb; Synonyms=cryII(b), cryV, cryV465;  
OS Bacillus thuringiensis (subsp. entomocidus).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1436;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BP465;  
RX MEDLINE=95314293; PubMed=7793960;  
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;  
RT Distribution of cryV-type insecticidal protein genes in Bacillus  
RT thuringiensis and cloning of cryV-type genes from Bacillus  
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.  
RT entomocidus.";  
RL Appl. Environ. Microbiol. 61:2402-2407(1995).  
CC -!- FUNCTION: Promotes colloidsomotic lysis by binding to the midgut  
CC epithelial cells of certain coleopteran and lepidopteran species.  
CC Active on Plutella xylostella but not on Bombyx mori.  
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
CC sporulation and is accumulated both as an inclusion and as part of  
CC the spore coat.  
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
CC terminus.  
CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; U07642; AAA82114.1; --  
CC FIR; I40590; I40590.  
CC HSSP; P02965; 1CIY.  
CC InterPro; IPR001178; Endotoxin.  
CC InterPro; IPR005638; endotoxin\_C.  
CC InterPro; IPR005639; endotoxin\_N.  
CC InterPro; IPR008979; Gal\_bind\_like.  
CC Pfam; PF03944; Endotoxin\_C; 1.  
CC Pfam; PF00555; Endotoxin\_M; 1.  
CC Pfam; PF03945; Endotoxin\_N; 1.  
KW Sporulation; Toxin.  
SQ SEQUENCE 719 AA; 81295 MW; E8210ABEA97688E CRC64;  
  
Query Match 92.9%; Score 3482.5; DB 1; Length 719;  
Best Local Similarity 92.4%; Pred. No. 1.4e-234;  
Matches 664; Conservative 31; Mismatches 23; Indels 1; Gaps 1;  
  
QY 1 MCLKNODKQHSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFVSASTI 60  
DB 1 MCLKNPDKQHSFSSNAKVDKIATDSLKNETDIELQNHEDCLKMEYENVEPFVSASTI 60

QY 61 QTGIGIAGKILGTGVFPAGQVASYLGFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVFPAGQVASYLGFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDKLGDLGALAVYHDSLESWGNRNNTARSVVKQYIALELMFVKQLPSPAVSG 180  
 Db 121 RNKALSDRLGDLGALAVYHDSLESWGNRNNTARSVVKQYIALELMFVKQLPSPAVSG 180  
 QY 181 EEEVPLLPYQAANLHLLLRDASIFCKEWGLSSSEISTFYNQVVERAGYSHVCKWYS 240  
 Db 181 EEEVPLLPYQAANLHLLLRDASIFCKEWGLSSSEISTFYNQVVERAGYSHVCKWYS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
 Db 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
 QY 301 GTVHPSPFTSTTWNNAEVSFAIAEAAVVRNPHLLDFLQVITYSLLSRWSNTQYNNMW 360  
 Db 301 GTVHPNOAFSTTWNNAEVSFAIAEAAVVRNPHLLDFLQVITYSLLSRWSNTQYNNMW 360  
 QY 361 GGKLEPRTTIGTLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTOPVN-VPR 419  
 Db 361 GGKLEPRTTIGTLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTOPVN-VPR 420  
 QY 420 VDFHWKFVTHPSADRTNTIENSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539  
 Db 420 VDFHWKFVTHPSADRTNTIENSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 481 ASHKVLYSWTHRSADRTNTIENSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 Db 481 ASHKVLYSWTHRSADRTNTIENSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 540 TGTFGDIRVNIINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSATWNRGEDLDYK 599  
 Db 541 TGTFGDIRVNIINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSATWNRGEDLDYK 600  
 QY 600 TFXVTGFTTFFSLDVGSTFTIGAWNFSSGNEVYDRIEFVPEVTVYEAAYDFEKAQEKV 659  
 Db 601 TFRITGFTTFFSDVQSTFTIGAWNFSSGNEVYDRIEFVPEVTVYEAAYDFEKAQEKV 660  
 QY 660 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDFFYLDKRELFVVKYAKQLHIERNM 718  
 Db 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDFFYLDKRELFVVKYAKQLHIERNM 719

## RESULT 8

CLID\_BACTU STANDARD; PRT; 719 AA.  
 AC Q9XDL1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryII (insecticidal delta-endotoxin  
 DE CryII(d)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryII; Synonyms=cryII(d), NRCryV;  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 CX NCBI\_taxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BR30;  
 RA MEDLINE=20374042; PubMed=10919402;  
 RA Chou S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;  
 RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein  
 RT gene".  
 RL Curr. Microbiol. 41:65-69(2000).  
 CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut  
 CC epithelial cells of many lepidopteran larvae. Active on Plutella  
 CC xylostella and on Bombyx mori.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-

CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC -----  
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 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC ENBL; AF047579; AAD44366.1; -.  
 DR HSP; P02965; 1CIY.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Sporulation; Toxin.  
 SQ SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;

Query Match 89.6%; Score 3359.5; DB 1; Length 719;  
 Best Local Similarity 89.3%; Pred. No. 5.7e-226;  
 Matches 642; Conservative 35; Mismatches 41; Indels 1; Gaps 1;  
 QY 1 MKLNQDQKQSPSSNAKVDKISTDSLKNETDIELQNIHEDCLKMEYENVEPVFSASTI 60  
 Db 1 MKSKNQWRSFSSNATVDKSFDDPLEHNTMELQNSHEDCLKMEYSEVFPVSVTI 60  
 QY 61 QTGIGIAGKILGTGVFPAGQVASYLGFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVFPAGQVASYLGFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDKLGDLGALAVYHDSLESWGNRNNTARSVVKQYIALELMFVKQLPSPAVSG 180  
 Db 121 RNKALADLKGDLGALAVYHDSLESWGNRNNTARSVVKQYIALELMFVKQLPSPAVSG 180  
 QY 181 EEEVPLLPYQAANLHLLLRDASIFCKEWGLSSSEISTFYNQVVERAGYSHVCKWYS 240  
 Db 181 EEEVPLLPYQAANLHLLLRDASIFCKEWGLSSSEISTFYNQVVERAGYSHVCKWYS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
 Db 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
 QY 301 GTVHPSPFTSTTWNNAEVSFAIAEAAVVRNPHLLDFLQVITYSLLSRWSNTQYNNMW 360  
 Db 301 GTVHPNASFASTTWNNAEVSFAIAEAAVVRNPHLLDFLQVITYSLLSRWSNTQYNNMW 360  
 QY 361 GGKLEPRTTIGTLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTOPVN-VPR 419  
 Db 361 GGKLEPRTTIGTLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTOPVNGVPR 420  
 QY 420 VDFHWKFVTHPSADRTNTIENSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539  
 Db 421 VDFHWKFVTHPSADRTNTIENSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 480 ASHKVLYSWTHRSADRTNTIENSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539  
 Db 481 ASHKVLYSWTHRSADRTNTIENSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 540 TGTFGDIRVNIINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSATWNRGEDLDYK 599  
 Db 541 TGTFGDIRVNIINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSATWNRGEDLDYK 600  
 QY 600 TFXVTGFTTFFSLDVGSTFTIGAWNFSSGNEVYDRIEFVPEVTVYEAAYDFEKAQEKV 659  
 Db 601 AFRVTGFTTFFSFAQSTFTIGAWNFSLGNEVYDRIEFVPEVTVYEAAYDFEKAQEKV 660  
 QY 660 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDFFYLDKRELFVVKYAKQLHIERNM 718  
 Db 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDFFYLDKRELFVVKYAKQLHIERNM 718

Db	661	TAMFTSTNLRLKNTVTDCHIDQVSNLVSLSDEFYLDKRELFEIVKAKQLNIERNM	719
RESULT 9			
C11C_BACTU			
ID	C11C_BACTU	STANDARD;	PRT; 719 AA.
AC	087404;		
DT	16-OCT-2001	(Rel. 40, Created)	
DT	16-OCT-2001	(Rel. 40, Last sequence update)	
DT	05-JUL-2004	(Rel. 44, Last annotation update)	
DE	Pesticidal crystal protein cryIIc (Insecticidal delta-endotoxin		
DE	CryII(c)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).		
GN	Name-cryIIc; Synonyms=cryII(c);		
OS	Bacillus thuringiensis.		
OG	Plasmid.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1428;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C18 / Egypt;		
RA	Oseman Y.A., Madkour M.A., Bulla L.A. Jr.;		
RL	Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.		
CC	-!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut		
CC	epithelial cells of insects.		
CC	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during		
CC	sporulation and is accumulated both as an inclusion and as part of		
CC	the spore coat.		
CC	-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-		
CC	terminus.		
CC	-!- SIMILARITY: Belongs to the delta endotoxin family.		
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or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
EMBL; AF056933; AAC62933.1; .			
DR	HSSP; P02965; 1CIV.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin_C.		
DR	InterPro; IPR005639; endotoxin_N.		
DR	InterPro; IPR008979; Gal bind like.		
DR	Pfam; PF03944; Endotoxin_C; 1		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		
KW	Plasmid; Sporulation; Toxin.		
SQ	SEQUENCE 719 AA; 81210 MW; 8370B3F06B905DFF CRC64;		
Query Match 89.6%; Score 3358.5; DB 1; Length 719;			
Best Local Similarity 89.6%; Pred. No. 6.7e-226;			
Matches 644; Conservative 33; Mismatches 41; Indels 1; Gaps 1;			
QY	1	MKLKNQDKHQSSNAKVDKISTDSLNKNETDIELQNHEDCLMKSEYENPFVSASTI	60
Db	1	MKLKNQDKHQSSNAKVDKISTDSLNKNETDIELQNHEDCLMKSEYENPFVSASTI	60
QY	61	QTGIGTAGKILGTLGVPPAGVASLYSFLGELWPKGKQWEIFMBHVEINQKISTYA	120
Db	61	QTGIGTAGKILGTLGVPPAGVASLYSFLGELWPKGKQWEIFMBHVEINQKISTYA	120
QY	121	RNKALTDLGLGDLALAVYHDSLESWGNNRNTARSVKSOYALRLMFQKLPSPAVSG	180
Db	121	RNKALTDLGLGDLALAVYHDSLESWGNNRNTARSVKSOYALRLMFQKLPSPAVSG	180
QY	181	EEVPLLPYIAQANLHLLLRDASIFGKEWGLSSSISTFYNRQVERAGDYSVHCYKWS	240
Db	181	EEVPLLPYIAQANLHLLLRDASIFGKEWGLSSSISTFYNRQVERAGDYSVHCYKWS	240
QY	241	TGLNNLRATNGSWRYNQFRKDIELMVLVDLVRVFPSTYDLVPIKTTSQLTRVYTDAL	300
Db	241	TGLNNLRATNGSWRYNQFRKDIELMVLVDLVRVFPSTYDLVPIKTTSQLTRVYTDAL	300

Db	241	TGLNNLRATNGSWRYNQFRKDIELMVLVDLVRVFPSTYDLVPIKTTSQLTRVYTDAL	300
QY	301	GTVHPHPSTTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYLLSRWSNTQTMNMW	360
Db	301	GTVHPHPSTTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYLLSRWSNTQTMNMW	360
QY	361	GGHLEFRITIGTALNISTOGSTNTSINPVTLSRDSRVTRTESLAGLNFLTOPVN-VPR	419
Db	361	GGHLEFRITIGTALNISTOGSTNTSINPVTLSRDSRVTRTESLAGLNFLTOPVN-VPR	419
QY	420	VFHMKFVTHPTASDNFYVPGVAGTGLQDSENELPPEATGPNPYESVSHRLSHGLIS	479
Db	420	VFHMKFVTHPTASDNFYVPGVAGTGLQDSENELPPEATGPNPYESVSHRLSHGLIS	479
QY	480	ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDIILRTN	539
Db	480	ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDIILRTN	539
QY	540	TGTFGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGELDYK	599
Db	540	TGTFGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGELDYK	599
QY	541	SGTFGHIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGELDYK	600
Db	541	SGTFGHIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGELDYK	600
QY	600	TFXTVGTFTPPSLDVQSTFTIGANFSSGNEVYDRIEFVPEVTEYAEYDFEKAQEKV	659
Db	600	TFXTVGTFTPPSLDVQSTFTIGANFSSGNEVYDRIEFVPEVTEYAEYDFEKAQEKV	659
QY	601	TFRTVGTFTPPSFDVQSTFTIGANFSSGNEVYDRIEFVPEVTEYAEYDFEKAQEKV	660
Db	601	TFRTVGTFTPPSFDVQSTFTIGANFSSGNEVYDRIEFVPEVTEYAEYDFEKAQEKV	660
QY	660	TALFTSTNPRGLTKDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKAKQLNIERNM	718
Db	660	TALFTSTNPRGLTKDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKAKQLNIERNM	718
QY	661	TALFTSTNPRGLTKDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKAKQLNIERNM	719
Db	661	TALFTSTNPRGLTKDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKAKQLNIERNM	719
RESULT 10			
C11B_BACTU			
ID	C11B_BACTU	STANDARD;	PRT; 1229 AA.
AC	045739;		
DT	30-MAY-2000	(Rel. 39, Created)	
DT	30-MAY-2000	(Rel. 39, Last sequence update)	
DT	05-JUL-2004	(Rel. 44, Last annotation update)	
DE	Pesticidal crystal protein cryIIBb (Insecticidal delta-endotoxin		
DE	CryIIB(b)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).		
GN	Name=cryIIBb; Synonyms=cryIIB5, cryIIB(b);		
OS	Bacillus thuringiensis.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1428;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=NREL B-21110 / EG5847;		
RA	Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;		
RT	"Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins		
RT	toxic to lepidopteran insects."		
RL	Patent number US5322687, 21-JUN-1994.		
CC	-!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut		
CC	epithelial cells of many lepidopteran larvae.		
CC	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during		
CC	sporulation and is accumulated both as an inclusion and as part of		
CC	the spore coat.		
CC	-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-		
CC	terminus.		
CC	-!- SIMILARITY: Belongs to the delta endotoxin family.		
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or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
EMBL; L32020; AAA2344.1; .			
DR	HSSP; P02965; 1CIV.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin_C.		
DR	InterPro; IPR005639; endotoxin_N.		

```

DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Sporulation; Toxin.
KW SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;
SQ
Query Match 64.4%; Score 2415; DB 1; Length 1229;
Best Local Similarity 65.1%; Pred. No. 1.2e-159;
Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;
QY 13 SSNAKVDKISTSLKN-ETDIEIQ-NINHEDCIKMSEYENVEPVSASTIQTGIGIAGKI 70
DB 7 NENEINALSIPVSNPSTQMLSPDARIEDSLCAEVNNDPVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPAGQVASYLSFTLGLMWPKGKQWEIFMEHVEEIIINQKISTYARKALTDLKG 130
DB 67 LGVLGVPPAGQVASYLSFTLGLMWPGRDPWEIFLHVQQLIRQVQVNTNTAIALLEG 126
QY 131 LGDALAVYHDSLSWVGNRRNTARSVVKSOYIALELMFVQKLPSFAVSGEEVPLPIYA 190
DB 127 LGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPLFRIRNEEVPLLMVYA 186
QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKYSTGLNNLRGTN 250
DB 187 QAAHLHLLLRDASLFGSEWGNASSDVNQYQEQIRYTEYSNHCVQWYNTGLNNLRGTN 246
QY 251 AESSWRYNQFRDMLTMDLVALPSPDYQMPYIKTTAQLTRVYTDATGTVHPHPSFT 310
DB 247 AESSWRYNQFRDMLTMDLVALPSPDYQMPYIKTTAQLTRVYTDATGTVHPHPSFT 306
QY 311 STTWYNNNAPSFAEAAVVRNPHLLDFEQVTIYSLLSRWNSNTQYMMWGGHKLFRIT 370
DB 307 STTWYNNNAPSFAEAAVVRNPHLLDFEQVTIYSLLSRWNSNTQYMMWGGHKLFRIT 366
QY 371 GGTLANISQTGST-NTSINPVTLPFTSRDVRVRESLAGNLFLETPVN-VPRVDFHWKFTV 428
DB 367 GGTLANISQTGST-NTSINPVTLPFTSRDVRVRESLAGNLFLETPVN-VPRVDFHWKFTV 422
QY 429 HPIASDNFYYPG-----YAGIGTQLODSENELPPEATGPNYESYSHRLSHIGLISAS 481
DB 423 --INPQNIYERGATTSYQYQGVIGLDFSELPETTERPNYESYSHRLSHIGLIGN 480
QY 482 HVKALVYSWTHRSADRTNTIENSITQIPLVKAFNLSSGAAVVRGPGFTGGDILARTNTG 541
DB 481 TURAPVYSWTHRSADRTNTIENRITQIPLVKALNLHSGVTVVGPGFTGGDILARTNTG 540
RESULT 11
CIBC_BACTM STANDARD; PRT; 1233 AA.
AC Q45774;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Peptidicidal crystal protein cryIbC (Insecticidal delta-endotoxin
DE CryIbC) (Crysaline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIbC; Synonyms=cryIb(c), cryIbC;
OS Bacillus thuringiensis (subsp. morrisoni).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1441;

```

[1]

SEQUENCE FROM N.A.  
 Bishop A.H., Bone E.J., Ellar D.J.;  
 "Cloning of novel *Bacillus thuringiensis* delta-endotoxin.";  
 Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
 -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut  
 epithelial cells of insects.  
 -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 sporulation and is accumulated both as an inclusion and as part of  
 the spore coat.  
 -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 terminus.  
 -!- SIMILARITY: Belongs to the delta endotoxin family.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL; Z46442; CAAB6568.1; -;  
 HSP; P02965; ICIY.

InterPro; IPR001178; Endotoxin.  
 InterPro; IPR005638; endotoxin\_C.  
 InterPro; IPR005639; endotoxin\_N.  
 InterPro; IPR008979; Gal\_bind\_like.

Pfam; PF03944; Endotoxin\_C; 1.  
 Pfam; PF00555; Endotoxin\_M; 1.  
 Pfam; PF03945; Endotoxin\_N; 1.

Sporulation; Toxin.  
 SQ SEQUENCE 1233 AA; 140451 MW; 7318382413529F21 CRC64;

Query Match 64.4%; Score 2415; DB 1; Length 1233;  
 Best Local Similarity 65.1%; Pred. No. 1.2e-159;

Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;

QY 13 SSNAKVDKISTSLKN-ETDIEIQ-NINHEDCIKMSEYENVEPVSASTIQTGIGIAGKI 70

DB 7 NENEINALSIPVSNPSTQMLSPDARIEDSLCAEVNNDPVSASTVQTGINIAGRI 66

QY 71 LGTLGVPPAGQVASYLSFTLGLMWPKGKQWEIFMEHVEEIIINQKISTYARKALTDLKG 130

DB 67 LGVLGVPPAGQVASYLSFTLGLMWPGRDPWEIFLHVQQLIRQVQVNTNTAIALLEG 126

QY 131 LGDALAVYHDSLSWVGNRRNTARSVVKSOYIALELMFVQKLPSFAVSGEEVPLPIYA 190

DB 127 LGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPLFRIRNEEVPLLMVYA 186

QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKYSTGLNNLRGTN 250

DB 187 QAAHLHLLLRDASLFGSEWGNASSDVNQYQEQIRYTEYSNHCVQWYNTGLNNLRGTN 246

QY 251 AESSWRYNQFRDMLTMDLVALPSPDYQMPYIKTTAQLTRVYTDATGTVHPHPSFT 310

DB 247 AESSWRYNQFRDMLTMDLVALPSPDYQMPYIKTTAQLTRVYTDATGTVHPHPSFT 306

QY 311 STTWYNNNAPSFAEAAVVRNPHLLDFEQVTIYSLLSRWNSNTQYMMWGGHKLFRIT 370

DB 307 STTWYNNNAPSFAEAAVVRNPHLLDFEQVTIYSLLSRWNSNTQYMMWGGHKLFRIT 366

QY 371 GGTLANISQTGST-NTSINPVTLPFTSRDVRVRESLAGNLFLETPVN-VPRVDFHWKFTV 428

DB 367 GGTLANISQTGST-NTSINPVTLPFTSRDVRVRESLAGNLFLETPVN-VPRVDFHWKFTV 422

QY 429 HPIASDNFYYPG-----YAGIGTQLODSENELPPEATGPNYESYSHRLSHIGLISAS 481

DB 423 --INPQNIYERGATTSYQYQGVIGLDFSELPETTERPNYESYSHRLSHIGLIGN 480

QY 482 HVKALVYSWTHRSADRTNTIENSITQIPLVKAFNLSSGAAVVRGPGFTGGDILARTNTG 541

DB 481 TURAPVYSWTHRSADRTNTIENRITQIPLVKALNLHSGVTVVGPGFTGGDILARTNTG 540

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QY 542 TFGDIRVNNPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSGATMNRGDLDTYKTF 601
DB 541 TFGDIRLNNVPLSQRYRVRIRYASTTDLQFHTSINGKAINQGNFSGATMNRGDLDTYKTF 600
QY 602 XTGVFTTSPSLDQVSTFTIGAWNPSGNEVYIDRIEFVPEVYTYBAEYDFEKAQEKVTA 661
DB 601 RTAGFSTPFLNQAOSTFTLGAQSFN-QEVYIDRIEFVPEVYTYBAEYDFEKAQEKVTA 659
QY 662 LFTSTNPRGLKTDVYHIDQVNSLVESLDEFLDEKRELFVYKAKQLHIERNM 718
DB 660 LFTSTNPRGLKTDVYHIDQVNSLVESLDEFLDEKRELFVYKAKQLHIERNM 716

RESULT 12
Q93T75 PRELIMINARY; PRT; 1228 AA.
ID Q93T75
AC Q93T75
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Delta-endotoxin Cry1Ba2.
GN Name-cry1Ba2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAK51084.1; -
DR HSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005639; endotoxin C.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match 60.0%; Score 2249; DB 2; Length 1228;
Best Local Similarity 62.3%; Pred. No. 4.9e-148;
Matches 446; Conservative 80; Mismatches 164; Indels 26; Gaps 7;

QY 23 TDSLKNETDTELQINHH-----EDCLKMEYENVEPFVBSASTTQTGIGAGKI 70
DB 2 TSNRKNENEINAVSNHSAQMDLLPDARIEDSLCIAEGNIDFPVBSASTVQTGINAGRI 61
QY 71 LGTLGVPPAGQVSLSYFLIGELWPKGNQWEIFMEHVEIINQKISTVARNKALDTLKG 130
DB 62 LGVLGVPPAGQVSLSYFLIGELWPKGNQWEIFMEHVEIINQKISTVARNKALDTLKG 121
QY 131 LGDALAVYHDSLSWSVGNRNTRARSVKSOYTALELMFVQKLPSFAVSGEEVPLPIYA 190
DB 122 LGDSFRAYQOQSLDLENRDARTSRVLTQYTALELDLFNAPLFAIRNQEVPLMVYA 181
QY 191 QANALHLLLRDASIFGKGLSSSETSTFYNQVERAGDYSYHCVKWTSTGLNLRGTN 250
DB 182 QANALHLLLRDASLGSFGLTSQELQRYEYQVERTRDYSYCVENYNTGLNLRGTN 241
QY 251 AEWRYNQPRRDMVLVDLVALFSPYDTQMTYPIKTTAQLTREVYDTAIGTVHPHSFT 310
DB 242 AASWRYNQPRRDLTGLVDLVALFSPYDTQMTYPIKTTAQLTREVYDTAIGTVHPHSFT 299
QY 311 STTWYNNAPSFSAIEAAVNRPHLLDPLFQVITYLSLLSWNSNTQYNNMGCHKLFRTI 370
DB 300 SMWYNNAPSFSAIEAAVNRPHLLDPLFQVITYLSLLSWNSNTQYNNMGCHKLFRTI 359
```

```
QY 371 GGTLNISTQGSTNTSINPVTLPFTSRDVRVYRTESLAGLNLF--LTOPVN-VPRVDFHWKVF 427
DB 360 GGTLNISTQGSTNTSINPVTLPFTSRDVRVYRTESLAGLNLF--LTOPVN-VPRVDFHWKVF 416
QY 428 THP-----IASDNFYYPGAGIGTQLODSENELPEATGCPNPVYESYSHRLSHIGLISASH 482
DB 417 TNPQNSIRGRTANYSQP-YESPLGLOKQSETELPPTETTERPNYESYSHRLSHIGLILQSR 475
QY 483 VKALVYSWTHRSADRTNTIEPNSITQIPLVAKAFNLSGAAVVRGPGFTCGDILRRNTTGT 542
DB 476 VNVFVYSWTHRSADRTNTIEPNSITQIPLVAKAFNLSGAAVVRGPGFTCGDILRRNTTGT 535
QY 543 FGDIRVNNPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSGATMNRGDLDTYKTF 602
DB 536 FGPRIVTNGLPTQRYRIGFRYASTVDFDFVSRGCTTVNNPFLRTMNSGDELKYGNFV 595
QY 603 TVGFTTSPSLDQVSTFTIGAWNPSGNEVYIDRIEFVPEVYTYBAEYDFEKAQEKVTA 662
DB 596 RRAFTTPTFTQIQDIIRTSIOGLSGNGEVYIDKIEIIPVTATFAEYDLERAQEAVAL 655
QY 663 FTSTNPRGLKTDVYHIDQVNSLVESLDEFLDEKRELFVYKAKQLHIERNM 718
DB 656 FTSTNPRGLKTDVYHIDQVNSLVESLDEFLDEKRELFVYKAKQLHIERNM 711

RESULT 13
CIBA_BACTK
ID CIBA_BACTK STANDARD; PRT; 1228 AA.
AC P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cry1Ba (insecticidal delta-endotoxin
DE Cry1B(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name-cry1Ba; Synonyms-cryA4, cry1B(a);
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1436;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
RX MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from
RT Bacillus thuringiensis subsp. thuringiensis.";
RL Nucleic Acids Res. 16:2723-2723(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL; X06711; CAA29898.1; -
CC EMBL; X95704; CAA65003.1; -
CC PIR; S00873; S00873.
CC HSP; P07130; 1DLC.
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RESULT 14	
Q93NM5	
ID	Q93NM5
AC	PRELIMINARY;
Q93NM5;	PRT; 1228 AA.
DT 01-DEC-2001	(TREMBLrel. 19, Created)
DT 01-DEC-2001	(TREMBLrel. 19, Last sequence update)
DT 01-WAR-2004	(TREMBLrel. 26, Last annotation update)
DE	Cry1Ba.
GN	Cry1Ba.
DN	Name=cry1Ba;



Query Match	57.7%	Score 2165	DB 2	Length 849
Best Local Similarity	59.0%	Pred. No. 2.1e-142		
Matches 421	Conservative 106	Mismatches 173	Indels 14	Gaps 4
Qy	13	SSNAKVDKISTDSLKN-----ETDTELQNIHEDCLMKSEYENVPFVSASTIQTGIG	65	
Db	7	NENEIINALSTPAPVNSHSAQNNLSTDARI-----EDSLCIAEGNNIDPFVSASTVQTGIN	61	
Qy	66	IAGKILGTLPVPPAGOVANLSYFPIGELWPKPKQWEI FMEHVEI INOKLSTVARNKAL	125	
Db	62	IAGRI LGVLGPVPPAGQATSFYSLVIGELWPRGRDPWEIFLEHVQLIRQQVTENTRDTAL	121	
Qy	126	TDLXGLGDALAAVYHDSLSVWGNENNRARSVWASQYIALBELMFVKLPSFAVSGEEVPL	185	
Db	122	ARLQGLGNSFRAYQOQSLDMLENDRDARTSRVLTQYIALSLDFLNAMPLFAIRNQEVPL	181	
Qy	186	LPIYAAQANLHLLLRDASIFGKKGWGLSSSISITFYNRQVERAGDYSYHCVKWTSTGLNN	245	
Db	182	LMVYAAQANLHLLLRDASLFGSGFGLTSQBIQRYERQVEKTRREYSYDCARWYNTGLNN	241	
Qy	246	LRGTNAESWRYNQFRDRMTLMVLDLVALPFSYDTQMYPIKTTAQLTREVYTDAGTVHP	305	
Db	242	LRGTNAESWLRVYNQFRDLTLGVLDLVALPFSYDTRVYPMNTSAQLTRIEYITDPIGRNA	301	
Qy	306	HPSTSTTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQPMNWGGHKL	365	
Db	302	PSGFASWFWNNAPSPSAIEAAVIRPPLHLLDPPEQLTIFVLGRSWSTQPMYMWGHRL	361	
Qy	366	BFRTIGGTLLNTSTQGSTWNTSINPVTLPFTSDRVYRTESLAGLNLFLTPQPVN -VPRVDPFW	424	
Db	362	ESRTIRGSLSTSTGNTWNTSINPVTLQFTSDRVYRTESFAGINILLTTPVNGVPMWRENW	421	
Qy	425	KFVTHPIASDNFYYPGVAGIGTQLODSNELPPEATQGNPYESYSHRULSHLGLISASHVK	484	
Db	422	RNPILNSLRGSLYLTIGYTGVTQQLPDSSETLPPEPPERNTESYSHRULSNLRLISGNLTR	481	
Qy	485	ALVYSWTHRSADRNTTTPENSIITQIPLKAFNLSSGAAVVRGPGTGDILRRNTGTGFG	544	
Db	482	APVYSWTHRSADRNTWTSSDIITQIPLVKSNFLNSGTSVSGPGPTGDDIIRTNVNGSVL	541	
Qy	545	DIRVNNIPPPAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAITMNRGEDLDYKTFKTV	604	

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2005, 20:32:21 ; Search time 16.5604 Seconds  
(without alignments)  
4171.616 Million cell updates/sec

Title: US-10-019-823B-54  
Perfect score: 3749  
Sequence: 1 MKLNQDKHQSFSSNAKVDK.....KRELFEIVKAKQLHIERNM 718  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3732.5	99.6	719	2 S25383	parasporal crystal
2	3724.5	99.3	719	2 I39814	insecticidal prote
3	3722.5	99.3	719	2 I39815	insecticidal prote
4	3482.5	92.9	719	2 I40590	cry465 protein -
5	2248	60.0	1228	2 S00873	parasporal crystal
6	1891	50.4	380	2 B42459	hypothetical prote
7	1480.5	39.5	1157	1 S49247	parasporal crystal
8	1462	39.0	1166	2 S32645	parasporal crystal
9	1455.5	38.8	1174	2 S32649	parasporal crystal
10	1448.5	38.6	1155	2 A26513	parasporal crystal
11	1441.5	38.5	1155	2 JD0002	parasporal crystal
12	1441.5	38.5	1156	2 A29125	parasporal crystal
13	1433	38.2	934	2 A22798	parasporal crystal
14	1432	38.2	1176	2 JT0241	parasporal crystal
15	1426	38.0	1176	2 JC2219	parasporal crystal
16	1424.5	38.0	1155	2 S02134	parasporal crystal
17	1424	38.0	1181	2 A41052	parasporal crystal
18	1422	37.9	1176	2 A02617	parasporal crystal
19	1422	37.9	1176	2 S02215	parasporal crystal
20	1420.5	37.9	1155	2 I39838	parasporal crystal
21	1354.5	36.1	1174	2 A42459	parasporal crystal
22	1340.5	35.8	1138	2 A48944	parasporal crystal
23	1319	35.2	1156	2 A29838	parasporal crystal
24	1310	34.9	823	2 S04181	parasporal crystal
25	1298	34.6	1189	2 S00944	parasporal crystal
26	1288.5	34.4	1154	2 S39536	parasporal crystal
27	1257.5	33.5	1171	2 I40572	parasporal crystal
28	1257.5	33.5	1171	2 A37829	parasporal crystal
29	1248.5	33.3	1176	2 A48970	parasporal crystal

30 1205.5 32.2 1160 2 S32647 parasporal crystal  
31 1197 31.9 1165 2 S11446 parasporal crystal  
32 1185 31.6 655 2 JC7140 prototoxin - Bacillu  
33 1184.5 31.6 1172 2 S32689 parasporal crystal  
34 1179.5 31.5 1160 2 I40589 parasporal crystal  
35 1149.5 30.7 1177 2 A43785 parasporal crystal  
36 1146 30.6 1178 1 USBSXH parasporal crystal  
37 1136.5 30.3 652 2 A27323 parasporal crystal  
38 1114.5 29.7 659 2 S10228 parasporal crystal  
39 1082 28.9 652 2 I39811 parasporal crystal  
40 977.5 26.1 649 1 JH0261 parasporal crystal  
41 921.5 24.6 618 2 S11445 parasporal crystal  
42 875.5 23.4 1156 2 S19306 parasporal crystal  
43 818.5 21.8 1136 1 USBS81 parasporal crystal  
44 686 18.3 934 2 B29838 parasporal crystal  
45 658.5 17.6 1180 2 I39870 parasporal crystal

ALIGNMENTS

RESULT 1

S25383

parasporal crystal protein cryIIa1 - Bacillus thuringiensis

N;Alternate names: delta-endotoxin; parasporal crystal protein cryV

C;Species: Bacillus thuringiensis

C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004

C;Accession: S25383

R;Tailor, R.; Tippet, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.

Mol. Microbiol. 6, 1211-1217, 1992

A;Title: Identification and characterization of a novel Bacillus thuringiensis delta-end

A;Reference number: S25383; MUID:92269582; PMID:1588820

A;Accession: S25383

A;Molecule type: DNA

A;Residues: 1-719 <TAI>

A;Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:940289; PIDN:CAA44633.1; PID:940290

C;Genetic:

C;Superfamily: parasporal crystal protein

C;Keywords: delta-endotoxin

Query Match 99.6%; Score 3732.5; DB 2; Length 719;  
Best Local Similarity 99.6%; Pred. No. 2.2e-250;  
Matches 716; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy	1	MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSEYENVEFPVSASTI	60
Db	1	MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSEYENVEFPVSASTI	60
Qy	61	QTGIGIAGKILGTGLGVFPAGQVASLYSFILGELWPKGKQWEIFMEHVEEIIINQKISTYA	120
Db	61	QTGIGIAGKILGTGLGVFPAGQVASLYSFILGELWPKGKQWEIFMEHVEEIIINQKISTYA	120
Qy	121	RNKALTDLKGLDALAVYHDSLESVGNRNTRPARSVKQSYIALELMFVKQLPSFAVSG	180
Db	121	RNKALTDLKGLDALAVYHDSLESVGNRNTRPARSVKQSYIALELMFVKQLPSFAVSG	180
Qy	181	EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSSISITFYNNQVRAGDYSHCVKWNYS	240
Db	181	EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSSISITFYNNQVRAGDYSHCVKWNYS	240
Qy	241	TGLNNLRGTNAESWVRYNQFRDMLTMLVDLVALFSPSYDTQMYPIKTTAQLTREVTYDAI	300
Db	241	TGLNNLRGTNAESWVRYNQFRDMLTMLVDLVALFSPSYDTQMYPIKTTAQLTREVTYDAI	300
Qy	301	GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSWSSTQYNNMW	360
Db	301	GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSWSSTQYNNMW	360
Qy	361	GGHKLFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRTESLAGLNFLFTQPVN-VPR	419
Db	361	GGHKLFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRTESLAGLNFLFTQPVN-VPR	420

Tue Feb 15 10:07:49 2005

420 VDFHWKFWTHPIASDNFYFPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479  
421 VDFHWKFWTHPIASDNFYFPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
480 ASHKALVYSWTHRSADRTNTEPNSITQIPLKAFNLSGAAVVRGPGFTGGDILRRTN 539  
481 ASHKALVYSWTHRSADRTNTEPNSITQIPLKAFNLSGAAVVRGPGFTGGDILRRTN 540  
540 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 599  
541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
600 TFXTVGFTTPELSDVQSTFTTIGAWNFSSGNEVVIDRIEFVPEVVTYEAEDFEKAQEKV 659  
601 TFXTVGFTTPELSDVQSTFTTIGAWNFSSGNEVVIDRIEFVPEVVTYEAEDFEKAQEKV 660  
660 TALFTSTNPRGLKTDVQKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQLHIERNM 718  
661 TALFTSTNPRGLKTDVQKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQLHIERNM 719

RESULT 2  
I39814  
insecticidal protein cryVI - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 26-Aug-1999  
C:Accession: I39814  
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A:Title: Distribution of cryv-type insecticidal protein genes in Bacillus thuringiensis  
tomocidus.  
A:Reference number: I39814; MUID:95314293; PMID:7793960  
A:Accession: I39814  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:Cross-references: GB:I36338; NID:G540281; PIDN:AAC36999.1; PID:G540282  
C:Genetics:  
A:Gene: cryVI  
C:Superfamily: parasporal crystal protein

Query Match 99.3%; Score 3724.5; DB 2; Length 719;  
Best Local Similarity 99.3%; Pred. No. 7.8e-250;  
Matches 714; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCCLKMSEYENVEPFVSASTI 60  
Db 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCCLKMSEYENVEPFVSASTI 60

Qy 61 QTGIGTAGKILGTLGVPPAGQVSLYSFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120  
Db 61 QTGIGTAGKILGTLGVPPAGQVSLYSFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120

Qy 121 RNKALTDLKGIGDALAVYHDSLSWGNRNNTARSVVKVSKQYIALELMFVKLPSPAVSG 180  
Db 121 RNKALTDLKGIGDALAVYHDSLSWGNRNNTARSVVKVSKQYIALELMFVKLPSPAVSG 180

Qy 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSVHCVKWYS 240  
Db 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSVHCVKWYS 240

Qy 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300  
Db 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300

Qy 301 GTVHPHPSFTTWTYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLSLSRWSNTQYNNMW 360  
Db 301 GTVHPHPSFTTWTYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLSLSRWSNTQYNNMW 360

Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYESIAGLNLFLOTQVNV -VPR 419  
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYESIAGLNLFLOTQVNVGVR 420

420 VDFHWKFWTHPIASDNFYFPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479  
421 VDFHWKFWTHPIASDNFYFPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
480 ASHKALVYSWTHRSADRTNTEPNSITQIPLKAFNLSGAAVVRGPGFTGGDILRRTN 539  
481 ASHKALVYSWTHRSADRTNTEPNSITQIPLKAFNLSGAAVVRGPGFTGGDILRRTN 540  
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601 TFXTVGFTTPELSDVQSTFTTIGAWNFSSGNEVVIDRIEFVPEVVTYEAEDFEKAQEKV 660  
660 TALFTSTNPRGLKTDVQKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQLHIERNM 718  
661 TALFTSTNPRGLKTDVQKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQLHIERNM 719

RESULT 3  
I39815  
insecticidal protein cryW - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I39815  
R:Gleave, A.P.; Williams, R.; Hedges, R.J.  
Appl. Environ. Microbiol. 59, 1683-1687, 1993  
A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for  
iensis subsp. kurstaki.  
A:Reference number: I39815; MUID:93298009; PMID:8517758  
A:Accession: I39815  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:Cross-references: UNIPROT:Q45752; GB:M98544; NID:G142767; PIDN:AAA22354.1; PID:G142768  
C:Genetics:  
A:Gene: cryW  
C:Superfamily: parasporal crystal protein

Query Match 99.3%; Score 3722.5; DB 2; Length 719;  
Best Local Similarity 99.4%; Pred. No. 1.1e-249;  
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Db 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCCLKMSEYENVEPFVSASTI 60

Qy 61 QTGIGTAGKILGTLGVPPAGQVSLYSFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120  
Db 61 QTGIGTAGKILGTLGVPPAGQVSLYSFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120

Qy 121 RNKALTDLKGIGDALAVYHDSLSWGNRNNTARSVVKVSKQYIALELMFVKLPSPAVSG 180  
Db 121 RNKALTDLKGIGDALAVYHDSLSWGNRNNTARSVVKVSKQYIALELMFVKLPSPAVSG 180

Qy 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSVHCVKWYS 240  
Db 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSVHCVKWYS 240

Qy 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300  
Db 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300

Qy 301 GTVHPHPSFTTWTYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLSLSRWSNTQYNNMW 360  
Db 301 GTVHPHPSFTTWTYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLSLSRWSNTQYNNMW 360

Qy 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYESIAGLNLFLOTQVNV -VPR 419  
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYESIAGLNLFLOTQVNVGVR 420

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QY 420 VDFHKKFVTHPIASDNFFYPGVAGIGTQLQDSENELPPEATQOPNYESYSHRLSHIGLIS 479
Db 421 VDFHKKFVTHPIASDNFFYPGVAGIGTQLQDSENELPPEATQOPNYESYSHRLSHIGLIS 480
QY 480 ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAENLSSGAAVRGPFTGGDILRRTN 539
Db 481 ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAENLSSGAAVRGPFTGGDILRRTN 540
QY 540 TGTFGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 599
Db 541 TGTFGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600
QY 600 TPXTVGFTTFFSLDVQSTFTTGAMNFFSGNEVYIDRIEFVPVEVYEAEDFEKAQEKV 659
Db 601 TERTVGFTTFFSLDVQSTFTTGAMNFFSGNEVYIDRIEFVPVEVYEAEDFEKAQEKV 660
QY 660 TALFTSTNPRGLTKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKOLHIERNM 718
Db 661 TALFTSTNPRGLTKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKOLHIERNM 719

RESULT 4
I40590
cryV465 protein - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40590
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis
tomocidus.
A:Reference number: I39814; MUID:95314293; PMID:7793960
A:Accession: I40590
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-719 <RES>
A:Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:g467234; PIDN:AAA82114.1; PID:g4672
C:Genetics:
A:Gene: cryV465
C:Superfamily: parasporal crystal protein

Query Match 92.9%; Score 3482.5; DB 2; Length 719;
Best Local Similarity 92.4%; Pred. No. 4.5e-233;
Matches 664; Conservative 31; Mismatches 23; Indels 1; Gaps 1;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNNHEDCLKSEYENRPFVSASTI 60
Db 1 MKLKNQDKHQSLSSNAKVDKIATDSLKNETDIELKNNEDYLKMSHESIDPFVSASTI 60
QY 61 QTGIGIAGKILGTVPPFAGQVASYLSFIILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTVPPFAGQIASYSFIILGELWPKGKQWEIFMEHVEEIIINQKILTYA 120
QY 121 RNKALTDLKGDLALAVYHDSLESWGNRNNTARSVVKSQYIALEIMFVKQLPSPAVSG 180
Db 121 RNKALSDLRGLDALAVYHDSLESWGNRNNTARSVVKQYIALEIMFVKQLPSPAVSG 180
QY 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSVHCVKWYS 240
Db 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNQVERTRDYSCHCKWYN 240
QY 241 TGLNNLRGNAESWRYNQFRDWTLMVLVDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300
Db 241 TGLNNLRGNAESWRYNQFRDWTLMVLVDLVALFPSYDTLPYIKTTAQLTREVTYDAI 300
QY 301 GTVHPHSPFTSTWYNNAPSPSAIEAAVVRNPHLLDPLEQVTIYSLLSRWNSQTQNNMW 360
Db 301 GTVHPNQFASTTWYNNAPSPSAIEAAVIRSPLHLLDPLEKVTIYSLLSRWNSQTQNNMW 360
QY 361 GGHKLEFRITGGTLANISTOGSTNTSINPVTLPFTSRDVRVETESLAGLNFLTPQVNV 419
Db 361 GGHRLSRPITGGALNTSTOGSTNTSINPVTLPFTSRDVRVETESLAGLNFLTPQVNGVR 420
```

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QY 420 VDFHKKFVTHPIASDNFFYPGVAGIGTQLQDSENELPPEATQOPNYESYSHRLSHIGLIS 479
Db 421 VDFHKKFVTHPIASDNFFYPGVAGIGTQLQDSENELPPEATQOPNYESYSHRLSHIGLIS 480
QY 480 ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAENLSSGAAVRGPFTGGDILRRTN 539
Db 481 ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAENLSSGAAVRGPFTGGDILRRTN 540
QY 540 TGTFGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 599
Db 541 TGTFGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600
QY 600 TPXTVGFTTFFSLDVQSTFTTGAMNFFSGNEVYIDRIEFVPVEVYEAEDFEKAQEKV 659
Db 601 TERTVGFTTFFSDVQSTFTTGAMNFFSGNEVYIDRIEFVPVEVYEAEDFEKAQEKV 660
QY 660 TALFTSTNPRGLTKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKOLHIERNM 718
Db 661 TALFTSTNPRGLTKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKOLHIERNM 719

RESULT 5
S00873
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis
N:Alternate names: parasporal crystal protein cryA4
C:Species: Bacillus thuringiensis subsp. thuringiensis
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S00873
R:Brizard, B.L.; Whiteley, H.R.
Nucleic Acids Res. 16, 2723-2724, 1988
A:Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus
A:Reference number: S00873; MUID:88203216; PMID:3362680
A:Accession: S00873
A:Molecule type: DNA
A:Residues: 1-1228 <BRI>
A:Cross-references: UNIPROT:P05517; EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PID:g58094
C:Genetics:
A:Gene: cryA4
A:Start codon: TTG
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 60.0%; Score 2248; DB 2; Length 1228;
Best Local Similarity 62.3%; Pred. No. 3.2e-147;
Matches 446; Conservative 80; Mismatches 164; Indels 26; Gaps 7;

QY 23 TDSLKNETDIELQNNH-----EDCLKSEYENRPFVSASTIQTGIGTAGKI 70
Db 2 TSNRRKNENIINAVSNHSAQMDLLPDARIEDSLCTAEGNNIDPFVSASTVQTGINIAGRI 61
QY 71 LGTLGVPPFAGQVASYLSFIILGELWPKGKQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
Db 62 LGVLGVPPFAGQLASFSYFLVGLWPMRGRDQWEIFLEHVEQLINQQLITENARNATALARLOG 121
QY 131 LGDALAVYHDSLESWGNRNNTARSVVKSQYIALEIMFVKQLPSPAVSGEEVPLPIYA 190
Db 122 LGDSPRAYQOQSLDLEWLENRDARTARSLVYQVYIALELDFLNAMPLFAIRNQEVPELLMVA 181
QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSVHCVKWYSTGLNNLRGNTN 250
Db 182 QAAHLHLLLRDASIFGSEFGITSQEIQRYERQVERTRDYSICYVEWNTGLNSURGTN 241
QY 251 AESWRYNQFRDWTLMVLVDLVALFPSYDTQMPYIKTTAQLTREVTYDAIGTVHPHSPFT 310
Db 242 AASWRYNQFRDWTLMVLVDLVALFPSYDTRYPINTSAQLTREVTYDAIGAT--GVNMA 299
QY 311 STTWYNNAPSPSAIEAAVVRNPHLLDPLEQVTIYSLLSRWNSQTQNNMWGGHKLSPRTI 370
Db 300 SMWYNNAPSPSAIEAAVIRSPLHLLDPLEQVTIYSLLSRWNSQTRMTYWRGHTIQSRPI 359
QY 371 GGTLANISTOGSTNTSINPVTLPFTSRDVRVETESLAGLNLF--LTQPVN-VPRVDFHWKFV 427
Db 360 GGGLNTSTHGATNTSINPVTLPFASRDVRVETESYAGVLLWGHYLEPIHGVTVPFRFNP--- 416
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Db 722 AAKRLSRERL 732

RESULT 8  
S32645  
paraasporal crystal protein crylGal - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S32645  
R:Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A:Reference number: S32645  
A:Accession: S32645  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1166 <LAM>  
A:Cross-references: UNIPROT:Q45746; EMBL:Z22510; NID:g295861; PIDN:CAA80233.1; PID:g2958  
C:Superfamily: paraasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 39.0%; Score 1462; DB 2; Length 1166;  
Best Local Similarity 45.7%; Pred. No. 7.9e-93;  
Matches 322; Conservative 101; Mismatches 207; Indels 74; Gaps 17;

QY 41 DCLKMEYE-----NVPEFVSASTIQGTIGIAGKILGTGLVPPFAGQVASLYSFLGELWPK 96  
DB 13 NCLNPESEIFNARNNSFGLVQVSSGL---TRFLLEAAVPEAGFALGLFDIHWGAL--- 66  
QY 97 GKQWEIFMEHVEEIIINQISTYARNKALTDLKGDLGDAVYHDSLESVWGNRNTRRS 156  
DB 67 GVDQMSLFRLQIEQLRIETELERNRATILGLSSSYLYEAUREWENDPNPASQE 126  
QY 157 VVKSQYIALELMFVQKLPFAVSGEVEPLPIYAQAANLHLLLRDASIFGKEWGLSSSE 216  
DB 127 RVTRFRLTDDAIVTGLPTLAIRNLVNLVSVTQAANLHLLSLRDVAVFGERMGLTQAN 186  
QY 217 ISTFYNRQVERAGDYSHCVKYSTGLNNLRGNAESWRYNORFRDMTLMVLVLP 276  
DB 187 IEDLYRLTSLNIOEQSHDCARWYNOGLNEIGGISR---RYLDFORDLTATSLVDI VALPP 242  
QY 277 SYDTQMPYIKTTAQLTRVYTDAL--GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNH 334  
DB 243 NYDIRTYPIPTQQLTRVYTSVPVAGNI-----NFGLSIANVLRAPH 285  
QY 335 LLDLFELQVITYSLLSWSNTQYNNMGHKLERTIG-GTLN-----ISTQGSTNTS 385  
DB 286 LMDFDIRIVITYNSVR--STPY---WAGHEVISRTTGGQGNIEIRFLPYGVAANAEPVY 340  
QY 386 INPVTLPFTSRDVRYES-----LAGNLFLTPQVNVPRVDFHWKFVTHPIASDNFYYP 439  
DB 341 IRPTGTDEQRQWRARSRVVSPRSSQDFSLVDVAVG-----FLT-IFSAVSIYRN 390  
QY 440 GYAGICTQLODSENLPEATQPNYESYSHRLSHGLISAS-----HVKALVYSWTHRS 494  
DB 391 GP-GFNT---DTIDEIPIEGTDP--FTGYSHRLCHVGFLASSPFIISQYARAPIFS WTHRS 444  
QY 495 ADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNNPFP 554  
DB 445 ATLNTIADPVIQIPLVKAFNLHSGATVKGFGFTGGDILRRNTVNGSGDGRVNTAPL 504  
QY 555 AQRYVRIRYASTTDLOFHTSINGKAINQGNFSAWNRGSDLDYKFTXTVGTFTPSLLD 614  
DB 505 SQRYVRIRYASTTDLOFVTNINGTITINIGFSSWMDSDGLQYGRFRVAGFTTPTFTSD 564  
QY 615 VQSTFTIGWTFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKVATLETSTNPRGLKTD 674  
DB 565 ANSTFTIGAFGSPNNEVYIDRIEFVPAEYDFEAEYDLEKAQAVNALFTSSNQIGLKTD 624  
QY 675 VKDYHIDQVSNLSLESDFYLDKEKELPEIVKYAKQLHIERNM 718  
DB 625 VTDYHIDKVSNUVECLSDFECLDEKELSEKVKHAKRLSDERNL 668

RESULT 9  
S32649  
paraasporal crystal protein crylFa3 - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S32649  
R:Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A:Reference number: S32645  
A:Accession: S32649  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1174 <LAM>  
A:Cross-references: UNIPROT:Q45749; EMBL:Z22512; NID:g295865; PIDN:CAA80235.1; PID:g29586  
C:Superfamily: paraasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 38.8%; Score 1455.5; DB 2; Length 1174;  
Best Local Similarity 44.7%; Pred. No. 2.3e-92;  
Matches 324; Conservative 101; Mismatches 205; Indels 95; Gaps 17;

QY 36 NINHE-----DCLKMEYENVEPFVGSASTIQTGTIGIA-GKILGTGLVPPFAGQVASLYSFL 90  
DB 4 NIQNCVPYCNCLSNPEVEILSEERSTGRPLDISLSTRFLSEFVPGVGVAFGLDLW 63  
QY 91 GELWPKGNQWEIFMEHVEEIIINQISTYARNKALTDLKGDLGDAVYHDSLESVWGNRN 150  
DB 64 GFITP---SEWSLFLQLIEQLRIETELERNRATILRLGLADSVLEVLEALREWEENPN 120  
QY 151 NTRASVVKSQYIALELMFVQKLPFAVSGEVEPLPIYAQAANLHLLLRDASIFGKEW 210  
DB 121 NAQLREDVRIRATDDALITAINNFTLSFPIPLSVYQAANLHLLSLRDVAVSGQG 180  
QY 211 GLSSSEISFTYNRQVERAGDYSHCVKYSTGLNNLRGNAESWRYNORFRDMTLMVL 270  
DB 181 GDIATVNNHYNRLNLHRYTEHCLDTYNOGLENLRGNTQWSRPNQFRRLTITVL 240  
QY 271 LVALPFSYDTQMPYIKTTAQLTRVYTDALGTVHPHPSFTSTTWYNNNAPS-PSAIEAAV 329  
DB 241 IVALFPYDARAYPIQTSQLTREIYTSV--IEDSP-----VSANIPNGFNRAEPG- 290  
QY 330 VRNPHLLDFLEQVITYSLLSRWSNTQYNNMGHKLERTIGTLNISTQGSTNTSINPV 389  
DB 291 VRPPLHMDPMN-----SLFVTAETVRSQTVWGGHLV-----SSRNTAGNPI 331  
QY 390 TLPP-----TSRDVYRTESLAGNLFLTPQVNVPRVDFHWKFVTHPIASD 434  
DB 332 NFPIYGIENPGGAIWAIEDPPFVRT-----LSDPVFV-RGGF-----GN 371  
QY 435 NFYFPGYAGIGTQLQ-----DSNELPPEATQPNYESYSHRLSHI----- 475  
DB 372 PHYVLGLRGVAFQQTGTHNTRFRNSGTIDSLDEIPPDNSGAPWNDYSHVLNHTVFW 431  
QY 476 -GLISASHV-KALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 533  
DB 432 PGEIAGSDSWRAPMFSWTHRSADRTNINPNITQIIPAVKAHNLHSGSTVVRGPGFTGGD 491  
QY 534 ILRRNTGTGDIRVNNPFPAAQRYVRIRYASTTDLOFHTSINGKAINQGNFSAWNRG 593  
DB 492 LURRNTGTGDIRVNNITGTLPSQRVRIRYASTTDLOFHTSINGKAINQGNFSAWNRG 551  
QY 594 ELDYKTFXTVGTFTTPFSLLDVQSTFTIGAMFSSGNEVYIDRIEFVPEVTEAEYDFE 653  
DB 552 GNLSGNPRTAGFTSPFSSNAQSTFTLTGTQAFSN-QEVYIDRIEFVPAEYDFEASSDLE 610  
QY 654 KQAEKVTALFTSTNPRGLKTDVKDHDIDQVSNLSLESDFYLDKEKELPEIVKYAKQLH 713  
DB 611 RAQKAVNALFTSTQGLKTNVTGYHIDQVSNLVACLSDFECLDEKELSEKVKHAKRLS 670  
QY 714 IERNM 718  
DB 671 DRRNL 675





Db	120	DPTPALREENKRIQFNQDNMSALTTPALPFAVQNYQVPLSVTVQANLHLSVLRDVSFG	179
Qy	208	KEWGLSSSEISFTFYNRQVERAGDYSYHCWKVYSTGLNLRGTAESWRYNQFRDMDTLM	267
Db	180	QRWGFDAAATINSRYNDLTRLIGNYTHDAVRWYNTGLERWGPDSRSDWRYNQFRRELTLT	239
Qy	268	VLDLVALPPSYDTOMYPTKTTAQLTREYVYTDAGTVHPHPFTSTWTNNNAPSF----	323
Db	240	VLDIVSUFPNYDSRTYPTVQSQTREIYTPV-----LENFDGSPRGSQAQ	285
Qy	324	AIEAAVVRNPHLLDFLEQVITYSLLSR-----WSNTQYMM-----WGHKLEFRTIGCTLNI	376
Db	286	GIEGS-IRSPHMLDILANSITIYDAHRGEYYWSGHQIMASPVGFSGPFTPLYXTMGNA	344
Qy	377	STQGSTWTSINPVLPTFSRDVRYTESLAGLNLFLTQPVNV-PRVDFWKFWTHPIASDN	435
Db	345	APOQRIVAQLGGQYVRTLSUSTLYRRFPFNIGIN---NQOLSVDLGDTEFAYG-----TSN	395
Qy	436	FYPYCYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI-----SASHVKALVY	488
Db	396	LPSAVYRKSGT--VDSLDEIIPQNNNVPRQGFSHRLSHVMSFRSGPNSSVSIIRAMPF	453
Qy	489	SWTHRSADRTNTIIPBNSITQPLVKAFNLSGAAVVRGPGTGGDILRTNTGTGDIRV	548
Db	454	SWIHRSAEFNNIIPSSQITQPLTKSTNLGSGTSVWKGPGFTGGDILRTSPGOISTLRV	513
Qy	549	NINPPPAQRYRVRYASTTDLOPHTSINGKAINQGNFSAWNRGDDLYKTFXTVGTTT	608
Db	514	NITAPLQORYRVRYASTTNLQPHTSIDGRPINQGNFSAWMSGSNLOSGSFRFTVGTTT	573
Qy	609	PFSLLDQGSTFTIGAMPSPSGNEVVYIDRIEFVPVEVTYEAEDFEKAQEKVYALTSTNP	668
Db	574	PFNFSNGSVFTLSNAHVNSGNEVVYIDRIEFVPAEVTFEAEVDLERAQKAVNELFTSSNQ	633
Qy	669	RLGTKDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM	718
Db	634	IGLKTVDYTHIDQVSNLVECLSDFECLDEKKEKSEKVKHAKRLSDENL	683

**RESULT 12**

RESULT 12  
 A29125  
 parasporal crystal protein Bt2 - *Bacillus thuringiensis* subsp. kurstaki (strain HD-1)  
 C;Species: *Bacillus thuringiensis* subsp. kurstaki  
 C;Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 09-Jul-2004  
 C;Accession: A29125  
 R;Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niedermeyer, J.  
 Bio/Technology 5, 807-813, 1987  
 A;Title: Insect tolerant transgenic tomato plants.  
 A;Reference number: A29125  
 A;Accession: A29125  
 A;Status: not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 1-1156 <PIS>  
 A;Cross-references: UNIPROT:Q9P296; UNIPROT:Q93T21  
 C;Superfamily: parasporal crystal protein  
 C;Keywords: delta-endotoxin

RESULT 13

RESULT 13  
A22798  
parasporal crystal protein - *Bacillus thuringiensis*  
C:Species: *Bacillus thuringiensis*  
C:Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 09-Jul-2004  
C:Accession: A22798  
R/Shibano, Y.; Yamagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, M.  
Gene 34, 243-251, 1985  
A:Title: Nucleotide sequence coding for the insecticidal fragment of the *Bacillus thuringiensis* parasporal crystal protein  
A:Reference number: A22798; MUID:85232070; PMID:2989108  
A:Accession: A22798  
A:Molecule type: DNA  
A:Residues: 1-934 <SH1>  
A:Crossa-references: UNIPROT:Q95SV8; GB:M10917; NID:q143100; PIDN:AAA22552.1; PID:g551713  
C:Comment: The authors translated the codon ACA for residue 264 as Ser.  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

	Query Match	38.2%; Score 1433; DB 2; Length 934;
	Best Local Similarity	43.1%; Pred. No. 5.7e-91;
	Matches	308; Conservative 119; Mismatches 221; Indels 66; Gaps 13;
QY	36	NINHEDCLKMWSEVYE-PFVSASTIQG-----IGIAGKITGLTGVPGFAGVASLYS 87
DB	4	NNINECIPNCLSNPEVEVLGERLETGYTPIDISLSTQFLSFE-VPGAGFVJGLVD 62
QY	88	FILGEIWPKGKNQEIMFBEHVBIINQKISTYARNKALTDLKGLDALAYTHDSLESWVG 147
DB	63	IIWGI F---GPSOWDAFLVQIEQLINORIEEFARNOAISRLGLESLNYQIYAESFREWEA 119
QY	148	NRNNTARSVKRKYOTALELMFVKLPSPSAVSGEEVPLLPITYAAOANHLHLLLRDASIFG 207
DB	120	DPTNPALREEMRIQFDNDMSALTATPILFAVQNYQVPILLSVYQAANHLHSUVRDVSFG 179
QY	208	KEWGLSSSIISTPYNRQVRAGDYSYHCWKWYSTGLNNLRGTNAESKVRYNQFRRDWTLM 267

Db 180 QRWGDAATINSYNDLRLIGNYTDYAVRWYNTGLERVMGPDSDRWVNRQFRRETLT 239  
Qy 268 VLDLVALPPSYDQWYPIKTAQTREVTDAIGTVHHPSPFTSTTWYNNAPSFSAIEA 327  
Db 240 VLDLVALFNSYDSRRYPIRTVSQUTREIYNTPV-----LENFDSFRGMAQ 285  
Qy 328 AV---VRNPHLLDFLEQVITYSLSRWSNTQYMMWGGHKLFRITGGT---LNISTQGS 381  
Db 286 RIEQNIRQPHLMDILNRIITYTDVHRG-----FNWMSGHQITASPVGSGPEPAPFLFGN 340  
Qy 382 TMTSINPVTLPFTSRDVRTESEL-----AGLN---LFLTPQVNVPRVDHFWKFTVH 429  
Db 341 AGNAAPPVLVLGLGIFRTLSPLRYRIILGSGPNQNELFV-----LDGTEFSFASLT 395  
Qy 430 PIASDNFYYPGAGIGTQLQDSENELPPEATGQNYESYHRLSHIGLISAS-----HVK 484  
Db 396 NLPSTIYRQGTV-----DSLDPVPPQDNSVPPRAGFSHRLSHVMTLSQAAGAVTLR 448  
Qy 485 ALVYSWTHRSADRNTIIPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTTGTG 544  
Db 449 APTFSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPFTGGDILRRTPGQIS 508  
Qy 545 DIRVNINPPAQRVRIRYASTTDLQHTSINKKAINOGNFSATMARGEDLDYKTFXTV 604  
Db 509 TLRVNITAPLSQRVRIRYASTTDLQHTSIDGRPINQGNFSATMSSGNSLQSGSPRTV 568  
Qy 605 GFTTTPFSLDQVSTFTIGAMWFSNGEVYIDRIEFVPEVTEYAEYDFEKAQKVTALEFT 664  
Db 569 GFTTTPFNSGSSVFTLSAHVFNSENEVYIDRIEFVPAEVTFEAYDLERAKAVNELFT 628  
Qy 665 STNPRGLKTDVKDHYDQVSNLVECLSDPEFCLDEKQELSEKVKHAKRLSDERNL 718  
Db 629 SSNIGLKTVDYDHYDQVSNLVECLSDPEFCLDEKQELSEKVKHAKRLSDERNL 682

## RESULT 14

JT0241  
parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)  
N:Alternate names: 135K insecticidal protein  
C:Species: Bacillus thuringiensis  
C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C:Accession: JT0241  
R:Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.  
Agric. Biol. Chem. 52, 1565-1573, 1988  
A:Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein  
A:Reference number: JT0241  
A:Accession: JT0241  
A:Molecule type: DNA  
A:Residues: 1-1176 <SHI>  
A:Cross-references: UNIPROT:P02965  
A:Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal proteins  
C:Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 38.2%; Score 1432; DB 2; Length 1176;  
Best Local Similarity 43.1%; Pred. No. 9, 6e-91;  
Matches 308; Conservative 118; Mismatches 222; Indels 66; Gaps 13;

Qy 36 NINHEDCUKMSYENVE-PFVSASTIQTG-----IGIAGKILGTGVFPAGQVASYLS 87  
Db 4 NENINECIPYNCLSNPEVEVLGGERIETGYTPTDLSLSTQFLSEF-VPGAGFVLGLVD 62  
Qy 88 FILGELWPKGNQWEIEFMEHVEEIIINOKISTYARNKALTDLKGDLALAVYHDSLESWVG 147  
Db 63 ILWIGIF---GPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGSLNLYQIYAESPREWEA 119  
Qy 148 NRNNTRARSVVKVSKQVIALELMFVQKLPSPAVSGEEVPLPIYQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMNSALTTPALFVQVNYQVPLSVYVQAANLHLSVLRDVSFVG 179  
Qy 208 KEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRGTNAESWRYNRQFRDWTLM 267

## RESULT 15

JC2219  
parasporal crystal protein cryIAa - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C>Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004  
C:Accession: JC2219  
R:Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.  
BioSci. Biotechnol. Biochem. 56, 830-835, 1994  
A:Title: Cloning of a new cryIA(a) gene from Bacillus thuringiensis strain FU-2-7 and analysis of its function  
A:Reference number: JC2219; MUID:94289859; PMID:7764972  
A:Accession: JC2219  
A:Molecule type: DNA  
A:Residues: 1-1176 <UDA>  
A:Cross-references: UNIPROT:Q45736; DDBJ:D17518; NID:9506190; PIDN:BA04468.1; PID:953578  
C:Genetics:  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 38.0%; Score 1426; DB 2; Length 1176;  
Best Local Similarity 43.0%; Pred. No. 2, 5e-90;  
Matches 307; Conservative 118; Mismatches 223; Indels 66; Gaps 13;

Qy 36 NINHEDCUKMSYENVE-PFVSASTIQTG-----IGIAGKILGTGVFPAGQVASYLS 87  
Db 4 NENINECIPYNCLSNPEVEVLGGERIETGYTPTDLSLSTQFLSEF-VPGAGFVLGLVD 62  
Qy 88 FILGELWPKGNQWEIEFMEHVEEIIINOKISTYARNKALTDLKGDLALAVYHDSLESWVG 147  
Db 63 ILWIGIF---GPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGSLNLYQIYAESPREWEA 119  
Qy 148 NRNNTRARSVVKVSKQVIALELMFVQKLPSPAVSGEEVPLPIYQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMNSALTTPALFVQVNYQVPLSVYVQAANLHLSVLRDVSFVG 179  
Qy 208 KEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRGTNAESWRYNRQFRDWTLM 267

Db 180 QRMGFDATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWRVYNQFRRELTLT 239  
Qy 268 VLDLVALFPSTYQMYPIKTAQLTREVYDAIGTVHPHPSFTSTWYNNAPSPSAIEA 327  
Db 240 VLDLVALFSYDGRYRIRTVSQTREIYNPV-----LENFDGSRGMAQ 285  
Qy 328 AV---VRNPHLLDFLEOVIIYSLLSWSNTQYMMWGGHKLPRITGGT---LNISTQGS 381  
Db 286 RISEQNRQPHMLDILNSITITVDVHRG-----FNYWSGHQITASPVGFGSGPEFAPLFGN 340  
Qy 382 TMTSINPVTLPFTSRDVRTESL-----AGLN---LFLTQPVNVPRVDFHMKFVTH 429  
Db 341 AGNAAPVVLSTGLGIFRLLSPLRYRIILGSGPNNQELFV-----LDGTEFSPASLTT 395  
Qy 430 PIASDNFPYPGYAGIGTQLODSNELPPEATGPNYESYSHRLSHIGLISAS-----HVK 484  
Db 396 NLPSTIYRQGTV-----DSLVDVIPPQDONSVPFRAGFSHRLSHVMTLSQAAGAVVTLR 448  
Qy 485 ALVYSWTHRSADRNTNIEPNSITQIPLVKAFLNLSGNAVVRGPGFTGGDILRETNTGTFG 544  
Db 449 APTFSWQHSRAEPNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRETSPQIS 508  
Qy 545 DIRVNIAPPQARYRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYKTFXTV 604  
Db 509 TLRVNIAPLSQRYRIRYASTTNLQFHTSIDGRPINQGNFSATWSSGNLQSGSFRIV 568  
Qy 605 GFTTFFSLLDVQSTFTTIGAWNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEKVTALET 664  
Db 569 GFTTFFNFSNGSVFTLSAHVFNNGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFT 628  
Qy 665 STNPRGLKTDVKDYHIDQVNLVESLSDEFYLDKRELFELIVKAKQLHIERNM 718  
Db 629 SSNQIGLKTVDYDHYDQVNLVECLSDFECLDEKQELSEKVKHAKRLSDERNL 682

Search completed: February 14, 2005, 21:00:45  
Job time : 19.5604 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:22:09 ; Search time 60.011 Seconds  
(without alignments)  
3909.384 Million cell updates/sec

Title: US-10-019-823B-54  
Perfect score: 3749  
Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KRELFEIVKYAKQLHIERN 718

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1376875 segs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications\_AA.\*
- 1: /cgn2\_6/prodata/2/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pep.\*
  - 4: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/prodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/prodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/prodata/2/pubpaa/US08\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/prodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/prodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/prodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/prodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/prodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/prodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/prodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
  - 17: /cgn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
  - 18: /cgn2\_6/prodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
  - 20: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3722.5	99.3	719	16	US-10-782-020-10 Sequence 10, Appl
2	3722.5	99.3	719	16	US-10-782-141-8 Sequence 8, Appl
3	3439	91.7	710	15	US-10-428-961-42 Sequence 42, Appl
4	2249	60.0	1228	16	US-10-809-953-10 Sequence 10, Appl
5	2236	59.6	1207	10	US-09-988-462-7 Sequence 7, Appl
6	2156	57.5	1227	15	US-10-428-961-63 Sequence 63, Appl
7	2141	57.1	1186	9	US-09-826-660-23 Sequence 23, Appl
8	2085.5	55.6	1228	15	US-10-428-961-38 Sequence 38, Appl
9	2085.5	55.6	1228	15	US-10-614-524-2 Sequence 2, Appl
10	1902	50.7	643	9	US-09-826-660-25 Sequence 25, Appl
11	1708	45.6	1167	14	US-10-089-678-1 Sequence 1, Appl
12	1658	44.2	653	15	US-10-428-961-6 Sequence 6, Appl
13	1652	44.1	1157	16	US-10-782-141-16 Sequence 16, Appl

14	1500.5	40.0	1206	13	US-10-032-717-2	Sequence 2, Appl
15	1500.5	40.0	1206	14	US-10-414-637-2	Sequence 2, Appl
16	1500.5	40.0	1206	15	US-10-606-320-2	Sequence 2, Appl
17	1477.5	39.4	1210	13	US-10-032-717-4	Sequence 4, Appl
18	1477.5	39.4	1210	14	US-10-414-637-4	Sequence 4, Appl
19	1477.5	39.4	1210	15	US-10-606-320-4	Sequence 4, Appl
20	1474	39.3	1156	14	US-10-093-285-72	Sequence 72, Appl
21	1474	39.3	1156	15	US-10-428-961-28	Sequence 28, Appl
22	1441.5	38.5	1155	9	US-09-756-643-2	Sequence 2, Appl
23	1441.5	38.5	1155	10	US-09-988-462-9	Sequence 9, Appl
24	1441.5	38.5	1155	15	US-10-136-998A-2	Sequence 2, Appl
25	1441.5	38.5	1177	14	US-10-035-060-6	Sequence 6, Appl
26	1441.5	38.5	1181	10	US-09-988-462-11	Sequence 11, Appl
27	1441.5	38.5	1181	10	US-09-988-462-13	Sequence 13, Appl
28	1441.5	38.5	1181	10	US-09-988-462-15	Sequence 15, Appl
29	1441.5	38.5	1181	10	US-09-988-462-17	Sequence 17, Appl
30	1441.5	38.5	1181	10	US-09-988-462-28	Sequence 28, Appl
31	1441.5	38.5	1181	15	US-10-136-998A-4	Sequence 4, Appl
32	1441.5	38.5	1181	15	US-10-136-998A-8	Sequence 8, Appl
33	1441.5	38.5	1181	15	US-10-136-998A-10	Sequence 10, Appl
34	1441.5	38.5	1181	15	US-10-136-998A-12	Sequence 12, Appl
35	1436.5	38.3	1177	14	US-10-035-060-2	Sequence 2, Appl
36	1434.5	38.3	1177	14	US-10-035-060-8	Sequence 8, Appl
37	1433.5	38.2	1177	14	US-10-102-469-24	Sequence 24, Appl
38	1422	37.9	1176	16	US-10-782-141-6	Sequence 6, Appl
39	1400	37.3	1176	11	US-09-837-961-2	Sequence 2, Appl
40	1380.5	36.8	1167	15	US-10-428-961-40	Sequence 2, Appl
41	1360.5	36.3	1177	9	US-09-873-873-26	Sequence 26, Appl
42	1360.5	36.3	1177	10	US-09-916-956A-26	Sequence 26, Appl
43	1360.5	36.3	1177	10	US-09-997-914-26	Sequence 26, Appl
44	1360.5	36.3	1177	14	US-10-365-645-26	Sequence 26, Appl
45	1360.5	36.3	1177	14	US-10-365-645-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1  
US-10-782-020-10  
; Sequence 10, Application US/10782020  
; Publication No. US20040197916A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Kozziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXM1-004, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for its Use  
; FILE REFERENCE: 045600/274139  
; CURRENT APPLICATION NUMBER: US/10/782,020  
; PRIOR FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,810  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-020-10

Query Match	99.3%	Score	3722.5	DB	16	Length	719
Best Local Similarity	99.4%	Pred. No.	4.5e-303				
Matches	715	Mismatches	0	Indels	1	Gaps	1
QY	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEFVSASTI	60				
DB	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEFVSASTI	60				
QY	61	QTGIGTAGKILCTGLGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEIINQKISTYA	120				
DB	61	QTGIGTAGKILCTGLGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEIINQKISTYA	120				

Qy	121	RNKALTDLKGIDALAVYHDSLSWGNRNNTARSVVKSQYIALELMFVQKLPSPAVSG	180
Db	121	RNKALTDLKGIDALAVYHDSLSWGNRNNTARSVVKSQYIALELMFVQKLPSPAVSG	180
Qy	181	BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVRAGDYSVHCVKWYS	240
Db	181	BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVRAGDYSVHCVKWYS	240
Qy	241	TGLNLRGTNAESWVRNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI	300
Db	241	TGLNLRGTNAESWVRNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI	300
Qy	301	GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW	360
Db	301	GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW	360
Qy	361	GGHKLFEFTIGTTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFTQPVN-VPR	419
Db	361	GGHKLFEFTIGTTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFTQPVN-VPR	419
Qy	420	VDHFWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS	479
Db	421	VDHFWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS	480
Qy	480	ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRTN	539
Db	481	ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRTN	540
Qy	540	TGTFGDIRVNIAPPFAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATNMRGEDLDYK	599
Db	601	TFTVGTFTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV	659
Qy	660	TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFFYLDEKRELFEIVKAKQLHIERNM	718
Db	661	TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFFYLDEKRELFEIVKAKQLHIERNM	719
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US-10-782-141-8			
; Sequence 8, Application US/10782141			
; Publication No. US20040197917A1			
; GENERAL INFORMATION:			
; APPLICANT: Carozzi, Nadine			
; APPLICANT: Hargies, Tracy			
; APPLICANT: Koziel, Michael G.			
; APPLICANT: Duck, Nicholas B.			
; APPLICANT: Carr, Brian			
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and			
; TITLE OF INVENTION: Methods for its Use			
; FILE REFERENCE: 045600/274143			
; CURRENT APPLICATION NUMBER: US/10782.141			
; CURRENT FILING DATE: 2004-02-20			
; PRIOR APPLICATION NUMBER: 60/448,632			
; PRIOR FILING DATE: 2003-02-20			
; NUMBER OF SEQ ID NOS: 23			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 8			
; LENGTH: 719			
; TYPE: PRT			
; ORGANISM: Bacillus thuringiensis			
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Best Local Similarity 99.4%; Pred. No. 4.5e-303;			
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;			
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; NAME/KEY: misc_feature
; LOCATION: (200)..(200)
; OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid
US-10-428-961-42

Query Match      91.7%; Score 3439; DB 15; Length 710;
Best Local Similarity 91.9%; Pred. No. 2.7e-279;
Matches 661; Conservative 15; Mismatches 33; Indels 10; Gaps 2;

Qy 1 MKLNQDKHQSPSSNAKVDKISDLSKNETDIEQLQNHEDCLKMSEYENVEPFFVSASTI 60
Db 1 MKSKNQMQSLNNATVDKNFTGSLNNNTNTEQLQPNH-----EGIEPFFVSSTI 51

Qy 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYTA 120
Db 52 QTGIGIAGKILGNLGVPPAGQVASYLSFILGELWPKGQWEIFMEHVEELINQKISTYA 111

Qy 121 RNKALTDLGLDALAVYHDSLESVGNRNNTARSVVKSYQIALBELMFVKLPSPAVSG 180
Db 112 RNKALADLGLDALAVYHDSLESWTENRNTRSVKSYQITLLEMFVQSLPSPAVSG 171

Qy 181 EEVPLPIVAQAANLHLLLRDASIFGKWLSSSISFTYNNQVRAGDYSVHCWKYS 240
Db 172 EEVPLPIVAQAANLHLLLRDASIFGKWLSSSISFTYNNQVSGKSEYSDHCWKYN 231

Qy 241 TGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPSYDTQYPIKTTAQLTREYVTDAT 300
Db 232 TGLNLRGMNAESWRYNQFRDMTLMVLDLVALFPSYDTQYPIKTTAQLTREYVTDAT 291

Qy 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQMNW 360
Db 292 GTVHPHPSFTSTWYNNAPSPSTIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQMNW 351

Qy 361 GGHKLFRTIGTLNLTSTGNTSINPVTLPSTRDVYRTESLAGLNLFLOPVN-VPR 419
Db 352 GGHKLFRTIGTLNLTSTGNTSINPVTLPSTRDVYRTESLAGLNLFLOPVNGVPR 411

Qy 420 VDFHWFVTHPIASDNFFYPGYAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 479
Db 412 VDFHWFVTHPIASDNFFYPGYAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 471

Qy 480 ASHVKALVSWTHRSADRTNTEIPNSITQIPLVKAFLNSGAAVVRGPGFTGGDILRRN 539
Db 472 ASHVKALVSWTHRSADRTNTEIPNSITQIPLVKAFLNSGAAVVRGPGFTGGDILRRN 531

Qy 540 TGTGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGDLDYK 599
Db 532 TGTGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGDLDYK 591

Qy 600 TFXTVGFTTPFSLDVQSTFTIGAMNFFSGNEVYIDRIEFPVPEVYEAEDPEKAQEV 659
Db 592 TFXTVGFTTPFSDVQSTFTIGAMNFFSGNEVYIDRIEFPVPEVYEAEDPEKAQEV 651

Qy 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELIVKYAKQLHBRNM 718
Db 652 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELIVKYAKQLHBRNM 710

RESULT 4
US-10-809-953-10
; Sequence 10, Application US/10809953
; Publication No. US2004018125A1
; GENERAL INFORMATION:
; APPLICANT: Van Mellaert, Herman
; APPLICANT: Botterman, Johan
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Joos, Henk
; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTICIDAL PROTEINS
; FILE REFERENCE: 021565-078
; CURRENT APPLICATION NUMBER: US/10/809,953
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/09/661,016
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; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: PCT/EP90/00905
; PRIOR FILING DATE: 1990-05-30
; PRIOR APPLICATION NUMBER: GB 89401499.2
; PRIOR FILING DATE: 1989-05-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-809-953-10

Query Match      60.0%; Score 2249; DB 16; Length 1228;
Best Local Similarity 62.3%; Pred. No. 4.5e-179;
Matches 446; Conservative 80; Mismatches 164; Indels 26; Gaps 7;

Qy 23 TDSLNKNETDIEQLQNH-----EDCLKMSEYENVEPFFVSASTIQTGIGIAGKI 70
Db 2 TSNRNKNEEIIINAVGNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61

Qy 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLAG 130
Db 62 LGVLGVPPAGQVASYLSFILGELWPRGDQWEIFLEHVEQLINQOITENARNALALQOG 121

Qy 131 LGDALAVYHDSLESVGNRNNTARSVVKSYQIALBELMFVKLPSPAVSGEBEVLPIYA 190
Db 122 LGDSFRAYQOSLEDMLNRRDDARTSVLHTQVIALLELDFLNAMPLFAIRNQEVPLLMVYA 181

Qy 191 QAANLHLLLRDASIFGKWLSSSISFTYNNQVRAGDYSVHCWKYSTGLNLRGNTN 250
Db 182 QAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVTRTDSYCVQEWYNTGLNSLRGTN 241

Qy 251 AESWRYNQFRDMTLMVLDLVALFPSYDTQYPIKTTAQLTREYVTDATGTVHPHPSFT 310
Db 242 AASWRYNQFRDMLTLGVLDLVALFPSYDTYPINTSAQLTREYVTDATGAT--GVNMA 299

Qy 311 STTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQMNWGGHKLFRFTI 370
Db 300 SNWYNNAPSPSAIEAAAIRSPHLLDFLEQLTIFSASSRWSNTRHMTYWRGHTIQSRPI 359

Qy 371 GGTLMISTGNTSINPVTLPSTRDVYRTESLAGLNLF--LTPQVN-VPRVDHFWKFV 427
Db 360 GGGLTSTHGATNTSINPVTLPSTRDVYRTESYAGVLLWGIYLEPIHGVPVTRFNF--- 416

Qy 428 THP-----IASDNFFYPGYAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLISASH 482
Db 417 TNPQWISDRGTANYSQP-YESFGLQKQSELTPELTERPNYESYSHRLSHIGLILQSR 475

Qy 483 VKALVYSWTHRSADRTNTEIPNSITQIPLVKAFLNSGAAVVRGPGFTGGDILRRNTGT 542
Db 476 VNPVYVSWTHRSADRTNTEIPNRIQIPMVKASELPQGTTVVRGPGFTGGDILRRNTGT 535

Qy 543 FGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGDLDYKTFX 602
Db 536 FGPVIRTVNGPLTQYRIGFRYASTVDFDFVSRGTTVNNFRFLRTMNSDELKYGNFV 595

Qy 603 TVGFTTPFSLDVQSTFTIGAMNFFSGNEVYIDRIEFPVPEVYEAEDPEKAQEVKAL 662
Db 596 RRAFTTPFTTQIDIIRTSIQGLSGNGEVIIDKLEIIPVTATFEAYEDLERAQEAVNAL 655

Qy 663 FTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELIVKYAKQLHIERNM 718
Db 656 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDCLDEKRELLKVKYAKRLSDERNL 711

RESULT 5
US-09-988-462-7
; Sequence 7, Application US/09988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
```

Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Lauais, Karen L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Syngenta Biotechnology, Inc.  
STREET: 3054 Cornwalis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/988,462  
FILING DATE: 20-NO. US20030046726A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/547,422  
FILING DATE: 11-APR-2000  
APPLICATION NUMBER: US 08/459,504  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-188051  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-988-462-7

Query Match 59.6%; Score 2236; DB 10; Length 1207;  
Best Local Similarity 63.9%; Pred. No. 5.4e-178;  
Matches 439; Conservative 78; Mismatches 156; Indels 14; Gaps 6;  
QY 40 EDCLKMSEYENPEFVSASTIOTGIGIAGKILGTGVPFAGQVASYLFIIGELWPKGN 99  
DB 10 EDCLCAEAGNIDPFVSASTVQTGINIAGRIILGVLPFAGQVASYLFIIGELWPKGRD 69  
QY 100 QWEIFMEHVEEIIINQKISTYARNKALTDKLGDLAVYHDSLEWVGNNRTRARSVK 159  
DB 70 QWEIFLEHVEQLINQITENARNALRLQGLGDSFRAYQOQSLDWNLRDARTSVLY 129  
QY 160 SQVIALELMFVQKLPFASVSGEVPPLPIYAQANLHLLLRDASTFGKEMGLSSSEIST 219  
DB 130 TQVIALELDFNAMPFLFARNQEVPLLMVYAQANLHLLLRDASTFGSEFGLTQEQIOR 189  
QY 220 FYNQVERAGDYSYHCVKWYSTGLNNLRGTNAESWRYNQPRDMLVLDLVALFPSSYD 279  
DB 190 YIERQVERTRDYSYCVIEWNTGLNSLRGTNAESWRYNQPRDMLVLDLVALFPSSYD 249  
QY 280 TQMPYPIKTAQLTREVTDAIGTVHPSPFTSTTNNNAPSFSAIEAAVVRPHLLDFL 339

250 TETYPINTSAQLTREVTDAIGAT--GVNMMASMMWYNNNAPSFSAIEAAAIRSPHLLDFL 307  
QY 340 EQVTIYSLLSRWSTNTQYNNMGGHKLBFRTTGGTLNISTOGSTNTSINPVTLPFTSRDVS 399  
DB 308 EQLTIFSSASRWSNTRHMTYWRGHTIOSRPJGGGLNTSTHGAINTSINPVTLPFTSRDVS 367  
QY 400 RTESLAGLNLF--LTQPVN-VRVDFHWKFVTHP-----IASDNFYFPGYAGIGTQLQDS 451  
DB 368 RTESVAGVLLWGIYLEPHGVPTVRNF--TNQNISDRGTANYSQP-YESPGLQLKDS 423  
QY 452 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVSWTHRSADRTNTPNSITQIPL 511  
DB 424 ETELPPETTERENYESYSHRLSHIGLILQSRVNPVSWTHRSADRTNTPNSITQIPL 483  
QY 512 VKAFNLSSGAAVVRGPGTGGDILARTNTGTGDIRVNINPFPFAQRYVRIRYASTTDLQ 571  
DB 484 VKASELPQGTTVVRGPGTGGDILARTNTGTGDIRVNINPFPFAQRYVRIRYASTVD 543  
QY 572 FHTSINGKAINQCNFSATNMGEDLDYKTFXVTGVTTPFSLDVGSTFTTIGAWNFSSNE 631  
DB 544 FVSRGGTTVNNFRFLRTMNSGDELKYNFVRRFTTPTFTQIQIIRTSIQGLSGNGE 603  
QY 632 VYIDRIEFPVPEVTEAEYDFEKAQKVTALFTSTNPRCLKTDVXDYHIDQVSNLVESIS 691  
DB 604 VYIDKIEIIPVTATEAEYDLERAQEAVALFTNPRRLKTDVTDYHIDQVSNLVACLS 663  
QY 692 DEFYLDKRELFEIVKYAKOLHIERNM 718  
DB 664 DEFCLDEKRELLEKVKYAKLSDERNL 690

RESULT 6  
US-10-428-961-63  
; Sequence 63, Application US/10428961  
; Publication NO. US200303237111A1  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Rupa, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
; FILE REFERENCE: Polynucleotides, Compositions, and Methods of Use (Amended)  
; CURRENT APPLICATION NUMBER: US/10/428,961  
; PRIOR FILING DATE: 2003-05-02  
; PRIOR FILING DATE: 09/661,322  
; PRIOR FILING DATE: 2000-09-13  
; PRIOR FILING DATE: 60/153,995  
; PRIOR FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 63  
; LENGTH: 1227  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-428-961-63

Query Match 57.5%; Score 2156; DB 15; Length 1227;  
Best Local Similarity 58.8%; Pred. No. 2.9e-171;  
Matches 420; Conservative 105; Mismatches 175; Indels 14; Gaps 4;  
QY 13 SSNAKVDKISTDLSKN-----ETDIELQINIHEDCLKMSEYENPEFVSASTIOTGIG 65  
DB 7 NENEIINALSTPAVSNHSAQNNLSTDAI-----EDSLCAEAGNIDPFVSASTVQTGIN 61  
QY 66 IAGKILGTGVPFAGQVASYLFIIGELWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 125  
DB 62 IAGRIILGVLPFAGQVASYLFIIGELWPKGRDPWEIFLEHVEHLIRQQVTRTAL 121  
QY 126 TDLKGLGDALAVYHDSLEWVGNNRTRARSVKQVIALELMFVQKLPFASVSGEVP 185



Db	122	ARLQGLGNSFRAYQOSLEDWLENRDDARTSRVLYQTQVIALEBDFLNMPLFAIRNQEVPL	181
Qy	186	LPIYAQAANLHLLLRDASIFKGEKGLSSSEISFTFYNNRQVERAGDYSYHCWKVYSTGLNN	245
Db	182	LMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEKTRREYSYDCARWYNTGLNN	241
Qy	246	LGRGTAESWRYNQPRRDMTLMVLDLVALPSPSYDTOMYPDKTTAQLTRREYVYDAIGTVHP	305
Db	242	LGRGTAESWLRYNQPRRDLTLGVLDLVALPSPSYDTRVYPMNTSAQLTRREYVYDPIGRGTA	301
Qy	306	HFSFTSTWYNNNAPSFAISAAVVRPHLLDPLEQVTIYSLLSRMSNTQYNNMGGHKL	365
Db	302	PGGFASFTWNNNAPSFAISAAVVRPHLLDPPPEQLTIIFSVLSRMSNTQYNNYVWGHKL	361
Qy	366	EPRTIGGTLNISTQGSTNTSINPVTLPFTSRDGVYRTESLAGNLFLTQPVN-VPRVDFHW	424
Db	362	ESRTIGSLSWTGHTNTSINPVTLPFTSRDGVYRTESFAGINILLTTPVNGVPMARFNV	421
Qy	425	KFVTHPIASDNFPYGYAGIGTQODSENELPPBATQOPNYESYSHRLSHIGLISASHVK	484
Db	422	RNPLASLRGSLTYTGYGVGTQTFDSSETLPPETTERPNYESYSHRLSNIRLISGNTLR	481
Qy	485	ALVYSWTHRSADRTWTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGFG	544
Db	482	APVSWTHRSADRTWTIISDSSITQIPLVKSNLMSGTSVVGSGPGFTGGDILRRNVGSL	541
Qy	545	DIRVINPFPFAQYRVRIYASTTDLPHTSINKAINQGNFATNMNRGEDLDYKTFXTV	604
Db	542	SNGLFNNTSLQYRVRYRYAASQTWVLRTVVGSTTFDQGFSTWSANESLTSQSFRPA	601
Qy	605	GTTTFPSLLDVQSTTTIGAMFSSGNEVYIDRIEFVPEVYTYBAEYDFEKAQEKVTALPT	664
Db	602	EPFVGISAGSQ-TAGISISNAGRQTQPHFKIEFIPITATFEAYDLERAQEAVALFT	660
Qy	665	STNPRCLKTDVKYHIDQVSNLVSLSDEFVLDKRELFLVKYAKQHLIERNM	718
Db	661	NTNPRRLKTVGTDYHIDEVSNLVAACLSDDEFCLDEKRELLEKVKYAKRLSDERNL	714
RESULT 7			
US-09-826-660-23			
; Sequence 23, Application US/09826660			
; Patent No. US20010026940A1			
; GENERAL INFORMATION:			
; APPLICANT: Cardineau, Guy A.			
; APPLICANT: Stelman, Steven J.			
; APPLICANT: Narva, Kenneth E.			
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins			
; FILE REFERENCE: MA-714XC2D1			
; CURRENT APPLICATION NUMBER: US/09/826,660			
; CURRENT FILING DATE: 2001-04-05			
; PRIOR APPLICATION NUMBER: 09/178,252			
; PRIOR FILING DATE: 1998-10-23			
; PRIOR APPLICATION NUMBER: 60/065,215			
; PRIOR FILING DATE: 1997-11-12			
; PRIOR APPLICATION NUMBER: 60/076,445			
; PRIOR FILING DATE: 1998-03-02			
; NUMBER OF SEQ ID NOS: 27			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 23			
; LENGTH: 1186			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene			
US-09-826-660-23			
Query Match 57.1%; Score 2141; DB 9; Length 1186;			
Best Local Similarity 58.5%; Pred. No. 5e-170;			
Matches 418; Conservative 108; Mismatches 174; Indels 14; Gaps			
Qy	13	SSNAKYDKISTSLKXN-----ETDIELQNHINHECLKMSYENVEPFFVSASTIQTGIG	65

```
Query Match 55.6%; Score 2085.5; DB 15; Length 1228;
Best Local Similarity 59.0%; Pred. No. 2.4e-165;
Matches 421; Conservative 98; Mismatches 183; Indels 11; Gaps 8;

QY 13 SNAKVDKISTSLKN-ETDIELO-NINHEDCLKMSEYENVEPVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66
QY 71 LGTGVPPAGQVASYFLIGELMPKGNOWEIPMEHVEEIIINQKISTYARNKALTDLKG 130
DB 67 LGVLGVPPAGQIASFYSLVGLMWRGRDQWEIFLEHVEQLINQIITENARNTALARQOG 126
QY 131 LGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPAVSGEEVPLPIYA 190
DB 127 LGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDLFNAMPFLAIRNQEVPLLMVYA 186
QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHVCWYKYSTGLNLRGTN 250
DB 187 QAAHLHLLLRDASLFGSEFGLTSQEIORYYERQVEQTRDYSCVWYNTGLNLRGTN 246
QY 251 AESWRYNQPRDMLVLDLVALPSPDYDTOMYIKTTAQLTRVYTDGATVTHPHPSFT 310
DB 247 AASWRYNQPRDMLVLDLVALPSPDYDTOMYIKTTAQLTRVYTDGATVTHPHPSFT 310
QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDPLEQVTIYSLSRWSNTQYNNMGGHKLFRTI 370
DB 305 SMWYNNAPSFSAIEATAVIRSPHLLDPLEQVTIYSLSRWSNTQYNNMGGHKLFRTI 364
QY 371 GGTLANISGTSTNTSINPVLPTFSRDVYRTESLAGLNLFP--LTQPVN-VPRVDFHWKFV 427
DB 365 GGGTNTSTHGTSTNTSINPVLPTFSRDVYRTESLAGLNLFP--LTQPVN-VPRVDFHWKFV 427
QY 428 --THPIASDNFYYPGAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLISASHVKA 485
DB 425 QNTFERGTANYSQP--YESPGLQKDSLETLPPTERRPNYESYSHRLSHIGLISASHVKA 483
QY 486 LVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTNTGTGFGD 545
DB 484 PYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTNTGTGFGD 545
QY 546 IRVNNPPPAQRYRVRIRYASQTQVLRVTVGGSTTFDQGFPTMSANESLTSQSFRFAE 603
DB 544 MGLNPNNTSLQRYRVRIRYASQTQVLRVTVGGSTTFDQGFPTMSANESLTSQSFRFAE 603
QY 606 FTTPFSLDLVQSTFTTIGAMNFGSGNEVYIDRIEFVPEVTEAEYDFEKAQEKVTALFTS 665
DB 604 FPVGISASGSQ--TAGISISNNAGRTQTFHDKIEFIPITATFEAYDLERAQEAVALFTN 662
QY 666 TNPRLGKTDVTDYHIDQVSNLVESLSDPEYLDKRELFEIVKYAKQLHIERNM 718
DB 663 TNPRLKTDVTDYHIDQVSNLVESLSDPEYLDKRELFEIVKYAKQLHIERNM 715

RESULT 10
US-10-614-524-2
; Sequence 2, Application US/10614524
; Publication No. US20040016020A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
; CURRENT APPLICATION NUMBER: US/10/614,524
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/739,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28

; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-614-524-2

Query Match 55.6%; Score 2085.5; DB 15; Length 1228;
Best Local Similarity 59.0%; Pred. No. 2.4e-165;
Matches 421; Conservative 98; Mismatches 183; Indels 11; Gaps 8;

QY 13 SNAKVDKISTSLKN-ETDIELO-NINHEDCLKMSEYENVEPVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66
QY 71 LGTGVPPAGQVASYFLIGELMPKGNOWEIPMEHVEEIIINQKISTYARNKALTDLKG 130
DB 67 LGVLGVPPAGQIASFYSLVGLMWRGRDQWEIFLEHVEQLINQIITENARNTALARQOG 126
QY 131 LGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPAVSGEEVPLPIYA 190
DB 127 LGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDLFNAMPFLAIRNQEVPLLMVYA 186
QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHVCWYKYSTGLNLRGTN 250
DB 187 QAAHLHLLLRDASLFGSEFGLTSQEIORYYERQVEQTRDYSCVWYNTGLNLRGTN 246
QY 251 AESWRYNQPRDMLVLDLVALPSPDYDTOMYIKTTAQLTRVYTDGATVTHPHPSFT 310
DB 247 AASWRYNQPRDMLVLDLVALPSPDYDTOMYIKTTAQLTRVYTDGATVTHPHPSFT 310
QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDPLEQVTIYSLSRWSNTQYNNMGGHKLFRTI 370
DB 305 SMWYNNAPSFSAIEATAVIRSPHLLDPLEQVTIYSLSRWSNTQYNNMGGHKLFRTI 364
QY 371 GGTLANISGTSTNTSINPVLPTFSRDVYRTESLAGLNLFP--LTQPVN-VPRVDFHWKFV 427
DB 365 GGGTNTSTHGTSTNTSINPVLPTFSRDVYRTESLAGLNLFP--LTQPVN-VPRVDFHWKFV 427
QY 428 --THPIASDNFYYPGAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLISASHVKA 485
DB 425 QNTFERGTANYSQP--YESPGLQKDSLETLPPTERRPNYESYSHRLSHIGLISASHVKA 483
QY 486 LVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTNTGTGFGD 545
DB 484 PYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTNTGTGFGD 545
QY 546 IRVNNPPPAQRYRVRIRYASQTQVLRVTVGGSTTFDQGFPTMSANESLTSQSFRFAE 603
DB 544 MGLNPNNTSLQRYRVRIRYASQTQVLRVTVGGSTTFDQGFPTMSANESLTSQSFRFAE 603
QY 606 FTTPFSLDLVQSTFTTIGAMNFGSGNEVYIDRIEFVPEVTEAEYDFEKAQEKVTALFTS 665
DB 604 FPVGISASGSQ--TAGISISNNAGRTQTFHDKIEFIPITATFEAYDLERAQEAVALFTN 662
QY 666 TNPRLGKTDVTDYHIDQVSNLVESLSDPEYLDKRELFEIVKYAKQLHIERNM 718
DB 663 TNPRLKTDVTDYHIDQVSNLVESLSDPEYLDKRELFEIVKYAKQLHIERNM 715

; Sequence 25, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
```

FILE REFERENCE: Q68921  
CURRENT APPLICATION NUMBER: US/10/089,678  
CURRENT FILING DATE: 2002-05-02  
PRIOR APPLICATION NUMBER: JP 2000-236140  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: PCT/JP01/06660  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 1  
LENGTH: 1167  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis  
FEATURE:  
OTHER INFORMATION: Toxin encoded by synthetic B.t. gene  
US-09-826-660-25

Query Match 50.7%; Score 1902; DB 9; Length 643;  
Best Local Similarity 57.2%; Pred. No. 2.2e-150;  
Matches 368; Conservative 100; Mismatches 161; Indels 14; Gaps 4;  
QY 13 SSNAKVDKISTSLK-----ETDIQLQNHEDCLMKSEYENVEPPVASTIQTGIG 65  
DB 7 NENEINALSIPAVNSHAQWNLSTDARI-----EDSLCIAEGNIDPFVASTVQTGIN 61  
QY 66 IAGKILGTGVPAGQVASYLFGELWPKGNQWEIFMEHVEEINQKISTYARKAL 125  
DB 62 IAGRIILGVLPAGQIASYSLFGELWPKGRDPWEIFLEHVEQLIRQOQVETRDAL 121  
QY 126 TDLKGLGDALAVHDSLESVWGNRNTARSVVKSOVIALLELMFVQKLPFAVSGEEVPL 195  
DB 122 ARIQGLGNSTRAVOQSLEDWLENRDDARTSVLTQYIALLELFLNAPLFAIRNQEVL 191  
QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDSYHCVKMYSTGLNN 245  
DB 182 LMVYAQAANLHLLLRDASIFGSEFGLTSQEIQRYYERQVEKREYSDYCARVNTGLNN 241  
QY 246 LRGTAESWRYNQFRDRTMLVLDVALPFSYDTOMYPIKTAQLTREVYDTAIGTVHP 305  
DB 242 LRGTAESWRYNQFRDRTMLVLDVALPFSYDTOMYPIKTAQLTREVYDTAIGTVHP 301  
QY 306 HPSFTSTWYNNAPSAEAAVVRNPHLLDFLEQVITYSLSRNSNTQYNNMGHKL 365  
DB 302 PSGFASNTWNNAPSAEAAVVRNPHLLDFLEQVITYSLSRNSNTQYNNMGHKL 361  
QY 366 EFRITIGTLNISTQSTNTSINPVTLPFTSRDVRYESLAGLNLFTQPVN-VPRVDFHW 424  
DB 362 ESRTIRGSLSTHGNTSINPVTLPFTSRDVRYESLAGLNLFTQPVN-VPRVDFHW 421  
QY 425 KFTVTHPIASDNFYVPGVAGITQLODSENELPEATGQPNYESYSHRLSHIGLISASHVK 494  
DB 422 RNPLNSLRGSLLYTIGTGVGTQLODSENELPEATGQPNYESYSHRLSHIGLISASHVK 491  
QY 485 ALVYSWTHRADRTNTEPNSITQIPLVAFNLSSGAAVVRGPGFTGGDILRENTGTG 544  
DB 482 APVYSWTHRADRTNTEPNSITQIPLVAFNLSSGAAVVRGPGFTGGDILRENTGTG 541  
QY 545 DIRWINPPAQRYRVRIRVASTTDLQFHTSINGKAINQGNFSAATMNRGDLDTKPTXV 604  
DB 542 SMGLNFNTSLQRYRVRVRAASQTMVLRVTVGSGTTFDQGFSTMSANESLTSQSFRFA 601  
QY 605 GPTTPFLLDQVSTFTTGAWNFSGNEVYIDRIEFVPEVTYE 647  
DB 602 EFPVGISASGSQ-TAGISISNAGRQTFHFDEKIEFIPITATLE 643

## RESULT 11

US-10-089-678-1  
Sequence 1, Application US/10089678  
Publication No. US20030017967A1  
GENERAL INFORMATION:  
APPLICANT: ASANO, Shinichiro  
TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A  
TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD

FILE REFERENCE: Q68921  
CURRENT APPLICATION NUMBER: US/10/089,678  
CURRENT FILING DATE: 2002-05-02  
PRIOR APPLICATION NUMBER: JP 2000-236140  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: PCT/JP01/06660  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 1  
LENGTH: 1167  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis  
FEATURE:  
OTHER INFORMATION: Toxin encoded by synthetic B.t. gene  
US-10-089-678-1  
Query Match 45.6%; Score 1708; DB 14; Length 1167;  
Best Local Similarity 47.4%; Pred. No. 1e-133;  
Matches 357; Conservative 126; Mismatches 222; Indels 48; Gaps 11;  
QY 1 MCLKNQDKHQ---SPSSNAKVDKISTDSLKNTDIELQNHEDCLMKSEYE-----NV 51  
DB 1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNNYKYLRMSEGENPELFGNP 60  
QY 52 EFPVSNSTIQTGIGTAGKILGTGVPAGQVASYLFGELWPKGNQWEIFMEHVEE 110  
DB 61 ETFISSSTVQTGIGIVGVLGALGVPFAGQIASFYSLVQGLWPSSTVSWEMIMKQVED 120  
QY 111 IINQKISTYARKALTDLKGGLDALAVHDSLESVWGNRNTARSVVKSOVIALLELMFV 170  
DB 121 LIDQKITDSVKTALAGLQGLGDLDVYQKSLKNWLENRDTARSVVVQYIALLELDFV 180  
QY 171 QKLPFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGD 230  
DB 181 AKIPSAISQGVPLLSVYAQAANLHLLLRDASIFGAEWGTGPGSEISTFYDRQVTRTAQ 240  
QY 231 YSHCVKMYSTGLNLRGTAESWRYNQFRDRTMLVLDVALPFSYDTOMYPIKTAQ 290  
DB 241 YSDYCVKMYNTGLDKLGTNAASWKLQHFREMTLLVLDLVALFPNYDTRTYPIETTAQ 300  
QY 291 LTRVVYDTAIGTVHPHPSFTSTWYNNAPSAEAAVVRNPHLLDFLEQVITYSLLS- 349  
DB 301 LTRVVYDTAIGTVHPHPSFTSTWYNNAPSAEAAVVRNPHLLDFLEQVITYSLLS- 360  
QY 350 -RWSNTQYNNMGHKLHLEFRTIGTLNISTQSTNTSINPVTLPFTSRDVRYESLAGL 407  
DB 361 LPLNTEYLEYVWGHISIKYKNTNASSALERNYGTITSNKIKYVDLANKDIFQVRSGLADL 420  
QY 408 NLFLTPQNVPRVDHFWKFTVHPHPSFTSTWYNNAPSAEAAVVRNPHLLDFLEQVITYSLLS- 453  
DB 421 ANYYAQVYGVYASFP-----TLDDKN---TCSGVSQVGGFTYSKPHTTWQVCTQNTYD 470  
QY 454 ELPPAATGQPNYESYSHRLSHIGLIS-----ASHVKALVYSWTHRADRTNTEPNS 505  
DB 471 EIPPE--NEPLSRGYSHRLSHITSYFSKQNASPARYGNLVPFAWTHRADRTNTEPNSDK 528  
QY 506 ITQIPLVAFNLSSGAAVVRGPGFTGGDILRENTGTGDIRVNIINPPFAQRYRVRIRYA 565  
DB 529 ITQIPLVAFNLSSGAAVVRGPGFTGGDILRENTGTGDIRVNIINPPFAQRYRVRIRYA 588  
QY 566 STTDLOFHTSINGKAINQGNFSAATMNRGDLDTKPTXVGTTPFLLDQVSTFTTGAWN 625  
DB 589 STTNLRLFVTISGTRIYSINVKNTWKNGDDLTFNTFDLATIGTAFSTFYSNLSLTGADS 648  
QY 626 FSSGNEVYIDRIEFVPEVTYEAEYDFEKAQKVTALTSTNPRGLKTDVCKYHIDQVSN 695  
DB 649 FASGGEVYVDFKELIPVNAATFAEEDLDVAKAVNGLFTSKKD-ALQTSVTDYQVNAAN 707  
QY 686 LVESLSDEFYLDKRELFEIVKYAKQLHTERNM 718  
DB 708 LVECLSDELYPNEKRWMLWDVAKEAKELVQARNL 740

## RESULT 12

```

US-10-428-961-6
; Sequence 6, Application US/10428961
; Publication No. US2003023711A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidodexan-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MBOC0201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-6

Query Match 44.2%; Score 1658; DB 15; Length 653;
Best Local Similarity 51.3%; Pred. No. 6.6e-130;
Matches 345; Conservative 104; Mismatches 175; Indels 48; Gaps 15;

QY 13 SSNAKVQKISTDSLKN---ETDIELQINHHEDCLKMSEYENVPFFVSASTIQIGIGIAGK 69
DB 2 NENEIINALSPAVNSHSAQMDLSL-DARIEDSLCIAEGNNINPLVSASTVQTGINIAGR 60

QY 70 ILGTGLVPFACQVASLVSFLIGELWPKGKNWEIEMEHVEEIIINOKISTYARNKALTDLK 129
DB 61 ILGLVGPFPAGQASFSYFLGELWPGGRDPWEIFLYEQILIRQQVETNRTAARLE 120

QY 130 GLGDALAVYHDSLESWGNRNNTARSVYKSQYIALEIMFVKQLPSFAVSGEEVPLPIY 189
DB 121 GLGRGYSYQQALETWLDNRNDARSRIILERYVALELDITTAIPLFRIRNEEVPLLMVY 180

QY 190 AQAAHLHLLLRDASIFKQEWGLSSSEISTPYNQOVERAGDYSHCVKYSTGLNNLRGT 249
DB 181 AQAAHLHLLLRDASLFGSEGMASDDNQYQIQIRYTEEYSHCVQYNTGLNNLRGT 240

QY 250 NAESHVRYNQRRDQMTLMVLDLVALFPSYDTQWYPIKTTAQLTREVYTDGIVTVPHPSP 309
DB 241 NAESHVRYNQRRDQMTLMVLDLVALFPSYDTQWYPIKTTAQLTREVYTDGIVTVPHPSP 300

QY 310 TSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYNNMMWGGHKLFRPT 369
DB 301 ASTNWFNNAPSFAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYNNMMWGGHKLFRPT 360

QY 370 IGGTINIQTGST-NTSINPVLTP-TRSDVYRATESLAGNLFTQPVN-VRPVDHEHWF 426
DB 361 IGGTINTSTQGTNNNTSINPVLTHVYSSRDVYRATESNAGTNILFTTPVNGVFWARFN--F 418

QY 427 VTHPTASDNFYYP-----GYAGIGTQLOQDSNEELPPEATGPNYESYSHRLSHIG-- 476
DB 419 IILRFMEKAPLPTVNRITRELGFNLYIQLNVHOK-----QQNDQIMNHVIDISYR 470

QY 477 LISASHKALVYSWTHRSADRNTTIEPSITQIPLVKAFNLSGGAUVRGFGFTGGDILR 536
DB 471 LIIGNTLRAPVYSWTHRSADRNTTIGPNRITQIPAVKGRFLFNG-SVTSGGFGFTGGDVVR 529

QY 537 -RTNCTGF---GDIRVNIN-PFFAQRVRYRIRYASTTDLOFHTSINGKALINQGNFSATMN 591
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QY 592 RGEDLDYKTFXTVGFPTPFSLLDVQSTFT-----IGAWNFSSGNEVYIDRIEFPVPEVT 645
DB 590 SLDNLO-----SGDEGVYEVINNAFTSATGNIVGARNFSANAEEVIDRFEFTPTVAT 640

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Db 523 SDKITQIPAVKGMMLYGGSSVQGGPGFTGGDILKRTNPNISILGTFATVTVNGSLSORVRRI 582  
Qy 563 RYASTTDQLQFHTSINGKAINQGFSPATMNRGEDIIDYKTFXTVGTFTPTPFSLLDVQSTFTIG 622  
Db 583 RYASTTDFE-LLVGLDPTIEKRNFKMTDNGASLTETFPFASFTDQFQRETKILLS 641  
Qy 623 ANPSSGNEVYDRIEFVPEVYEAEDPEKAQKVTAFTSTNPRGLTKTDVQVHIDQ 682  
Db 642 MGFSSGQEVYDRIEFVPEVYEAEDPEKAQKVTAFTSTNPRGLTKTDVQVHIDQ 700  
Qy 683 VSNLVSLSDEFYLDKRELFVYKAKQLHIERNM 718  
Db 701 AANLVECLSDDLYPNEKRLFFDAVREAKLSGARNL 736  
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US-10-032-717-2  
; Sequence 2, Application US/10032717  
; Publication No. US20020151709A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With  
; Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/032,717  
; CURRENT FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/242,838  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1206  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-032-717-2  
Query Match 40.0%; Score 1500.5; DB 13; Length 1206;  
Best Local Similarity 44.2%; Pred. No. 2.8e-116;  
Matches 336; Conservative 129; Mismatches 230; Indels 65; Gaps 22;  
Qy 1 MCLKNQDKHQSFSSNAKVDKISTDS----LKNETDIELQNHEDCLKM-----SEYE-N 50  
Db 1 MSPNNQNEYIIDATPST-SVSNDSNRYFPANPTNALQNDYKYLKMSAGNASEYPGS 59  
Qy 51 VEPFVSA-STIQTGIGIAGKILGTVFPFAGQVASYLSFYLGLWPKG-KNOMEIFMEHV 108  
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Qy 109 EEINQKISTYARNKALTDLKGLGDALAVYHDSLESVWGNRNTRARVSVKQSYALIELM 168  
Db 120 EEINQKIAYARNKALSELEGLNNYQLYLTALAEENPNPNSRALRDVNRFEILDLSL 179  
Qy 169 FVOKLPSFVSGREVPLPIYAQAANLHLLLDASIFGKEMGLSSSEISTFTYNROVERA 228  
Db 180 FTQMPFSFRVNTPEVFPFLTVYAAANLHLLLDKASIFGEEWGSTTTNNYDRQMKLT 239  
Qy 229 GDYSHCVKVKYSTGLNNLRGNTAESVRYNQFRDMLVLDLVALPPSYDTQWPIKTT 288  
Db 240 AYSDDHCVKVYETGLAKLGTSAQWVDYQNFREMTLAVLDVVALPNDYTRTPMETK 299  
Qy 289 AQLTREYVTDGATVPHPHFTSTTWNNNAPSFSAEAAVARNPHLLDPLEQVITYSL 348  
Db 300 AQLTREYVTDPLGAVNVS---SIGSWY-DKAPSGVIESSVIRPPHFVFDYITGLTVYTS 355  
Qy 349 SRMSNTQYMNWGHKLEFRITGTLNISTQGSNTSINPV-TLPFTSRDVRVETESLAGL 407  
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Qy 408 NULFTOP-----VNPRVDFHWKFTVTHPIASDN-----FYYPGAGIGTQLQDSNELPPE 458  
Db 416 LLDIVYPGVYTIYFFGPEVEF---FMVNQLNNRTRKTKYNPVSKDIIASTRDSELELPPE 472  
Qy 459 ATGQPNYESVSHLSHIGLISAS-HVKAL--VYSWTHRSADRTNTEPNSITQIPLVKAF 515  
Db 473 TSDQPNYESVSHRLCHITSIPATGNTGLVPFVSWTHRSADLNNITYSDKITQIPAVKCW 532  
Qy 516 NISSGAAVVRGPGFTGGDILR-RTNTGTFGDI---RVNINPPPPAQRVRYRIRVASTTDLQ 571  
Db 533 DNLPPFVVKVPGHGTGDDLLQYNRSTGSGVGLTFLARYGLALEKAGKYRVLRYLATDADIV 592  
Qy 572 FHTSINGKAINQGNFSATMNRGDDLYKTF-----XTVGFTTFFPSLL-----DVQST 618  
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Qy 619 FTIGAMNFSNGNEVYDRIEFVPEVYEAEDPEKAQKVTAFTSTNPRGLTKTDVQV 678  
Db 648 LS-----GLVYVDRIEFVPEVYEAEDPEKAQKVTAFTSTNPRGLTKTDVQV 697  
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; Sequence 2, Application US/10414637  
; Publication No. US20030177528A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With  
; Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/414,637  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: US/10/032,717  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/242,838  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1206  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-414-637-2  
Query Match 40.0%; Score 1500.5; DB 14; Length 1206;  
Best Local Similarity 44.2%; Pred. No. 2.8e-116;  
Matches 336; Conservative 129; Mismatches 230; Indels 65; Gaps 22;  
Qy 1 MCLKNQDKHQSFSSNAKVDKISTDS----LKNETDIELQNHEDCLKM-----SEYE-N 50  
Db 1 MSPNNQNEYIIDATPST-SVSNDSNRYFPANPTNALQNDYKYLKMSAGNASEYPGS 59  
Qy 51 VEPFVSA-STIQTGIGIAGKILGTVFPFAGQVASYLSFYLGLWPKG-KNOMEIFMEHV 108  
Db 60 PEVLVSGQDAKAAIDIVGKLLSGLGVPFVGPVLSVLTQLIDILWPSGKSKQWEIFMEQV 119  
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Qy 169 FVOKLPSFVSGREVPLPIYAQAANLHLLLDASIFGKEMGLSSSEISTFTYNROVERA 228  
Db 180 FTQMPFSFRVNTPEVFPFLTVYAAANLHLLLDKASIFGEEWGSTTTNNYDRQMKLT 239



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:24:54 ; Search time 22.2992 Seconds  
(without alignments)  
2403.590 Million cell updates/sec

Title: us-10-019-823b-54

Perfect score: 3749

Sequence: 1 MKLKNQDRHQSFSSNAKVDK.....KRELFEIVYAKQLHIERN 718

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

1: /cgn2\_6/prodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/prodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/PCUTUS COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3718.5	99.2	719	3	US-08-286-870A-8
2	3439	91.7	710	4	US-09-661-322A-42
3	3360.5	89.6	648	3	US-08-286-870A-4
4	3358.5	89.6	719	2	US-09-003-217-2
5	3356.5	89.5	719	3	US-09-218-942-2
6	2778.5	74.1	535	3	US-08-286-870A-6
7	2415	64.4	1229	1	US-08-100-709-4
8	2415	64.4	1229	1	US-08-176-865-4
9	2415	64.4	1229	1	US-08-474-038-4
10	2415	64.4	1229	1	US-08-779-046-4
11	2415	64.4	1229	2	US-08-881-340-4
12	2319	61.9	488	1	US-08-448-170-10
13	2319	61.9	488	3	US-08-961-803-10
14	2236	59.6	1207	1	US-07-951-715A-7
15	2236	59.6	1207	2	US-08-459-448A-7
16	2236	59.6	1207	3	US-08-459-595A-7
17	2236	59.6	1207	3	US-08-459-504B-7
18	2236	59.6	1207	3	US-08-459-444-7
19	2236	59.6	1207	3	US-09-053-549-8
20	2236	59.6	1207	3	US-09-347-422-7
21	2236	59.6	1207	4	US-09-988-462-7
22	2235	59.6	1227	3	US-09-053-549-2
23	2165	57.7	1227	1	US-08-448-170-8
24	2165	57.7	1227	3	US-08-961-803-9
25	2156	57.5	1227	4	US-09-661-322A-63
26	2141	57.1	1186	3	US-09-178-252-23
27	2141	57.1	1186	4	US-09-826-660-23

28 2085.5 55.6 1228 4 US-09-661-322A-38 Sequence 38, Appl  
29 1902 50.7 643 3 US-09-178-252-25 Sequence 25, Appl  
30 1902 50.7 643 4 US-09-826-660-25 Sequence 25, Appl  
31 1891 50.4 380 5 PCT-US91-02560-4 Sequence 4, Appl  
32 1658 44.2 653 4 US-09-661-322A-6 Sequence 6, Appl  
33 1652 44.1 1157 1 US-07-876-280-30 Sequence 30, Appl  
34 1652 44.1 1157 1 US-07-812-180A-2 Sequence 2, Appl  
35 1652 44.1 1157 1 US-08-315-468-2 Sequence 2, Appl  
36 1652 44.1 1157 3 US-07-941-650A-2 Sequence 2, Appl  
37 1482 39.5 1176 1 US-08-257-999-2 Sequence 5, Appl  
38 1480.5 39.5 1157 2 US-08-532-547-5 Sequence 5, Appl  
39 1480.5 39.5 1157 2 US-08-379-656B-5 Sequence 5, Appl  
40 1480.5 39.5 1157 3 US-08-455-838-5 Sequence 5, Appl  
41 1480.5 39.5 1157 3 US-09-019-809-5 Sequence 5, Appl  
42 1480.5 39.5 1157 4 US-09-471-177-5 Sequence 5, Appl  
43 1480.5 39.3 1157 4 US-09-220-806-5 Sequence 5, Appl  
44 1474 39.3 1156 3 US-09-002-285-72 Sequence 72, Appl  
45 1474 39.3 1156 4 US-09-589-477-72 Sequence 72, Appl

#### ALIGNMENTS

RESULT 1  
US-08-286-870A-8  
; Sequence 8, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PAUL N. KOKULIS  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 70608/220720  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-286-870A-8

Query Match 99.2%; Score 3718.5; DB 3; Length 719;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 714; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

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DB 61 Q T G I G I A G K I L G T L G V P F A G Q V A S I Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N K I S T Y A 120

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DB 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E M F V K L P S F A V S G 180

QY 181 E V P L L P I Y A Q A A N I H L L L R D A S I F G K E W G L S S E I S T F Y N R O V E R A G D Y S H C V K W Y S 240  
DB 181 E V P L L P I Y A Q A A N I H L L L R D A S I F G K E W G L S S E I S T F Y N R O V E R A G D Y S H C V K W Y S 240

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DB 241 T G L A N L R G T N A E S W Y R Y N Q F R D M T L M V L D L V A L P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 300

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DB 361 G G H K L E F R I G T L N I S T G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420

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DB 481 A S H V K A L V S W T H R S A D R T N T I E P N S I T O I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540

QY 540 T G T F G D I R V N I N P P P A Q R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 599  
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RESULT 2  
US-09-661-322A-42  
; Sequence 42, Application US/09661322A  
; Patent No. 6593293  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chin-Rel  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Rupar, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo  
; TITLE OF INVENTION: and Methods of Use  
; FILE REFERENCE: MECO201  
; CURRENT APPLICATION NUMBER: US/09/661,322A  
; CURRENT FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 42  
; LENGTH: 710  
; TYPE: PRT

ORGANISM: Bacillus thuringiensis  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (2007..(2000)  
OTHER INFORMATION: No. 6593293-Coding  
US-09-661-322A-42

Query Match 91.7%; Score 3439; DB 4; Length 710;  
Best Local Similarity 91.9%; Pred. No. 1.2e-299;  
Matches 661; Conservative 15; Mismatches 33; Indels 10; Gaps 2;

QY 1 M K L K N Q D K H Q S F S N A K V D K I S T S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60  
DB 1 M K S K N Q N H Q S L S N A T V D K N F T G S L E N T N T E L Q N F N H -----E G I E P P V S U S T I 51

QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S I Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N K I S T Y A 120  
DB 52 Q T G I G I A G K I L G T L G V P F A G Q V A S I Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N K I S T Y A 111

QY 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E M F V K L P S F A V S G 180  
DB 112 R N K A L A D L K G L G D A L A V Y H S L E S W I E N R N T R T R S V V K S Q Y I T L E L M F V Q S L P S F A V S G 171

QY 181 E V P L L P I Y A Q A A N I H L L L R D A S I F G K E W G L S S E I S T F Y N R O V E R A G D Y S H C V K W Y S 240  
DB 172 E V P L L P I Y A Q A A N I H L L L R D A S I F G K W G L S D S E I S T F Y N R Q S G K S E Y S H D C V K W Y N 231

QY 241 T G L A N L R G T N A E S W Y R Y N Q F R D M T L M V L D L V A L P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 300  
DB 232 T G L N L R M G N A E S W Y R Y N Q F R D M T L M V L D L V A L P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 291

QY 301 G T V H P H P S F T S T T W N N N A P S F A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y N M W 360  
DB 292 G T V H P H P S F T S T T W N N N A P S F T I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y N M W 351

QY 361 G G H K L E F R I G T L N I S T G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N - V P R 419  
DB 352 G G H K L E F R I G T L N I S T G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 411

QY 420 V D F H W K F V T H P I A S D N F Y P P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 479  
DB 412 V D F H W K F V T H P I A S D N F Y P P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 471

QY 480 A S H V K A L V S W T H R S A D R T N T I E P N S I T O I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 539  
DB 472 A S H V K A L V S W T H R S A D R T N T I E P N S I T O I P L V K A F N L S S G A A V V R G P G T G G D I L R R K N 531

QY 540 T G T F G D I R V N I N P P P A Q R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 599  
DB 532 T G T F G D I R V N I N P P P A Q R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 591

QY 600 T F T V G T F T P F S L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V Y E A E Y D F E K A Q E K V 659  
DB 592 T F T V G T F T P F S D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V Y E A E Y D F E K A Q E V 651

QY 660 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q L H I E R N M 718  
DB 652 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D K F Y L D E K R E L F E I V K A Q L H I E R N M 710

RESULT 3  
US-08-286-870A-4  
; Sequence 4, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: RLY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENN, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN



ADDRESSEE: Intellectual Property Group of  
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/286,870A  
FILING DATE: 05-AUG-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520228  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8910624.9  
FILING DATE: 09-MAY-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: PAUL N. KOKULIS  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 70608/220720  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 648 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-286-870A-4

Query Match 89.6%; Score 3360.5; DB 3; Length 648;  
Best Local Similarity 99.4%; Pred. No. 1.1e-292;  
Matches 644; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMGSEYENVEPFSASTI 60  
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMGSEYENVEPFSASTI 60  
QY 61 QTGIGTAGKILGTGVPPAGQVASYFLGELMPKGNQWEIFMEHVVEIINOKISTYA 120  
DB 61 QTGIGTAGKILGTGVPPAGQVASYFLGELMPKGNQWEIFMEHVVEIINOKISTYA 120  
QY 121 RNKALTDLKGLDALAVYHDSLSWVGNRNNTARSVVKVSKQYIALELMFVKLPSFAVSG 180  
DB 121 RNKALTDLKGLDALAVYHDSLSWVGNRNNTARSVVKVSKQYIALELMFVKLPSFAVSG 180  
QY 181 EYVPLPIYAQAANLHLLLRDASIFGKEWGLSSSBISTFYNNQVRAGDYSYHCVKWYS 240  
DB 181 EYVPLPIYAQAANLHLLLRDASIFGKEWGLSSSBISTFYNNQVRAGDYSYHCVKWYS 240  
QY 241 TGLNLRGNTNAESWRYNQPRDMLVLDLVALFSDYDQMPYIKTTAQLTRVYTDAL 300  
DB 241 TGLNLRGNTNAESWRYNQPRDMLVLDLVALFSDYDQMPYIKTTAQLTRVYTDAL 300  
QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 360  
DB 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 360  
QY 361 GGHKLFRITGGLTINISTQGSTNTSINPVTLPFTSRDVRKTESLAGNLFLTPQVNV 419  
DB 361 GGHKLFRITGGLTINISTQGSTNTSINPVTLPFTSRDVRKTESLAGNLFLTPQVNV 420  
QY 420 VDFHWKFTVPIASDNFYPYAGIGTQLODSENLPEATGQPNYESYSHRLSHGLIS 479  
DB 421 VDFHWKFTVPIASDNFYPYAGIGTQLODSENLPEATGQPNYESYSHRLSHGLIS 480

QY 480 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGDIILRRTN 539  
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGDIILRRTN 540  
QY 540 TGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 599  
DB 541 TGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600  
QY 600 TEXTVGFTTFFSLDVQSTFTTIGANFSSGNEVYIDRIEFVPEVITYE 647  
DB 601 TFRVTGFTTFFSLDVQSTFTTIGANFSSGNEVYIDRIEFVPEVITYE 648

## RESULT 4

US-09-003-217-2  
Sequence 2, Application US/09003217  
Patent No. 5986177  
GENERAL INFORMATION:  
APPLICANT: Osman, Yehia A.  
APPLICANT: Madkour, Magdy A.  
APPLICANT: Bulla, Lee A.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH  
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESS: W. Murray Spruill (Alston & Bird, LLP)  
STREET: 3605 Glenwood Ave. Suite 310  
CITY: Raleigh  
STATE: NC  
COUNTRY: US  
ZIP: 27622  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/003,217  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: 5718-3  
TELEPHONE: 919 420 2202  
TELEFAX: 919 881 3175  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 719 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-003-217-2

Query Match 89.6%; Score 3358.5; DB 2; Length 719;  
Best Local Similarity 89.6%; Pred. No. 2e-292;  
Matches 644; Conservative 33; Mismatches 41; Indels 1; Gaps 1;  
QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMGSEYENVEPFSASTI 60  
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMGSEYENVEPFSASTI 60  
QY 61 QTGIGTAGKILGTGVPPAGQVASYFLGELMPKGNQWEIFMEHVVEIINOKISTYA 120  
DB 61 QTGIGTAGKILGTGVPPAGQVASYFLGELMPKGNQWEIFMEHVVEIINOKISTYA 120  
QY 121 RNKALTDLKGLDALAVYHDSLSWVGNRNNTARSVVKVSKQYIALELMFVKLPSFAVSG 180  
DB 121 RNKALTDLKGLDALAVYHDSLSWVGNRNNTARSVVKVSKQYIALELMFVKLPSFAVSG 180  
QY 181 EYVPLPIYAQAANLHLLLRDASIFGKEWGLSSSBISTFYNNQVRAGDYSYHCVKWYS 240

Db 181 EEVPLLPYQAANLHLLLRDASIFKNGGLSASEISTFYNRQVRTRDYSYHCVKWN 240  
Qy 241 TGLNLRGTNAESVVRNQFRDWTMLVLDLVALFSDYDQMYPIKTTAQLTREVYTDI 300  
Db 241 TGLNLRGTNAESVVRNQFRDWTMLVLDLVALFSDYDQMYPIKTTAQLTREVYTDI 300  
Qy 301 GTVHPHPSFTSTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVITYSLLSRWSTQYMNW 360  
Db 301 GTVDPNQALRSTTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVITYSLLSRWSTQYMNW 360  
Qy 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTOPV-NVR 419  
Db 361 GGHLESRIPIGALNTSTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTOPVNGVR 420  
Qy 420 VDFHWKFTPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479  
Db 421 VDFHWKFTPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
Qy 480 ASHKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539  
Db 481 GSHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTX 540  
Qy 540 TCTFGDIRVNIINPPFAQRYRVRIRYASTDLOQFHTSINGKAINQGNFSATMNRGDLDYK 599  
Db 541 SGTFGHIRVNIINPPFAQRYRVRIRYASTDLOQFHTSINGKAINQGNFSATMNRGDLDYK 600  
Qy 600 TFXTVGFTTPFSLDVQSTFTIGAMNFSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 659  
Db 601 TFRVGTFTTPFSDVQSTFTIGAMNFSGNEVYIGRIEFVPEVTEAEYDFEKAQEKV 660  
Qy 660 TALFTSTNPRGLTKDVKYHIDQVSNLVESLSDLEYLDEKELFEIVKYAKQIHIERNM 718  
Db 661 TALFTSTNPRGLTKDVKYHIDQVSNLVESLSDLEYLDEKELFEIVKYAKQIHIERNM 719

RESULT 5  
US-09-218-942-2  
; Sequence 2, Application US/09218942  
; Patent No. 6232439  
; GENERAL INFORMATION:  
; APPLICANT: Osman, Yehia  
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum  
; FILE REFERENCE: Crv11  
; CURRENT APPLICATION NUMBER: US/09/218,942  
; CURRENT FILING DATE: 1998-12-22  
; EARLIER APPLICATION NUMBER: 60/035,361  
; EARLIER FILING DATE: 1997-01-10  
; EARLIER APPLICATION NUMBER: 09/003,217  
; EARLIER FILING DATE: 1998-01-06  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 719  
; TYPE: PR1  
; ORGANISM: Bacillus thuringiensis  
US-09-218-942-2

Query Match 89.5%; Score 3356.5; DB 3; Length 719;  
Best Local Similarity 89.6%; Pred. No. 3e-292;  
Matches 644; Conservative 33; Mismatches 41; Indels 1; Gaps 1;

Qy 1 MLLKNQKHQSFSNAKVDKISTDSLNQETDIELQNIHEDCLKMEYENVERFVCASTI 60  
Db 1 MLLKNPKGHQTLSSNAKVDKIATDSLNQETDIELKNNNEDYLRMSEHESIDPFVSASTI 60  
Qy 61 QTGIGIAGKIILGTIGVFPAGVASYLSFILGELWPKGNQWELFMHVEIINOKISTVA 120  
Db 61 QTGIGIAGKIILGTIGVFPAGVASYLSFILGELWPKGNQWELFMHVEIINOKISTVA 120  
Qy 121 RNKALTDLKGLDALAVVHDSLESWGVNRRNTRARSVVKSYQYIALELMFVQKLPSPAVSG 180  
Db 121 RNKALTDLKGLDALAVVHDSLESWGVNRRNTRARSVVKSYQYIALELMFVQKLPSPAVSG 180

Qy 181 EEVPLLPYQAANLHLLLRDASIFKNGGLSASEISTFYNRQVRTRDYSYHCVKWN 240  
Db 181 EEVPLLPYQAANLHLLLRDASIFKNGGLSASEISTFYNRQVRTRDYSYHCVKWN 240  
Qy 241 TGLNLRGTNAESVVRNQFRDWTMLVLDLVALFSDYDQMYPIKTTAQLTREVYTDI 300  
Db 241 TGLNLRGTNAESVVRNQFRDWTMLVLDLVALFSDYDQMYPIKTTAQLTREVYTDI 300  
Qy 301 GTVHPHPSFTSTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVITYSLLSRWSTQYMNW 360  
Db 301 GTVDPNQALRSTTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVITYSLLSRWSTQYMNW 360  
Qy 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTOPV-NVR 419  
Db 361 GGHLESRIPIGALNTSTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTOPVNGVR 420  
Qy 420 VDFHWKFTPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479  
Db 421 VDFHWKFTPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
Qy 480 ASHKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539  
Db 481 ASHKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTK 540  
Qy 540 TCTFGDIRVNIINPPFAQRYRVRIRYASTDLOQFHTSINGKAINQGNFSATMNRGDLDYK 599  
Db 541 SGTFGHIRVNIINPPFAQRYRVRIRYASTDLOQFHTSINGKAINQGNFSATMNRGDLDYK 600  
Qy 600 TFXTVGFTTPFSLDVQSTFTIGAMNFSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 659  
Db 601 TFRVGTFTTPFSDVQSTFTIGAMNFSGNEVYIGRIEFVPEVTEAEYDFEKAQEKV 660  
Qy 660 TALFTSTNPRGLTKDVKYHIDQVSNLVESLSDLEYLDEKELFEIVKYAKQIHIERNM 718  
Db 661 TALFTSTNPRGLTKDVKYHIDQVSNLVESLSDLEYLDEKELFEIVKYAKQIHIERNM 719

RESULT 6  
US-08-286-870A-6  
; Sequence 6, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENN, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBAY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989

```
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-870A-6

Query Match 74.1%; Score 2778.5; DB 3; Length 535;
Best Local Similarity 99.6%; Pred. No. 1.5e-240;
Matches 533; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MRLKQDKHQSFSSNAKVKIDSLKNETDIELQINHEDECLKMSEYENVEPVSASTI 60
DB 1 MRLKQDKHQSFSSNAKVKIDSLKNETDIELQINHEDECLKMSEYENVEPVSASTI 60
QY 61 QTGIGTAGKTLGTPPAGQVASYFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGTAGKTLGTPPAGQVASYFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGDLALAVYHDSLSWGNNRNRARSVVKSOYIALELMFVKLPSFAVSG 180
DB 121 RNKALTDLKGDLALAVYHDSLSWGNNRNRARSVVKSOYIALELMFVKLPSFAVSG 180
QY 181 EYVPLPIYAAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWTYS 240
DB 181 EYVPLPIYAAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWTYS 240
QY 241 TGLNLRGTVNAESWVRYNQPRDMTLMVLVLFPSSYDTQMPYIKTTAQLTREVTYDAI 300
DB 241 TGLNLRGTVNAESWVRYNQPRDMTLMVLVLFPSSYDTQMPYIKTTAQLTREVTYDAI 300
QY 301 GTVHPHPSFTSTWYNNAPSAEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTWYNNAPSAEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 360
QY 361 GGHKLEFRITGGTLNISTQSTNTSINPVTLPFTSRDVRVYTESLAGLNFLTPQVNV- 419
DB 361 GGHKLEFRITGGTLNISTQSTNTSINPVTLPFTSRDVRVYTESLAGLNFLTPQVNV- 420
QY 420 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 479
DB 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480
QY 480 ASHVKALVYSWTHRSADRTNTIIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 534
DB 481 ASHVKALVYSWTHRSADRTNTIIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
; Sequence 4, Application US/08100709
; Patent No. 5322687
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yeping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; NUMBER OF INVENTIONS: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
```

```
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,709
; FILING DATE: 19930729
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-100-709-4

Query Match 64.4%; Score 2415; DB 1; Length 1229;
Best Local Similarity 65.1%; Pred. No. 2.5e-207;
Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLKMSEYENVEPVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPTVSNPSTOMNLSDPARTIEDSLCAEVANNIDPFVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPAGQVASYFILGELWPKGKQWEIFMEHVEEIIINQKISTYARNKALDCLKG 130
DB 67 LGVLGVPPAGQVASYFILGELWPKGKQWEIFMEHVEEIIINQKISTYARNKALDCLKG 126
QY 131 LGDALAVYHDSLSWGNNRNRARSVVKSOYIALELMFVKLPSFAVSGEVPPLPIYA 190
DB 127 LGGRYSYQOALETWLDNRNDARSIIILERYVALELDITAIPLPRINEEVPPLMVYA 186
QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWTYSTGLNLRGTVN 250
DB 187 QAANLHLLLRDASIFGSEWGNASDVNQYQOIRYEEYSNHCYQWYNTGLNLRGTVN 246
QY 251 ASWVRYNQPRDMTLMVLVLFPSSYDTQMPYIKTTAQLTREVTYDAITGVHPHPSFT 310
DB 247 ASWVRYNQPRDMTLMVLVLFPSSYDTQMPYIKTTAQLTREVTYDAITGVHPHPSFT 306
QY 311 STTWYNNAPSAEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNWGGHKLFRIT 370
DB 307 STTWYNNAPSAEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNWGGHKLFRIT 366
QY 371 GGTLANISTQGST-NTSINPVTLPFTSRDVRVYTESLAGLNFLTPQVNV-VRPVDHMKFVT 428
DB 367 GGTLANISTQGST-NTSINPVTLPFTSRDVRVYTESLAGLNFLTPQVNV-VRPVDHMKFVT 422
QY 429 HPIASDNFYYPG-----YAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLISAS 481
DB 423 --INPQNIYERGATTYSQPYQGVIGLFDSETELPEPPTERRPNERPYESYSHRSLHIGLIS 480
QY 482 HVKALVYSWTHRSADRTNTIIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 541
DB 481 TURAPVYTHRSADRTNTIIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 540
QY 542 TFGDIRVNIINPPFAQRVRIYASTTDIQFHTSINGKAINQGNFATNMNRGSDLDYKTF 601
DB 541 TFGDIRVNIINPPFAQRVRIYASTTDIQFHTSINGKAINQGNFATNMNRGSDLDYKTF 600
QY 602 XTGVGTFPPSLDVQSTFTTIGAWNSSGNEVIDRIEFVPEVTEYAEVDFEQAQKAVTA 661
DB 601 RTAGFSTPFNFNAQSTFTTIGAWNSSGNEVIDRIEFVPEVTEYAEVDFEQAQKAVTA 659
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247 AESWLRYNQPRRDITLGVLDLVALFPSYDRTPTINTSQAQLTREIYTDPIGRTNAPSGFA 306
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311 STTWYNNAPSFAISAEEAVVRNPHLLDFLEQVTIYSLLRWSNTQVMNWGGHKLFRFI 370
    |||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3307 STNWNNNAPSFAISAERAI FRPPELLDFEOLATIIYASSRWSSTQHMNVVGHRLNFRFI 366
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371 GGTNLISQTGST-NTSINPVTLPTFSDVRTRPSLACLNLFLTPQVN -PRVUDFHKKFVT 428
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367 GGTNLNTSQGLTNNTSINPVTLQFTRSDRVRTESNAGTNILFTTPVNGVPAERFNF- 422
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429 HPIASDNFYPG-----YAGITQLOQDSNELPPEATQPNYESYSHLSHIGLISAS 481
    |||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
423 --INPQNIYERGATTYSQPYQGVGIQLFDSETELPPTTERPNYESYSHLSHIGLIGN 480
    |||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
482 HVKALVYSWTHRSADRTNTNIPNSITQIPLKAFNLSSGAAVRGPGETGGDILRRNTG 541
    |||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
481 TURAPVYSWTHRSADRTNTIGNRITQIPLVKALNLHSGVTVWVGPGPTGGDILRRNTG 540
    |||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
542 TFGDIRVNIINPFFAQRYRIRIYASTDIQPHSTINGKAINOGNFSAIWNRGEDLDYKTF 601
    |||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
541 TFGDIRLNIINVLPSQRYRIRIYASTDIQPFTRINGTIVNIGNFSPRTWNRGDNLEYSRF 600
    |||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
602 XTGVGFTTPSLLDVQSTFTIIGAWNFSSGNEVYIDRIEFVPEVTYAEAYDEKQAQKVTA 661
    |||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
601 RTAGFSTPFNFLLNAQSTFTLIGAQSFN -QEVYIDRVEFVPAEVTPEAYDYLERAQKAYNA 659
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662 LFTSTNPRGLKTDVQKVHIDQVSNLVESLDSFYLDEKRELEFIVKYAKQLHIERNM 718
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660 LFTSTNPRRLKTDVTDYHIDQVSNVACLSDSFCLDEKRELEFKVKYAKRLSDERNL 716
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## RESULT 9

US-08-474-038-4  
; Sequence 4, Application US/08474038  
; Patent No. 5679343  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yeping  
; APPLICANT: Jany, Christine S.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
; ADDRESSEE: Nadel  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/474,038  
; APPLICATION NUMBER: US/08/474,038  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/176,865  
; FILING DATE: 30-DEC-1993  
; APPLICATION NUMBER: US 08/100,709  
; FILING DATE: 29-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Egolf, Christopher  
; REGISTRATION NUMBER: 27633  
; REFERENCE/DOCKET NUMBER: 7205-49  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-757-1590  
; INFORMATION FOR SEQ ID NO: 4:

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662 LFTSTNPRGLKTDVKYDHIDQVSNLYESLSDEFLVDEKRELFEIVKYAKQLHIERNM 718
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660 LFTSTNPRRLKTDVTDYHIDQVSNMVACLSDSEFLCDEKRELFEKVYAKRLSDERNL 716
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
US-08-176-865-4
; Sequence 4, Application US/08176865
; Patent No. 5616319
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yeping
; APPLICANT: Jan, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CrYET4 AND CrYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,865
; FILING DATE: 30-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-176-865-4
; Query Match 64.4%; Score 2415; DB 1; Length 1229;
; Best Local Similarity 65.1%; Pred. No. 2.5e-207;
; Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;

QY 13 SSNAKWDKISTDLKQ-ETDIEIQ-NINHEDCLKMSEVNEPFFVSASTIQTGIGIAGKI 70
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
7 NENEIINALSIPTVSNPSTQMLSPDARIEDSLCAEVANNIDPFFVSASTVQTGINIAGRI 66
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Db 71 LGTVGPAGQVASLYSFIIGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 LGVLGVPAGQASLYSFIIGELWPSGRDPWEIFLEHVEQLIRQQVTRNTARTARLEG 126
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 131 LGDALAVYHDSLEWGVGNRRNTRARSVVKSYQYIALELMFVKLPSFVSGSEVPLLPIYA 190
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 127 LGRGYRSYQQALETWLDNRNDARSRISILERYVALELDITTAIPLERINEEVPLLMVYA 186
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 191 QAAHLHLLLRDASTEGKEWGLSGSSEISTFVNROVERAGDYSYCHVKVYSTGLNNLRGTN 250
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 187 QAAHLHLLLRDASLFGSEWNASDVNQYQEQIRYVTEYSNHCYQWNTGLNNLRGTN 246
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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SEQUENCE CHARACTERISTICS:  
LENGTH: 1229 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-474-038-4

Query Match 64.4%; Score 2415; DB 1; Length 1229;  
Best Local Similarity 65.1%; Pred. No. 2.5e-207;  
Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;  
Qy 13 SSNAKVKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPFSASTIQTGIGIAGKI 70  
Db 7 NENEINALSIPTVSNPSTOMNLSDPARIEDSLCAEVNNDIPFVSASTVQTGINIAGRI 66  
Qy 71 LGTLGVPPFAGQVASYLFGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130  
Db 67 LGVLGVPPFAGQVASYLFGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 126  
Qy 131 LGDALAVYHDSLSWGNRNNTARSVKVQYIALELMFVQKLPSPAVSGEEVPLPIYA 190  
Db 127 LGRGYSYQOALETLDNRDARSIIILERYVALELDITTAIPLRIRNEEVPLLMVYA 186  
Qy 191 QANLHLLLRDASIFGKESGLSSSEISTFYNNQVERAGDYSYHCVKYSTGLNNLRGTN 250  
Db 187 QANLHLLLRDASIFGSEWGMASSDVQYQEIYRYTEYSNHCYQWYNTGLNNLRGTN 246  
Qy 251 AESWRYNQPRDMTLVLDLVALPFSYDTQMPYIKTTAQLTREVYTDGIVTVPHPST 310  
Db 247 AESWRYNQPRDMTLVLDLVALPFSYDTQMPYIKTTAQLTREVYTDGIVTVPHPST 306  
Qy 311 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLLSRWNTQYMMWGGHKLFRTI 370  
Db 307 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLLSRWNTQYMMWGGHKLFRTI 366  
Qy 371 GGTNLNISTQGST-NTSINPVTLPFTSRDVRVYTESLAGLNLFTQPVN-VRPVDFFHKKFT 428  
Db 367 GGTNLNISTQGST-NTSINPVTLPFTSRDVRVYTESLAGLNLFTQPVN-VRPVDFFHKKFT 422  
Qy 429 HPIASDNFYYPG-----YAGIGTQLOQSENELPPEATQPNYESYSHRLSHIGLISAS 481  
Db 423 --INPQNIYERGATTYSQPYQGVIGLFPSETLPPTETTERPNYESYSHRLSHIGLIGN 480  
Qy 482 HVKALVYSWTHRSADRTNITPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTG 541  
Db 481 TLRAPVYSWTHRSADRTNITPNSITQIPLVKALNLSGAAVVRGPGFTGGDILRRNTG 540  
Qy 542 TFGDIRVNINPPAQRVYRIRYASTDLOPHTSINGKAINQGNFSAATWNRGDDLYKTF 601  
Db 541 TFGDIRVNINPPAQRVYRIRYASTDLOPHTSINGKAINQGNFSAATWNRGDDLYKTF 600  
Qy 602 XTGVFTTPTFSLDVQSTFTTICANNFSGNEVYIDRIEFVFEVYEAAYDFEKAQEKVTA 661  
Db 601 RTAGSTFPFNFLAQSFTFLGAQSPN-QEVIDRVEFPVPAETVFAEYDLERAQAKVA 659  
Qy 662 LFTSTNPRGLKTDVYHIDQVNLVSVLSDEFYLDKRELFEIVKYAKQLHIERNM 718  
Db 660 LFTSTNPRGLKTDVYHIDQVNLVSVLSDEFYLDKRELFEIVKYAKQLHIERNM 716

RESULT 10  
US-08-779-046-4  
Sequence 4, Application US/08779046  
Patent No. 5854053  
GENERAL INFORMATION:  
APPLICANT: Donovan, William P.  
APPLICANT: Tan, Yiping  
APPLICANT: Jan, Christine S.  
APPLICANT: Gonzalez Jr., Jose M.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5  
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
ADDRESSEE: Nadel  
STREET: 1601 Market Street, 36th Floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19103

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/779,046  
FILING DATE: 06-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/100,709  
FILING DATE: 29-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Egolf, Christopher  
REGISTRATION NUMBER: 27633  
REFERENCE/DOCKET NUMBER: 7205-49  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-757-1590  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1229 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-779-046-4

Query Match 64.4%; Score 2415; DB 2; Length 1229;  
Best Local Similarity 65.1%; Pred. No. 2.5e-207;  
Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;  
Qy 13 SSNAKVKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPFSASTIQTGIGIAGKI 70  
Db 7 NENEINALSIPTVSNPSTOMNLSDPARIEDSLCAEVNNDIPFVSASTVQTGINIAGRI 66  
Qy 71 LGTLGVPPFAGQVASYLFGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130  
Db 67 LGVLGVPPFAGQVASYLFGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 126  
Qy 131 LGDALAVYHDSLSWGNRNNTARSVKVQYIALELMFVQKLPSPAVSGEEVPLPIYA 190  
Db 127 LGRGYSYQOALETLDNRDARSIIILERYVALELDITTAIPLRIRNEEVPLLMVYA 186  
Qy 191 QANLHLLLRDASIFGKESGLSSSEISTFYNNQVERAGDYSYHCVKYSTGLNNLRGTN 250  
Db 187 QANLHLLLRDASIFGSEWGMASSDVQYQEIYRYTEYSNHCYQWYNTGLNNLRGTN 246  
Qy 251 AESWRYNQPRDMTLVLDLVALPFSYDTQMPYIKTTAQLTREVYTDGIVTVPHPST 310  
Db 247 AESWRYNQPRDMTLVLDLVALPFSYDTQMPYIKTTAQLTREVYTDGIVTVPHPST 306  
Qy 311 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLLSRWNTQYMMWGGHKLFRTI 370  
Db 307 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLLSRWNTQYMMWGGHKLFRTI 366  
Qy 371 GGTNLNISTQGST-NTSINPVTLPFTSRDVRVYTESLAGLNLFTQPVN-VRPVDFFHKKFT 428  
Db 367 GGTNLNISTQGST-NTSINPVTLPFTSRDVRVYTESLAGLNLFTQPVN-VRPVDFFHKKFT 422  
Qy 429 HPIASDNFYYPG-----YAGIGTQLOQSENELPPEATQPNYESYSHRLSHIGLISAS 481  
Db 423 --INPQNIYERGATTYSQPYQGVIGLFPSETLPPTETTERPNYESYSHRLSHIGLIGN 480  
Qy 482 HVKALVYSWTHRSADRTNITPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTG 541  
Db 481 TLRAPVYSWTHRSADRTNITPNSITQIPLVKALNLSGAAVVRGPGFTGGDILRRNTG 540

542 TFGDIRVNINPFAQRYRIRVASTTDLQFHTSINGKAINQNFSAATMNRGDLDYKTF 601  
541 TFGDIRVNINPVSQRIRVIRVASTTDLQFHTSINGKAINQNFSAATMNRGDLDYKTF 600  
602 XTGVFTTFFSLDQVSTFTIGANFSGNVEYIDRIEFVPEVTEAEYDFEKAQEKVTA 661  
601 RTAGSIFPFNLAQSTFTLGAQSFN-QEYVIDRVEFPAEYTFEAYDLERAQKAVNA 659  
662 LFTSTNPRGLKTDVYKHIDOVSNLVSLSDEFVLDEKRELFEIVKAKOLHIERNM 718  
660 LFTSTNPRGLKTDVYKHIDOVSNLVSLSDEFVLDEKRELFEIVKAKOLHIERNM 716

RESULT 11  
US-08-881-340-4  
; Sequence 4, Application US/08881340  
; Patent No. 5942658  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yiping  
; APPLICANT: Jan, Christine S.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
; ADDRESSEE: Nadel  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,340  
; FILING DATE: 24-JUN-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/100,709  
; FILING DATE: 29-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Egolf, Christopher  
; REGISTRATION NUMBER: 27633  
; REFERENCE/DOCKET NUMBER: 7205-49  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-757-1590  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1229 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-881-340-4

Query Match 64.4%; Score 2415; DB 2; Length 1229;  
Best Local Similarity 65.1%; Pred. No. 2.5e-207;  
Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;  
13 SSNAVKDKISTDLKKN-ETDIELQ-NINHECLKMKSENVNPPVPSASTTQTGIGAKI 70  
7 NENEINALSIFTVSNPSTQMLSPDARIEDSLCAEVNNDPVPVSASTVQTGINAGRI 66  
71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEIWEHVEELINOKISTYARNKALDLKG 130  
67 LGVLGVPPAGQVASYLSFILGELWPKGNQWEIWEHVEELINOKISTYARNKALDLKG 126  
131 LGDALAVYHDSLSWVGNNRNRTRASVVKVSKYVIALELMFVOKLPSFAVSGEEVLLIYA 190

127 LGRGYSYQQALETWLDNRDARSRSIILERYVALELDTITAIPLFIRNEEVLPMVYA 186  
191 QAAHLHLILIRLSDASIFGKEWGLSSSBSISTFYNRQVERAGDYSYHCVKYSTGLNNLRGTN 250  
187 QAAHLHLILIRLSDASIFGKEWGLSSSBSISTFYNRQVERAGDYSYHCVKYSTGLNNLRGTN 246  
251 AESVVRYNQFRDRMTLMVLDAVLPFSPYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 310  
247 AESVVRYNQFRDRMTLMVLDAVLPFSPYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 306  
311 STTWYNNAPSFSAIEAAVVRNPHLLDFEQVTIYSLLSRWSNTQYNNMWGKHLEFRIT 370  
307 STWYNNAPSFSAIEAAVVRNPHLLDFEQVTIYSLLSRWSNTQYNNMWGKHLEFRIT 366  
371 GGTINISTQGST-NTSINPVTLPFTSRDVTYRTSLAGNLFLTPQVN-VPVDFHMKFVT 428  
367 GGTINISTQGST-NTSINPVTLPFTSRDVTYRTSLAGNLFLTPQVN-VPVDFHMKFVT 422  
429 HPIASDNFYPFG-----YAGIGTQLOQDSNELPPEATGQPNVSYSHSLSHIGLISAS 481  
423 --INPQNIYERGATTYSQY 480  
482 HVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGCDILRRNTG 541  
481 TURAPVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGCDILRRNTG 540  
542 TFGDIRVNINPFAQRYRIRVASTTDLQFHTSINGKAINQNFSAATMNRGDLDYKTF 601  
541 TFGDIRVNINPVSQRIRVIRVASTTDLQFHTSINGKAINQNFSAATMNRGDLDYKTF 600  
602 XTGVFTTFFSLDQVSTFTIGANFSGNVEYIDRIEFVPEVTEAEYDFEKAQEKVTA 661  
601 RTAGSIFPFNLAQSTFTLGAQSFN-QEYVIDRVEFPAEYTFEAYDLERAQKAVNA 659  
662 LFTSTNPRGLKTDVYKHIDOVSNLVSLSDEFVLDEKRELFEIVKAKOLHIERNM 718  
660 LFTSTNPRGLKTDVYKHIDOVSNLVSLSDEFVLDEKRELFEIVKAKOLHIERNM 716

RESULT 12  
US-08-448-170-10  
; Sequence 10, Application US/08448170  
; Patent No. 5723758  
; GENERAL INFORMATION:  
; APPLICANT: Payne, Jewel  
; APPLICANT: Cummings, David A.  
; APPLICANT: Cannon, Raymond J.C.  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Stelman, Steve  
; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted  
; TITLE OF INVENTION: B.t. PSI58C2, Active Against Lepidopteran Pests, and Genes  
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/448,170  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/069,902  
; FILING DATE: 01-JUNE-1993  
; CLASSIFICATION: 424

```

;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Salwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-448-170-10

Query Match 61.9%; Score 2319; DB 1; Length 488;
Best Local Similarity 89.3%; Pred. No. 2.3e-199;
Matches 444; Conservative 13; Mismatches 30; Indels 10; Gaps 2;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMSEYENVEPFFVSASTI 60
DB 1 MMSKNQNMHOSLNNAATVDKNFTGSLNNTNTELQNFH-----EGIEPFFVSSTI 51
QY 61 QTGIGTAGKILGTLPVFPAGQVASYLSFILGELWPKGKQWEI FMEHVBEI INQKISTYA 120
DB 52 QTGIGIVGKILGNLGVFPAGQVASYLSFILGELWPKGKQWEI FMEHVBEI INQKISTYA 111
QY 121 RNKALTDLKGGLDALAVYHDSLSWGNNRNTARSVVKSQYIALBELMFVKLPSPFVSG 180
DB 112 RNKALADLKGGLDALAVYHESLSWENRNTRTSRVVKSQYITLBELMFVQSLPSPFVSG 171
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWTYS 240
DB 172 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQSKSKEYSDHCVKWYN 231
QY 241 TGLNLRGTNAESWVRYNQFRDMLTMDLVALPFSYDTQMYPIKTTAQLTREVYTDAL 300
DB 232 TGLNLRGMNAESWVRYNQFRDMLTMDLVALPFSYDTQMYPIKTTAQLTREVYTDAL 291
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMNW 360
DB 292 GTVHPHPSFTSTWYNNNAPSFTIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMNW 351
QY 361 GGHKLBPRTTGGTINTSTQSTNTSINPVTLPFTSRDVRTESSLAGINLFLTPQVNV 419
DB 352 GGHKLBPRTTGGTINTSTQSTNTSINPVTLPFTSRDVRTESSLAGINLFLTPQVNGVPR 411
QY 420 VDFHMKFVTHPIASDNFYPGYAGICTQLODSNELPPEATGPNYESYSHRSLHGLIS 479
DB 412 VDFHMKFVTHPIASDNFYPGYAGICTQLODSNELPPEATGPNYESYSHRSLHGLIS 471
QY 480 ASHVKALVYSWTHRSAD 496
DB 472 ASHVKALVYSWTHRSAD 488

RESULT 13
US-08-961-803-10
; Sequence 10, Application US/08961803
; Patent No. 6150589
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 6150589e1 Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
;
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,170
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: M/S 102DCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-961-803-10

Query Match 61.9%; Score 2319; DB 3; Length 488;
Best Local Similarity 89.3%; Pred. No. 2.3e-199;
Matches 444; Conservative 13; Mismatches 30; Indels 10; Gaps 2;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMSEYENVEPFFVSASTI 60
DB 1 MMSKNQNMHOSLNNAATVDKNFTGSLNNTNTELQNFH-----EGIEPFFVSSTI 51
QY 61 QTGIGTAGKILGTLPVFPAGQVASYLSFILGELWPKGKQWEI FMEHVBEI INQKISTYA 120
DB 52 QTGIGIVGKILGNLGVFPAGQVASYLSFILGELWPKGKQWEI FMEHVBEI INQKISTYA 111
QY 121 RNKALTDLKGGLDALAVYHDSLSWGNNRNTARSVVKSQYIALBELMFVKLPSPFVSG 180
DB 112 RNKALADLKGGLDALAVYHESLSWENRNTRTSRVVKSQYITLBELMFVQSLPSPFVSG 171
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWTYS 240
DB 172 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQSKSKEYSDHCVKWYN 231
QY 241 TGLNLRGTNAESWVRYNQFRDMLTMDLVALPFSYDTQMYPIKTTAQLTREVYTDAL 300
DB 232 TGLNLRGMNAESWVRYNQFRDMLTMDLVALPFSYDTQMYPIKTTAQLTREVYTDAL 291
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMNW 360
DB 292 GTVHPHPSFTSTWYNNNAPSFTIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMNW 351
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Best Local Similarity 63.9%; Pred. No. 2.8e-191;  
Matches 439; Conservative 78; Mismatches 156; Indels 14; Gaps 6;  
40 BDCLKMEYENVEPVASASTQIGTAGKILGTGVPPAGQVASYSLFGLBWPGRKN 99  
10 EDSLCIAEGNNIDFPVSASTVQTGINAGRLGVLPVPPAGQLASFYSFLVGLWPRGRD 69  
100 QWEIFMEHVEBIIINOKISTYARNKALTDLKLGDALAVYHDSLESWGVNRRNTRARSVK 159  
70 QWEIFLEHVEQLNQITENARTALRQLGDSFRAYQOQSLDMLWLENDDARTRSVLY 129  
160 SOYTALELMFVKLPSPFAVSGEYVPLPIYAQAANLHLLLRDASIFGKMGWGLSSSIST 219  
130 TOYTALELDFLNAMPFAIRNOEVPLLMVYAQAANLHLLLRDASLFGSEGLTSQIQIR 189  
220 FYNROVERAGDYSYHCVKWSYSTGLNNLRGTNAESWRYNQFRDMTLMVLDLVALFFSYD 279  
190 YIERQVTRDYSDYCVWYNTGLNSLRGTNAASWRYNQFRDLTLGLVDLVALFFSYD 249  
280 TOMYPKTQAQTRREYVTDALGTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFL 339  
250 TRTYPINTSAQTRREYVTDALGT--GVNMAWMWYNNAPSFSAIEAAVVRNPHLLDFL 307  
340 EQVTIYSLSRWSNTQYMMWGGHKLPRITGGTINISTQSTNTSINPVTLPFTSRDYY 399  
308 EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLTSTHGATNTSINPVTLPFTSRDYY 367  
400 RTESLAGLNLFP--LTQPVN--VPRVDFHMKFVTHP-----IASDNFYYPGYAGIGTQLODS 451  
368 RTESYAGVLLWGLYLEPHTGVPTVRFNF---TNPQNISDRGTANYSQP--YESPGQLKDS 423  
452 ENELPPEATQPNYESYSHRSLSHIGLISASHVKALVYSWTHRSADRTNTIPNSITQIPL 511  
424 ETELPEPETERPNYESYSHRSLSHIGLIIQSRVNVVYSWTHRSADRTNTIGNRITQIPM 483  
512 VKAFNLSSGAADVVRGPGFTGGDILRRTNTGTGDIRVNVINPPFAQRYVRIRYASTDQ 571  
484 VKASELPQGTTVVRGPGFTGGDILRRTNTGGFPIRVTVNGPLTORIRYRIGFYASTVD 543  
572 FHTSINGKAINQGNFSATWNGEDLDYKTFXTVGTFTTPELSDVOSTFTIGAWNFSSGNE 631  
544 FVSRGGTTVNFRFLRTMNSGDELKYGNFVRRRAFTTPTFTQIQDIIRTSQGLSGNCE 603  
632 VYIDRIEFVPEVTEYEAEDFEKAQSKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESUS 691  
604 VYIDKHEIIPVATFPAEYDLEAQAQVAVNALFTNTNPRKLTGDTVDYHIDQVSNLVACLS 663  
692 DEFYLDKRELFEIVYAKOLHIERNM 718  
664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 15  
US-08-459-448A-7  
; Sequence 7, Application US/08459448A  
; Patent No. 5859336  
; GENERAL INFORMATION:  
; APPLICANT: Kozziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, John L.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.

361 GGHKLEPRTGGTINISTQSTNTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNV-VP 419  
352 GGHKLEPRTGGTINISTQSTNTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNGVPR 411  
420 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSNELPPEATQPNYESYSHRSLSHIGLIS 479  
412 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSNELPPEATQPNYESYSHRSLSHIGLIS 471  
480 ASHVKALVYSWTHRSAD 496  
472 ASHVKALVYSWTHRSAD 488

RESULT 14  
US-07-951-715A-7  
; Sequence 7, Application US/07951715A  
; Patent No. 5625136  
; GENERAL INFORMATION:  
; APPLICANT: Kozziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/951,715A  
; FILING DATE: 25-SEP-1992  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 541-8615  
; TELEFAX: (919) 541-8689  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1207 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-951-715A-7

Query Match 59.6%; Score 2236; DB 1; Length 1207;



Query Match	59.6%;	Score 2236;	DB 2;	Length 1207;
Best Local Similarity	63.9%;	Pred. No. 2.8e-191;		
Matches	439;	Conservative 78;	Mismatches 156;	Indels 14; Gaps 6;
Qy	40	EDCIKMEYENVEPVASASTIQTGIGTAGKILGTGLGVFPAGQVASLVSFILGELWPKGKN	99	
Db	10	EDSLCIAGNNIDFPVSGASTVQTGINTAGRILGVLPFPAGQLASFSFLVGEUWPRGD	69	
Qy	100	QWEIFMBEVBESIINQKISTYARNKALTDLKGIGDALAVYHDSLESWVGNRRNNTARSVVK	159	
Db	70	QWEIFLEHVEQLINQOITENARNALTALRQLGSDSFRAYQQSLEDWLENRDDARTSVLY	129	
Qy	160	SOYIALELMFVKQLPSFAVSGEEVPLPIYAAQANHLHLLLRDASIFGKEWGLSSSEIST	219	
Db	130	TQYIALELDFLNAMPLEFAIRNOEVLPLMVYAAQANHLHLLLRDASLFGSEFGLTSQBIQR	189	
Qy	220	FYNQVERAGYSYHCVKWSYTGNNLRGTNAESWVRYNQFRDWTLMVLDLVLFPSYD	279	
Db	190	YYEQRVERTRDYSYCVEMWTNGLSLGTNAASWVRYNQFRDLTLGVLDLVLFPYSYD	249	
Qy	280	TQMTPIKTTAOLTRVYTDALGTVHPHPSFTSTTWNNAWPSFAIEAAVVRNPHLLDFL	339	
Db	250	TRTYPINTSAQLTRVYTDALGAT--GVNMAASMNWYNNNAWPSFAIEAAIIRSPHLLDFL	307	
Qy	340	EQVTIYLLSSWSNTQYNNMGHGKLEPRTIGTTLNTSQGSTNTSINPVTLPFTSRDVI	399	
Db	308	EQLTIYFASASWSNRHTYWRGHTIQSRPLCGGLNTSTHGATNTSINPVTLPFASRDVI	367	
Qy	400	RTESLAGLNLF--LTQPVN-VPRYDFHWKFVTHP-----IASDNFYPGYAGIGTQLQDS	451	
Db	368	RTESVAGLLWGIYLEPHTHGVTYVRNF---TNPONTSDRGATANYSDP-YESPGLOLKDS	423	

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2005, 20:20:21 ; Search time 98.2147 Seconds  
(without alignments)  
2827.419 Million cell updates/sec

Title: US-10-019-823B-54

Perfect score: 3749

Sequence: 1 MKLQNDKHQSSNAKVDK.....KRELFEIVKYAKQLHIERNM 718

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3747	99.9	718	4	AAB66907 Insectici
2	3747	99.9	718	6	AAB66907 Insectici
3	3736.5	99.7	719	2	AAR08041 81 kD end
4	3732.5	99.6	719	4	AU02095 Bacillus
5	3724.5	99.3	719	4	AAB66909 Insectici
6	3724.5	99.3	719	6	AAB66909 Insectici
7	3722.5	99.3	719	4	AAB66908 Insectici
8	3722.5	99.3	719	6	AAB66908 Insectici
9	3722.5	99.3	719	8	ADR99421 Insectici
10	3718.5	99.2	719	4	AAB66910 Insectici
11	3718.5	99.2	719	6	AAB66910 Insectici
12	3711.5	99.0	719	4	AAB66911 Insectici
13	3711.5	99.0	719	6	AAB66911 Insectici
14	3513.5	93.7	719	7	ADM74717 B. thurin
15	3482.5	92.9	719	4	AAB66912 Insectici
16	3482.5	92.9	719	6	AAB66912 Insectici
17	3439	91.7	710	3	AAB07073 Bacillus
18	3359.5	89.6	719	3	AAB07073 Bacillus
19	3358.5	89.6	719	2	AAB07073 Bacillus
20	3280.5	87.5	1217	4	AU02092 Bacillus
21	2704.5	72.1	1208	4	AU02093 Bacillus
22	2416.5	64.5	1230	8	ADK98484 B. thuring
23	2416.5	64.5	1230	8	ADK98489 B. thuring
24	2416.5	64.5	1230	8	ADK98481 B. thuring
25	2416.5	64.5	1230	8	ADK98491 B. thuring

26	2416.5	64.5	1230	8	ADK98487	Adk98487 B. thuring
27	2415	64.4	1229	2	AAR54074	Aar54074 CryET5. 2
28	2415	64.4	1229	2	AAW35259	Aaw35259 Bacillus
29	2415	64.4	1229	2	AAW17699	Aaw17699 CryET5. 3
30	2415	64.4	1229	2	AAW87633	Aaw87633 CryET5. pr
31	2415	64.4	1229	2	AAV30923	Aav30923 B. thurin
32	2415	64.4	1229	8	ADK98479	Adk98479 B. thuring
33	2319	61.9	488	2	AAW44322	Aaw44322 Bacillus
34	2319	61.9	488	4	AAW19947	Aaw19947 Bacillus
35	2249	60.0	1228	2	AAR50955	Aar50955 Bacillus
36	2244	59.9	1209	4	AAU02094	Aau02094 Chimeric
37	2235	59.6	1227	2	AAV31990	Aav31990 Chimeric
38	2165	57.7	1227	2	AAW44321	Aaw44321 Bacillus
39	2165	57.7	1227	4	AAU02046	Aau02046 Bacillus
40	2156	57.5	1227	4	AAU02046	Aau02046 B. thurin
41	2141	57.1	1186	2	AAV16796	Aav16796 Amino aci
42	2121	56.6	1221	4	AAU00421	Aau00421 B. thurin
43	2107	56.2	1221	4	AAU00420	Aau00420 B. thurin
44	2085.5	55.6	1228	4	AAB84628	Aab84628 Amino aci
45	2085.5	55.6	1228	4	AAU02039	Aau02039 B. thurin

ALIGNMENTS

RESULT 1

AAB66907  
ID AAB66907 standard; protein; 718 AA.

AC AAB66907;

DT 12-APR-2001 (first entry)

DE Insecticidal protein cryIIaI.

KW Insecticide; transgenic plant; insect-resistance.

OS Paecilomyces sp.

PN WO200100841-A1.

PD 04-JAN-2001.

PF 23-JUN-2000; 2000WO-GB002457.

PR 29-JUN-1999; 99GB-00015215.

PR 23-DEC-1999; 99GB-00030536.

PA (ZENE ) ZENECA LTD.

PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
Vincent JL, Lee MD;

DR WPI; 2001-123015/13.

PT Novel insecticidal protein obtained from species of Paecilomyces for  
controlling insects, and for insect-resistant transgenic plant  
production.

PS Claim 14; Page 53-55; 72pp; English.

CC The present invention relates to novel insecticidal proteins obtained  
from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
insecticidal proteins can be used to produce transgenic plants, which are  
insect-resistant. Also, the insecticidal proteins are useful for  
controlling insects by providing them at a locus where insects feed

SQ Sequence 718 AA;

Query Match 99.9%; Score 3747; DB 4; Length 718;  
Best Local Similarity 100.0%; Pred. No. 9.4e-296; Indels 0; Gaps 0;  
Matches 718; Conservative 0; Mismatches 0;

[illegible]

RESULT 2	
AAE36271	
ID	AAE36271 standard; protein; 718 AA.
XX	
AC	
XX	AAE36271;
XX	
DT	26-JUN-2003 (first entry)
XX	
DE	B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa1.
DE	
XX	Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX	
OS	Bacillus thuringiensis.
XX	
PN	WO200298911-A2.
XX	
PD	. 12-DEC-2002.
XX	
XX	
PF	30-MAY-2002; 2002WO-GB002666.
XX	
PR	07-JUN-2001; 2001GB-00013900.
XX	
PA	(SYGN ) SYNGENTA LTD.
XX	

Pt	Vincent JL, Viner R;
Dx	WPI; 2003-175137/17.
Xx	New insecticidal protein comprising an X-glycine motif at the amino-
Pt	terminus, useful as an active ingredient of a pesticide.
Xx	Claim 12; Page 42-44; 67pp; English.
P8	The invention relates to insecticidal protein comprising an X-glycine
Cc	motif at the amino-terminus. Polynucleotide or DNA constructs of the
Cc	invention are useful for producing plants or plant parts that are
Cc	resistant to insects. The protein or synergistic combination is useful as
Cc	an active ingredient of a pesticide or for controlling insects.
Cc	Antibodies raised to the insecticidal proteins can be used to identify
Cc	other proteins with insecticidal activity. The present sequence is
Cc	Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This
Cc	sequence is used in the invention
Xx	Sequence 718 AA;
SQ	Query Match      99.9%; Score 3747; DB 6; Length 718; Best Local Similarity    99.9%; Pred. No. 9.4e-296; Matches 717; Conservative    0; Mismatches    1; Indels    0; Gaps    0;
Qy	1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHDCLXKSEYENVEPFPVSASTI 60
Db	1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNINHDCLXKSEYENVEPFPVSASTI 60
Qy	61 QTGTGIGAKILGTGVPPAGOVASLYSPFELGELPKGNQWEIFMEHVVEEIIINQKISTYA 120
Db	61 QTGTGIGAKILGTGVPPAGOVASLYSPFELGELPKGNQWEIFMEHVVEEIIINQKISTYA 120
Qy	121 RNKALTDLKLGDALAVYHDSLESWGVRNNTRARSVVKSQYIALELMFVKQLPSFAVSG 180
Db	121 RNKALTDLKLGDALAVYHDSLESWGVRNNTRARSVVKSQYIALELMFVKQLPSFAVSG 180
Qy	181 BEVPLLPYQAANLHLULLRDASFGEKWGLSSEISFTFYNRQVERAGDYSYHCWKWYS 240
Db	181 BEVPLLPYQAANLHLULLRDASFGEKWGLSSEISFTFYNRQVERAGDYSYHCWKWYS 240
Qy	241 TGLNLRGTNAESWRYNQPRRDMTLMVLVALPPSYDTOMYPITKTAAQLTREVTDAI 300
Db	241 TGLNLRGTNAESWRYNQPRRDMTLMVLVALPPSYDTOMYPITKTAAQLTREVTDAI 300
Qy	301 GTVHPHPGSTTWYNNAPSFSAEAAVVRNPHELLDFLEQVTIYSLLSRWNTQMNMW 360
Db	301 GTVHPHPGSTTWYNNAPSFSAEAAVVRNPHELLDFLEQVTIYSLLSRWNTQMNMW 360
Qy	361 GGKLEFRITIGTLNISTQGSTNTSINPVTLPTSRDVYRTESLAGLNFLTPQVNVPRV 420
Db	361 GGKLEFRITIGTLNISTQGSTNTSINPVTLPTSRDVYRTESLAGLNFLTPQVNVPRV 420
Qy	421 DPHWFVTHPIASDNFFPYGYAGIGTOLODSNEELPPEATGPNYESYSHRLSHIGLIISA 480
Db	421 DPHWFVTHPIASDNFFPYGYAGIGTOLODSNEELPPEATGPNYESYSHRLSHIGLIISA 480
Qy	481 SHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRPGTGDDILRRNT 540
Db	481 SHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRPGTGDDILRRNT 540
Qy	541 GTFGDIRVNINPPFAQRVRYRYASTTDLQPHTSINGKAINOGNFSAWNMGEDLDYKT 600
Db	541 GTFGDIRVNINPPFAQRVRYRYASTTDLQPHTSINGKAINOGNFSAWNMGEDLDYKT 600
Qy	601 EKVTVGGTFPFSLLDVGOSTETIGAWNFSSNGEVVIDRIEFVPVEVTYEAEPDYFEKAQEKVT 660
Db	601 FRIVGGTFPFSLLDVGOSTETIGAWNFSSNGEVVIDRIEFVPVEVTYEAEPDYFEKAQEKVT 660
Qy	661 ALPTSNNPGLKTDVVDKYHHDOVSNLVESIDEFYLDEKRELFPIVKYAKQLHIERNM 718
Db	661 ALPTSNNPGLKTDVVDKYHHDOVSNLVESIDEFYLDEKRELFPIVKYAKQLHIERNM 718

```

RESULT 3
AAR08041
ID AAR08041 standard; protein; 719 AA.
XX
AC AAR08041;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 27-FEB-1991 (first entry)
XX
DE 81 kD endotoxin deduced from DNA carried on pJH12.
XX
KW Crystal; insecticide; toxin; delta endotoxin.
XX
OS Bacillus thuringiensis; JHCC 4353 and 4835.
XX
PN WO9013651-A.
XX
PD 15-NOV-1990.
XX
PF 09-MAY-1989; 89GB-00010624.
XX
PR 09-MAY-1989; 89GB-00010624.
XX
PA (ICIL ) IMPERIAL CHEM IND PLC.
XX
PI Blenk RG, Ely S, Tailor RH, Tippett JM;
DR WPI; 1990-361486/48.
DR N-PSDB; AAQ06636.
XX
XX
PT Bacillus thuringiensis strains - used for producing an endotoxin for
protecting plants against insects, partic. Lepidoptera and Coleoptera.
XX
PS Claim 5; Fig 5-10; 66pp; English.
XX
CC The sequence carried on pJH12 which was isolated from B. thurin- giensis
strains JHCC4835 and JHCC 4353 (NCIB 40091 and 40090 resp.). The DNA can
be used to produce transformants E.coli strain MC12022/pJH12 (NCIB 40278,
or bacteriophage EMBL4 vector (NCIB 40279) or E.coli strain BL21/pJH11
(NCIB 40275). The delta-endo- toxin produced by the transformants can be
used in formulations for combating Lepidoptera and Coleoptera pests.
CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to
standardise OS field)
XX
SQ Sequence 719 AA;

Query Match          99.7%; Score 3736.5; DB 2; Length 719;
Best Local Similarity 99.9%; Pred. No. 6.8e-295;
Matches 718; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
DB 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
QY 61 Q T G I G A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N O W E I F M E H V E I I N Q I S T V A 120
DB 61 Q T G I G A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N O W E I F M E H V E I I N Q I S T V A 120
QY 121 R N K A L T D L K G L G D A L A V Y H D S L S E S V G N R N N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180
DB 121 R N K A L T D L K G L G D A L A V Y H D S L S E S V G N R N N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180
QY 181 E E V P L I P I Y A Q A A N H L L L R D A S I F G K E W L S S S E I S T F Y N Q R V E R A G D Y S H C V K W Y S 240
DB 181 E E V P L I P I Y A Q A A N H L L L R D A S I F G K E W L S S S E I S T F Y N Q R V E R A G D Y S H C V K W Y S 240
QY 241 T G L N N L R G T N A E S W R Y N Q P R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A O L T R E V T Y D A I 300
DB 241 T G L N N L R G T N A E S W R Y N Q P R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A O L T R E V T Y D A I 300
QY 301 G T V H P H P S F T S T T W Y N N A P S F A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360

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Db 301 G T V H P H P S F T S T T W Y N N A P S F A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360
QY 361 G G H K L E F R I G T L N I S T Q S T N T S I N P V T L P T S R D V Y R T E S L A G L N L F L T O P V N - V P R 419
Db 361 G G H K L E F R I G T L N I S T Q S T N T S I N P V T L P T S R D V Y R T E S L A G L N L F L T O P V N G V P R 420
QY 420 V D F H W K F V T H P I A S D N F Y Y P G Y A G I G T Q L Q D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 479
Db 421 V D F H W K F V T H P I A S D N F Y Y P G Y A G I G T Q L Q D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 480
QY 480 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R P G P T G G D I L R R T N 539
Db 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R P G P T G G D I L R R T N 540
QY 540 T G T F G D I R V N I N P P P A Q R Y R V R I Y A S T T D L O F H T S I N K A I N Q G N F S A T M N R G E D L D Y K 599
Db 541 T G T F G D I R V N I N P P P A Q R Y R V R I Y A S T T D L O F H T S I N K A I N Q G N F S A T M N R G E D L D Y K 600
QY 600 T P X T V G F T T P F S L L D V Q S T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 659
Db 601 T P X T V G F T T P F S L L D V Q S T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660
QY 660 T A L F T S T N P R G L K T D V K D Y H I D O V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 718
Db 661 T A L F T S T N P R G L K T D V K D Y H I D O V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719

RESULT 4
AAR02095
ID AAR02095 standard; protein; 719 AA.
XX
AC AAR02095;
XX
DT 07-SEP-2001 (first entry)
XX
DE Bacillus thuringiensis partial mutant CryIIa.
XX
KW Crystal protein; CryIIa; CryIa; moth; butterfly; Colorado potato beetle;
mutant; mutein.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT Peptide 1..19 /label= Signal_peptide
FT Protein 20..719 /label= Mature_CryIIa
FT EP1099760-A1.
XX
PN 16-MAY-2001.
XX
PF 09-NOV-1999; 99EP-00203723.
XX
PR 09-NOV-1999; 99EP-00203723.
XX
PA (CPRO-) CPRO-DLO CENT PLANTENVEREDELINGS REPROD.
XX
PI De Maagd RA, Bosch HJ;
XX
DR WPI; 2001-337141/36.
DR N-PSDB; AAS04855.
XX
PT New hybrid Bacillus thuringiensis hybrid toxins comprising structural
domains derived from at least 2 different crystal proteins, such as
CryIIa and CryIa, and having insecticidal activity, useful for combating
insects.
XX
PS Example; Page 30-32; 43pp; English.
XX
CC The sequence is B. thuringiensis (Bt) crystal protein CryIIa, the DNA
encoding which was mutated to allow cloning of domain III or domains I

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CC and II, to make the hybrid protoxins of the invention. The hybrid toxins  
CC of the invention, having structural domains I, II and III in this order  
CC starting from the N-terminal derived from at least 2 different crystal  
CC proteins, are useful for protecting plants against pest insects, e.g.  
CC moths, butterflies and Colorado potato beetle or for combating insects  
XX  
XX Sequence 719 AA;

Query Match 99.6%; Score 3732.5; DB 4; Length 719;  
Best Local Similarity 99.6%; Pred. No. 1.4e-294;  
Matches 716; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
QY 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNIHEDCLKMSYENVEPFSASTI 60  
DB 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNIHEDCLKMSYENVEPFSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIEMHEVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIEMHEVEEIIINQKISTYA 120  
QY 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNTARSVVKSQYIALELMFVKLPSFAVSG 180  
DB 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNTARSVVKSQYIALELMFVKLPSFAVSG 180  
QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSHCVKQWYS 240  
DB 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSHCVKQWYS 240  
QY 241 TGLNLRGNTAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREVTYDAI 300  
DB 241 TGLNLRGNTAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREVTYDAI 300  
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLRSNSTQYMMNW 360  
DB 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLRSNSTQYMMNW 360  
QY 361 GGKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVRVTSAGLNLFLTQPVN-VPR 419  
DB 361 GGKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVRVTSAGLNLFLTQPVN-VPR 420  
QY 420 VDFHMKVTHPIASDNFYPGYAGICTQDSENELPPEATQPNYESYSHRLSHIGLIS 479  
DB 420 VDFHMKVTHPIASDNFYPGYAGICTQDSENELPPEATQPNYESYSHRLSHIGLIS 480  
QY 480 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 539  
DB 480 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
QY 540 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 599  
DB 540 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
QY 600 TFXTVGFTTPSLDVGSTFTIGAWNPSGNEVYIDRIEFPVVEVTEAYEYDPEKAOEKV 659  
DB 600 TFXTVGFTTPSLDVGSTFTIGAWNPSGNEVYIDRIEFPVVEVTEAYEYDPEKAOEKV 660  
QY 660 TALFTSTNPRGLKTDVKDHYHDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIBRNW 718  
DB 660 TALFTSTNPRGLKTDVKDHYHDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIBRNW 719

RESULT 5  
AAB66909 standard; protein; 719 AA.  
XX AAB66909;  
XX 12-APR-2001 (first entry)  
XX Insecticidal protein cryIIa3.  
XX Insecticide; transgenic plant; insect-resistance.  
XX

OS Paecilomyces sp.  
XX WO200100841-A1.  
XX 04-JAN-2001.  
XX 23-JUN-2000; 2000WO-GB002457.  
XX 29-JUN-1999; 99GB-00015215.  
XX 23-DEC-1999; 99GB-00030536.  
XX (ZENE ) ZENECA LTD.  
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
XX Vincent JL, Lee MD;  
XX WPI; 2001-123015/13.  
XX Novel insecticidal protein obtained from species of Paecilomyces for  
XX controlling insects, and for insect-resistant transgenic plant  
XX production.  
XX Claim 14; Page 57-59; 72pp; English.  
XX The present invention relates to novel insecticidal proteins obtained  
XX from Paecilomyces sp. (see AAB6699 to AAB6691 and AAB66913). The  
XX insecticidal proteins can be used to produce transgenic plants, which are  
XX insect-resistant. Also, the insecticidal proteins are useful for  
XX controlling insects by providing them at a locus where insects feed  
XX  
XX Sequence 719 AA;

Query Match 99.3%; Score 3724.5; DB 4; Length 719;  
Best Local Similarity 99.3%; Pred. No. 6.4e-294;  
Matches 714; Conservative 1; Mismatches 3; Indels 1; Gaps 1;  
QY 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNIHEDCLKMSYENVEPFSASTI 60  
DB 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNIHEDCLKMSYENVEPFSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIEMHEVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIEMHEVEEIIINQKISTYA 120  
QY 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNTARSVVKSQYIALELMFVKLPSFAVSG 180  
DB 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNTARSVVKSQYIALELMFVKLPSFAVSG 180  
QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSHCVKQWYS 240  
DB 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSHCVKQWYS 240  
QY 241 TGLNLRGNTAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREVTYDAI 300  
DB 241 TGLNLRGNTAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREVTYDAI 300  
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLRSNSTQYMMNW 360  
DB 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLRSNSTQYMMNW 360  
QY 361 GGKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVRVTSAGLNLFLTQPVN-VPR 419  
DB 361 GGKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVRVTSAGLNLFLTQPVN-VPR 420  
QY 420 VDFHMKVTHPIASDNFYPGYAGICTQDSENELPPEATQPNYESYSHRLSHIGLIS 479  
DB 420 VDFHMKVTHPIASDNFYPGYAGICTQDSENELPPEATQPNYESYSHRLSHIGLIS 480  
QY 480 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 539  
DB 480 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
QY 540 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 599  
DB 540 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 599

|||||  
 541 TGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGELDLYK 600  
 600 TFXTVGFTTTPFSLDQSTFTTIGAMNPFSSGNEVYIDRIEFVPEVVEYEAEDPEKAQEKV 659  
 601 TFRVGTFTTTPFSLDQSTFTTIGAMNPFSSGNEVYIDRIEFVPEVVEYEAEDPEKAQEKV 660  
 660 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFELVYKAKQLHIERNM 718  
 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFELVYKAKQLHIERNM 719

RESULT 6  
 AAE36273 standard; protein; 719 AA.  
 AC AAE36273;  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.  
 XX  
 KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 PN WO200298911-A2.  
 XX  
 PD 12-DEC-2002.  
 XX  
 PF 30-MAY-2002; 2002WO-GB002666.  
 XX  
 PR 07-JUN-2001; 2001GB-00013900.  
 XX  
 PA (SYGN ) SYNGENTA LTD.  
 XX  
 PI Vincent JL, Viner R;  
 DR WPI; 2003-175137/17.  
 XX  
 PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PT  
 XX  
 PS Claim 12; Page 47-50; 67pp; English.  
 XX  
 CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 CC  
 XX  
 SQ Sequence 719 AA;  
 Query Match 99.3%; Score 3724.5; DB 6; Length 719;  
 Best Local Similarity 99.3%; Pred. No. 6.4e-294;  
 Matches 714; Conservative 1; Mismatches 3; Indels 1; Gaps 1;  
 QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCLKMSEYENVEPFVSASTI 60  
 DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCLKMSEYENVEPFVSASTI 60  
 QY 61 QTGIGTAGKILGTLGVPPFACQVSLYSFILGELWPKGNQWEIFMEHVEBIINQKISTYA 120  
 DB 61 QTGIGTAGKILGTLGVPPFACQVSLYSFILGELWPKGNQWEIFMEHVEBIINQKISTYA 120  
 QY 121 RNKALTDLKGLDALAVYHDSLSGWNRRNTRARSVVKSQYIALELMFVKQLPSFAVSG 180  
 DB 121 RNKALTDLKGLDALAVYHDSLSGWNRRNTRARSVVKSQYIALELMFVKQLPSFAVSG 180

QY 181 BEVPLLPITYAQAANLHLLLRDASIPGKEWGLSSSEISTFYNRQVRAGDYSYHCVKWYS 240  
 DB 181 BEVPLLPITYAQAANLHLLLRDASIPGKEWGLSSSEISTFYNRQVRAGDYSYHCVKWYS 240  
 QY 241 TGLNLRGNAESWRYNQFRDMLMWLDLVALPSPYDTOMYPIKTTAQLTREVTDAI 300  
 DB 241 TGLNLRGNAESWRYNQFRDMLMWLDLVALPSPYDTOMYPIKTTAQLTREVTDAI 300  
 QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQTMNMW 360  
 DB 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQTMNMW 360  
 QY 361 GGHKLEFRTIGTGLNISTQSTNTSINPVTLPFTSRDVTRTESLAGINLFLTOPVNGVPR 419  
 DB 361 GGHKLEFRTIGTGLNISTQSTNTSINPVTLPFTSRDVTRTESLAGINLFLTOPVNGVPR 420  
 QY 420 VDFHMKFVTHPIASDNFYYPGVAGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 479  
 DB 421 VDFHMKFVTHPIASDNFYYPGVAGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 480 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGGAAVVRGPGFTGGDILRRTN 539  
 DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGGAAVVRGPGFTGGDILRRTN 540  
 QY 540 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGELDLYK 599  
 DB 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGELDLYK 600  
 QY 600 TFXTVGFTTTPFSLDQSTFTTIGAMNPFSSGNEVYIDRIEFVPEVVEYEAEDPEKAQEKV 659  
 DB 601 TFRVGTFTTTPFSLDQSTFTTIGAMNPFSSGNEVYIDRIEFVPEVVEYEAEDPEKAQEKV 660  
 QY 660 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFELVYKAKQLHIERNM 718  
 DB 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFELVYKAKQLHIERNM 719

RESULT 7  
 AAB66908 standard; protein; 719 AA.  
 ID AAB66908;  
 AC AAB66908;  
 XX  
 DT 12-APR-2001 (first entry)  
 XX  
 DE Insecticidal protein cryIIa2.  
 XX  
 KW Insecticide; transgenic plant; insect-resistance.  
 XX  
 OS Paecilomyces sp.  
 XX  
 PN WO200100841-A1.  
 XX  
 PD 04-JAN-2001.  
 XX  
 PF 23-JUN-2000; 2000WO-GB002457.  
 XX  
 PR 29-JUN-1999; 99GB-00015215.  
 PR 23-DEC-1999; 99GB-00030536.  
 XX  
 PA (ZENE ) ZENECA LTD.  
 XX  
 PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 XX  
 DR WPI; 2001-123015/13.  
 XX  
 PT Novel insecticidal protein obtained from species of Paecilomyces for controlling insects, and for insect-resistant transgenic plant production.  
 PT  
 XX  
 XX Claim 14; Page 55-57; 72pp; English.  
 XX

Tue Feb 15 10:07:49 2005

CC The present invention relates to novel insecticidal proteins obtained  
 CC from *Paecilomyces* sp. (see AAB6699 to AAB6691) and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 CC  
 XX Sequence 719 AA;

OS	Bacillus thuringiensis.
XX	WO200298911-A2.
XX	12-DEC-2002.
XX	30-MAY-2002; 2002WO-GB002666.
XX	07-JUN-2001; 2001GB-00013900.
PA	(SYGN ) SYNGENTA LTD.
XX	Vincent JL, Viner R;
XX	WPI; 2003-175137/17.
DR	New insecticidal protein comprising an X-glycine motif at the amino-
PT	terminus, useful as an active ingredient of a pesticide.
XX	Claim 12; Page 44-47; 67pp; English.
XX	The invention relates to insecticidal protein comprising an X-glycine
CC	motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC	invention are useful for producing plants or plant parts that are
CC	resistant to insects. The protein or synergistic combination is useful as
CC	an active ingredient of a pesticide or for controlling insects.
CC	Antibodies raised to the insecticidal proteins can be used to identify
CC	other proteins with insecticidal activity. The present sequence is
CC	Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This
CC	sequence is used in the invention
XX	Sequence 719 AA;

OS	Bacillus thuringiensis.	OS	Bacillus thuringiensis.
XX	WO200298911-A2.	XX	WO200298911-A2.
XX	12-DEC-2002.	XX	12-DEC-2002.
XX	30-MAY-2002; 2002WO-GB002666.	XX	30-MAY-2002; 2002WO-GB002666.
XX	07-JUN-2001; 2001GB-00013900.	XX	07-JUN-2001; 2001GB-00013900.
PA	(SYGN ) SYNGENTA LTD.	PA	(SYGN ) SYNGENTA LTD.
XX	Vincent JL, Viner R;	XX	Vincent JL, Viner R;
XX	WPI; 2003-175137/17.	XX	WPI; 2003-175137/17.
DR	New insecticidal protein comprising an X-glycine motif at the amino-	DR	New insecticidal protein comprising an X-glycine motif at the amino-
PT	terminus, useful as an active ingredient of a pesticide.	PT	terminus, useful as an active ingredient of a pesticide.
XX	Claim 12; Page 44-47; 67pp; English.	XX	Claim 12; Page 44-47; 67pp; English.
XX	The invention relates to insecticidal protein comprising an X-glycine	XX	The invention relates to insecticidal protein comprising an X-glycine
CC	motif at the amino-terminus. Polynucleotide or DNA constructs of the	CC	motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC	invention are useful for producing plants or plant parts that are	CC	invention are useful for producing plants or plant parts that are
CC	resistant to insects. The protein or synergistic combination is useful as	CC	resistant to insects. The protein or synergistic combination is useful as
CC	an active ingredient of a pesticide or for controlling insects.	CC	an active ingredient of a pesticide or for controlling insects.
CC	Antibodies raised to the insecticidal proteins can be used to identify	CC	Antibodies raised to the insecticidal proteins can be used to identify
CC	other proteins with insecticidal activity. The present sequence is	CC	other proteins with insecticidal activity. The present sequence is
CC	Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This	CC	Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This
CC	sequence is used in the invention	CC	sequence is used in the invention
XX	Sequence 719 AA;	XX	Sequence 719 AA;

Query Match 99.3%; Score 3722.5; DB 6; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 9.3e-294;  
 Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQINHEDECLKMSYENVEPFFVASTI 60  
 DB 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQINHEDECLKMSYENVEPFFVASTI 60  
 QY 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELMPKGNQWEIEMHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELMPKGNQWEIEMHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLGLGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFVSG 180  
 DB 121 RNKALTDLGLGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDYSHCVKWS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDYSHCVKWS 240  
 QY 241 TGLNNRGNAESWRYNQFRDMTLMVLDLVALPFSYDTQMPYIKTTAQLTREVTDAI 300  
 DB 241 TGLNNRGNAESWRYNQFRDMTLMVLDLVALPFSYDTQMPYIKTTAQLTREVTDAI 300  
 QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMW 360  
 QY 361 GGHKLEFRTTIGTTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVN- 419  
 DB 361 GGHKLEFRTTIGTTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVN- 419  
 QY 420 VDFHWKFTHTPIASDNFYVPGVAGIGTQDSENELPEATQPNVYESYSHRSLHIGLIS 479  
 DB 420 VDFHWKFTHTPIASDNFYVPGVAGIGTQDSENELPEATQPNVYESYSHRSLHIGLIS 479  
 QY 480 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539  
 DB 480 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539  
 QY 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540

RESULT 8  
 AAE36272  
 ID AAE36272 standard; protein; 719 AA.  
 AC AAE36272;  
 XX AAE36272;  
 XX AAE36272;  
 DT 26-JUN-2003 (first entry)  
 XX B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.  
 XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 KW  
 XX



Qy 540 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLIDYK 599  
Db 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLIDYK 600  
Qy 600 TFXTVGTTTFFSLDDVOSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEKAEKV 659  
Db 601 TFRIVGTTTFFSLDDVOSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEKAEKV 660  
Qy 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFVVKYAKQLHIERNM 718  
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFVVKYAKQLHIERNM 719

RESULT 9  
ADR89421  
ID ADR89421 standard; protein; 719 AA.  
AC ADR89421;  
Xt 18-NOV-2004 (first entry)  
Xx cryIIa.  
Kw delta-endotoxin; delta-endotoxin associate polypeptide;  
Kw expression cassette; transformation; transgenic; plant; bacteria;  
Kw lepidoptera; coleoptera; pest; pesticide; resistance;  
Kw pesticidal activity.  
Xx Bacillus thuringiensis.  
Xx WO2004074462-A2.  
Xx 02-SEP-2004.  
Xx 20-FEB-2004; 2004WO-US005829.  
Xx 20-FEB-2003; 2003US-0448632P.  
Xx 20-FEB-2003; 2003US-0448633P.  
Xx 20-FEB-2003; 2003US-0448797P.  
Xx 20-FEB-2003; 2003US-0448806P.  
Xx 20-FEB-2003; 2003US-0448810P.  
Xx 20-FEB-2003; 2003US-0448812P.  
Xx 19-FEB-2004; 2004US-00781979.  
Xx 19-FEB-2004; 2004US-00782020.  
Xx 19-FEB-2004; 2004US-00782096.  
Xx 19-FEB-2004; 2004US-00782141.  
Xx 19-FEB-2004; 2004US-00782570.  
Xx 19-FEB-2004; 2004US-00783417.  
Xx (ATHE-) ATHENIX CORP.  
Xx Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;  
Xx WPI; 2004-635574/61.  
Xx New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
Xx and polypeptides, useful for killing lepidopteran or coleopteran pests or  
Xx for producing organisms with pesticide resistance.

Example 6; SEQ ID NO 33; 178pp; English.

This sequence represents a delta-endotoxin crystal protein. This protein was included in the scope of the invention as a comparison to the delta-endotoxins of the invention. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved

CC delta-endotoxin or delta-endotoxin-associated proteins that have  
CC pesticidal activity, or for detecting the presence of delta-endotoxin or  
CC delta-endotoxin-associated proteins or nucleic acids in products or  
CC organisms.  
Xx  
Sq Sequence 719 AA;  
Query Match 99.3%; Score 3722.5; DB 8; Length 719;  
Best Local Similarity 99.4%; Pred. No. 9.3e-294;  
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
Qy 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60  
Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60  
Qy 61 QTGIGIAGKILGTGLGVPPAGQVASYLSFILGELWPKGKQWEIFMHEVBEIINQKISTYA 120  
Db 61 QTGIGIAGKILGTGLGVPPAGQVASYLSFILGELWPKGKQWEIFMHEVBEIINQKISTYA 120  
Qy 121 RNKALTDLKGLGDALAVYHDSLESWVGNNRNTARSVVKSQYIALELMFVKLPSFAVSG 180  
Db 121 RNKALTDLKGLGDALAVYHDSLESWVGNNRNTARSVVKSQYIALELMFVKLPSFAVSG 180  
Qy 181 EYVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCYKWS 240  
Db 181 EYVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCYKWS 240  
Qy 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAL 300  
Db 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAL 300  
Qy 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
Db 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
Qy 361 GGHKLEFRITGTLNISTQSTNTSINPVTLPFTSRDVRTESLAGLNLELTQPVN-VPR 419  
Db 361 GGHKLEFRITGTLNISTQSTNTSINPVTLPFTSRDVRTESLAGLNLELTQPVN-VPR 420  
Qy 420 VDPHWKFPVTHPIASDNFYYPGVAGIGTQLQDSNELPPEATGPNYESYSHRSLSHGLIS 479  
Db 421 VDPHWKFPVTHPIASDNFYYPGVAGIGTQLQDSNELPPEATGPNYESYSHRSLSHGLIS 480  
Qy 480 ASHKALVYSWTHRSADRTNITPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRTN 539  
Db 481 ASHKALVYSWTHRSADRTNITPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRTN 540  
Qy 540 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLIDYK 599  
Db 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLIDYK 600  
Qy 600 TFXTVGTTTFFSLDDVOSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEKAEKV 659  
Db 601 TFRIVGTTTFFSLDDVOSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEKAEKV 660  
Qy 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFVVKYAKQLHIERNM 718  
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFVVKYAKQLHIERNM 719

RESULT 10  
AAB66910  
ID AAB66910 standard; protein; 719 AA.  
Xx  
Xx AAB66910;  
Xx 12-APR-2001 (first entry)  
Xx Insecticidal protein cryIIa4.  
Xx Insecticide; transgenic plant; insect-resistance.  
Xx Paecilomyces sp.



Db 181 EEEVLLPIYAQAANLHLLLRDASIFGKENGSSSISTFYNRQVRAGDYSVHCVKWYS 240  
QY 241 TGLNNLRGTNAESWRYNQPRRDMTLMWLDLVALFPSYDTOMYPIKTTAQLTRFVYTDAI 300  
Db 241 TGLNNLRGTNAESWRYNQPRRDMTLMWLDLVALFPSYDTOMYPIKTTAQLTRFVYTDAI 300  
QY 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYMMNW 360  
Db 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYMMNW 360  
QY 361 GGHKLEFRTIGGLTNI STOGSTNTSINPVTLPFTSRDVYRTESLAGLNFLTOPVNV 419  
Db 361 GGHKLEFRTIGGLTNI STOGSTNTSINPVTLPFTSRDVYRTESLAGLNFLTOPVNV 420  
QY 420 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGPNYESYSHRLSHGLIS 479  
Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGPNYESYSHRLSHGLIS 480  
QY 480 ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539  
Db 481 ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
QY 540 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINOGNFSATMNRGEDLDYK 599  
Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINOGNFSATMNRGEDLDYK 600  
QY 600 TPTVGTFTTFFSLDVQSTFTIGAMNFFSGNEVYIDRIEFVPEVTEYAEYDEKAEQKV 659  
Db 601 TPTVGTFTTFFSLDVQSTFTIGAMNFFSGNEVYIDRIEFVPEVTEYAEYDEKAEQKV 660  
QY 660 TALFTSTNPRGLTKDVKDYHIDQVSNLVESLSDPEFYLDKRELFEIVKYAKQLHIERNM 718  
Db 661 TALFTSTNPRGLTKDVKDYHIDQVSNLVESLSDPEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 12

AAE36275  
ID AAE36275 standard; protein; 719 AA.  
XX AAE36275;  
AC AAE36275;  
XX AAE36275;  
DT 12-APR-2001 (first entry)  
DE Insecticidal protein cryIIa5.  
DE Insecticide; transgenic plant; insect-resistance.  
KW Paecilomyces sp.  
OS WO200100841-A1.  
XX 04-JAN-2001.  
XX 23-JUN-2000; 2000WO-GB002457.  
PF 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX (ZENE ) ZENECA LTD.  
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX WPI; 2001-123015/13.  
XX Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PT production.  
XX Claim 14; Page 62-64; 72pp; English.  
PS The present invention relates to novel insecticidal proteins obtained  
XX

CC from Paecilomyces sp. (see AAB66901 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX  
SQ Sequence 719 AA;  
Query Match 99.0%; Score 3711.5; DB 4; Length 719;  
Best Local Similarity 99.0%; Pred. No. 7.4e-293;  
Matches 712; Conservative 2; Mismatches 4; Indels 1; Gaps 1;  
QY 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDTELQNIHEDCLKSEYENVEPFVSASTI 60  
Db 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDTELQNIHEDCLKSEYENVEPFVSASTI 60  
QY 61 QTGIGIAGKILGTLPVFPAGQVASYLSYFILGELMFKGNQWEIFMEHVBEIINQKISTYA 120  
Db 61 QTGIGIAGKILGTLPVFPAGQVASYLSYFILGELMFKGNQWEIFMEHVBEIINQKISTYA 120  
QY 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNNTRARSVVKVQYIALELMFVQKLPSPAVSG 180  
Db 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNNTRARSVVKVQYIALELMFVQKLPSPAVSG 180  
QY 181 EBPVLLPIYAQAANLHLLLRDASIFGKENGSSSISTFYNRQVRAGDYSVHCVKWYS 240  
Db 181 EBPVLLPIYAQAANLHLLLRDASIFGKENGSSSISTFYNRQVRAGDYSVHCVKWYS 240  
QY 241 TGLNNLRGTNAESWRYNQPRRDMTLMWLDLVALFPSYDTOMYPIKTTAQLTRFVYTDAI 300  
Db 241 TGLNNLRGTNAESWRYNQPRRDMTLMWLDLVALFPSYDTOMYPIKTTAQLTRFVYTDAI 300  
QY 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYMMNW 360  
Db 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYMMNW 360  
QY 361 GGHKLEFRTIGGLTNI STOGSTNTSINPVTLPFTSRDVYRTESLAGLNFLTOPVNV 419  
Db 361 GGHKLEFRTIGGLTNI STOGSTNTSINPVTLPFTSRDVYRTESLAGLNFLTOPVNV 420  
QY 420 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGPNYESYSHRLSHGLIS 479  
Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGPNYESYSHRLSHGLIS 480  
QY 480 ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539  
Db 481 ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
QY 540 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINOGNFSATMNRGEDLDYK 599  
Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINOGNFSATMNRGEDLDYK 600  
QY 600 TPTVGTFTTFFSLDVQSTFTIGAMNFFSGNEVYIDRIEFVPEVTEYAEYDEKAEQKV 659  
Db 601 TPTVGTFTTFFSLDVQSTFTIGAMNFFSGNEVYIDRIEFVPEVTEYAEYDEKAEQKV 660  
QY 660 TALFTSTNPRGLTKDVKDYHIDQVSNLVESLSDPEFYLDKRELFEIVKYAKQLHIERNM 718  
Db 661 TALFTSTNPRGLTKDVKDYHIDQVSNLVESLSDPEFYLDKRELFEIVKYAKQLHIERNM 719  
RESULT 13  
AAE36275  
ID AAE36275 standard; protein; 719 AA.  
XX AAE36275;  
AC AAE36275;  
XX AAE36275;  
DT 26-JUN-2003 (first entry)  
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa5.  
XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
XX Bacillus thuringiensis.

XX	WO200298911-A2.	Db	541	TGTFGDIRVNNPPFAQRYVRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYK	600
XX	12-DEC-2002.	Qy	600	TFXTVGTTPFSLDVQSTFTIGAWNFSSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV	659
XX	30-MAY-2002; 2002WO-GB002666.	Db	601	TFRTVGTTPFSLDVQSTFTIGAWNFSSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV	660
XX	07-JUN-2001; 2001GB-00013900.	Qy	660	TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFETVKYAKOLHIERNM	718
XX	(SYCN ) SYNGENTA LTD.	Db	661	TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFETVKYAKOLHIERNM	719
XX	Vincent JL, Viner R;				
XX	WPI; 2003-175137/17.	RESULT 14			
XX	New insecticidal protein comprising an X-glycine motif at the amino-	ADM74717			
XX	terminus, useful as an active ingredient of a pesticide.	ID	ADM74717 standard; protein; 719 AA.		
XX	Claim 12; Page 53-56; 67pp; English.	XX	ADM74717;		
XX	The invention relates to insecticidal protein comprising an X-glycine	AC	XX		
XX	motif at the amino-terminus. Polynucleotide or DNA constructs of the	DT	03-JUN-2004 (first entry)		
XX	invention are useful for producing plants or plant parts that are	XX	B. thuringiensis cryIIel SEQ ID NO:2.		
XX	resistant to insects. The protein or synergistic combination is useful as	DE	cryI; toxicity; lepidoptera; cryIa; cryIb; coleoptera; diptera;		
XX	an active ingredient of a pesticide or for controlling insects.	KW	cryIIel.		
XX	Antibodies raised to the insecticidal proteins can be used to identify	XX	Bacillus thuringiensis.		
XX	other proteins with insecticidal activity. The present sequence is	OS	CN1401772-A.		
XX	Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This	PN	12-MAR-2003.		
XX	sequence is used in the invention	PD	20-AUG-2001; 2001CN-00124163.		
XX	Sequence 719 AA;	PF	20-AUG-2001; 2001CN-00124163.		
XX	Query Match 99.0%; Score 3711.5; DB 6; Length 719;	PR	(PLAN-) PLANT PROTECTION INST CHINESE ACAD AGRIC.		
XX	Best Local Similarity 99.0%; Pred. No. 7.4e-293;	PA	Song F, Zhang J, Huang D;		
XX	Matches 712; Conservative 2; Mismatches 4; Indels 1; Gaps 1;	PI	WPI; 2003-442339/42.		
Qy	1 MKLKNQDKHQSSNAKVDKISTDSLKNETDIELQNHEDCLMKSEYENVEPFVSASTI 60	XX	N-PSDB; ADM74716.		
Db	1 MKLKNQDKHQSSNAKVDKISTDSLKNETDIELQNHEDCLMKSEYENVEPFVSASTI 60	DR	Bacillus thuringiensis cryI gene, expression vector, nucleotide sequence		
Qy	61 QTGIGIAGKILGTGVPFAGOVASLYSFLGELWPKGNQWEIFMEHVEEIIINQISTYA 120	XX	with high-toxicity to lepidoptera pests, encoded protein, primer		
Db	61 QTGIGIAGKILGTGVPFAGOVASLYSFLGELWPKGNQWEIFMEHVEEIIINQISTYA 120	PT	sequences and the shuttle vector pSXY422b, useful as a pesticide.		
Qy	121 RNKALTDKGLDALAVYHDSLSWSVGNRNNTARSVVKSQVIALFMVQKLPFAVSG 180	PT	Example 3; SEQ ID NO 2; 29pp; Chinese.		
Db	121 RNKALTDKGLDALAVYHDSLSWSVGNRNNTARSVVKSQVIALFMVQKLPFAVSG 180	PS	The invention relates to a novel Bacillus thuringiensis cryI gene, gene		
Qy	181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWS 240	CC	combination, expression vector, nucleotide sequence of the B		
Db	181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWS 240	CC	thuringiensis cryI gene with high-toxicity to lepidoptera pests and the		
Qy	241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFPSYDTOMYPIKTTAQLTRVYTDI 300	CC	amino acid sequence of the protein encoded by it, cooperative use of the		
Db	241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFPSYDTOMYPIKTTAQLTRVYTDI 300	CC	cryI gene with the expression product of cryIa or cryIb, primer		
Qy	301 GTVHPHPSFTSTTWNNAFSFAIAEAVVRNPHLLDFLEQVTIYSLLRWSNTQYMNW 360	CC	sequences for expressing the genes, and the constructed shuttle vector		
Db	301 GTVHPHPSFTSTTWNNAFSFAIAEAVVRNPHLLDFLEQVTIYSLLRWSNTQYMNW 360	CC	pSXY422b. The gene in combination with the cryIa or cryIb genes		
Qy	361 GGHKLEPFTIGTINISQGSTNTSINPVLPTFSRDVYTESLAGNLFLTQPNV 419	CC	displays high toxicity to the lepidoptera, coleoptera and diptera pests.		
Db	361 GGHKLEPFTIGTINISQGSTNTSINPVLPTFSRDVYTESLAGNLFLTQPNV 419	CC	The present sequence represents the cryIIel protein.		
Qy	420 VDFHWKFVTHPTASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479	XX	Query Match 93.7%; Score 3513.5; DB 7; Length 719;		
Db	421 VDFHWKFVTHPTASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480	XX	Best Local Similarity 93.0%; Pred. No. 9.7e-277;		
Qy	480 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVAFNLSSGAAVVRGPGFTGGDILRTN 539	XX	Matches 669; Conservative 26; Mismatches 23; Indels 1; Gaps 1;		
Db	481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVAFNLSSGAAVVRGPGFTGGDILRTN 540	Qy	1 MKLKNQDKHQSSNAKVDKISTDSLKNETDIELQNHEDCLMKSEYENVEPFVSASTI 60		
Qy	540 TGTFGDIRVNNPPFAQRYVRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYK 599	Db	1 MKLKNQDKHQSSNAKVDKISTDSLKNETDIELQNHEDCLMKSEYENVEPFVSASTI 60		

Db 121 RNTALADKGLGDALAYTHESLESWKRNNAATSVMKSYQYIALELLFVKLPFAVSG 180  
Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVRAGDYSYHCVKWS 240  
Db 181 EEPVLLPIYAQAANLHLLLRDASVFGKEWGLSSQISTFYNNQVRSYDSDHCVKWS 240  
Qy 241 TGLNLRGTNAESWRYNQRRDMLMVLVALPFSYDQMPYPIKTTAQLTREVTDAI 300  
Db 241 TGLNLRGTNAESWRYNQRRDMLMVLVALPFSYDQMPYPIKTTAQLTREVTDAI 300  
Qy 301 GTVHPHPSFTSTWYNNAPSFSAIEAAYVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW 360  
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Qy 420 VDFHMKFVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATGQPNYESYSHRSLHIGLIS 479  
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Qy 480 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDIILRTN 539  
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Qy 600 TPTVGTFTPFSLDVGSTFTTIGAMNFSNGNEVYIDRIEFPVPEVTEYAEYDFEKAQEKV 659  
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Qy 660 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFVYKAKQIHIERNM 718  
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFVYKAKQIHIERNM 719

RESULT 15  
AAB66912 standard; protein; 719 AA.

XX ID AAB66912  
XX AC AAB66912;  
XX DT 12-APR-2001 (first entry)  
XX DE Insecticidal protein cryIb1.  
XX KW Insecticide; transgenic plant; insect-resistance.  
XX OS Paecilomyces sp.  
XX PN WO200100841-A1.  
XX PD 04-JAN-2001.  
XX PF 23-JUN-2000; 2000WO-GB002457.  
XX PR 29-JUN-1999; 99GB-00015215.  
XX PR 23-DEC-1999; 99GB-00030536.  
XX PA (ZENE ) ZENECA LTD.  
XX PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
XX PI Vincent JL, Lee MD;  
XX DR WPI; 2001-123015/13.  
XX PT Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PT production.

XX Claim 14; Page 64-66; 72pp; English.  
XX The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX Sequence 719 AA;  
SQ

Query Match 92.9%; Score 3482.5; DB 4; Length 719;  
Best Local Similarity 92.4%; Pred. No. 3.2e-274;  
Matches 664; Conservative 31; Mismatches 23; Indels 1; Gaps 1;  
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Db 1 MKLKNPDKHQSSNAKVDKIATDSLKNETDLELKNMNEDEYLRMSEHSIDPFVASTI 60  
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Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSASEISTFYNNQVRSYDSDHCVKWN 240  
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Db 241 TGLNLRGTNAESWRYNQRRDMLMVLVALPFSYDQMPYPIKTTAQLTREVTDAI 300  
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Db 301 GTVHPNAPSFSTWYNNAPSFSAIEAAYVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW 360  
Qy 361 GGHKLEFRTTGGTLNTSTQSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTOPVN-VPR 419  
Db 361 GGHKLEFRTTGGTLNTSTQSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTOPVNGVR 420  
Qy 420 VDFHMKFVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATGQPNYESYSHRSLHIGLIS 479  
Db 421 VDFHMKFATLPIASDNFYLYGAVGTQLQDSNELPPEATGQPNYESYSHRSLHIGLIS 480  
Qy 480 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDIILRTN 539  
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDIILRTN 540  
Qy 540 TGTFGDIRVNIINPPFAQRYVRIRYASTTDLQPHTSINGKAINQGNFSAATMNRGEDLDYK 599  
Db 541 TGTFGDIRVNIINPPFAQRYVRIRYASTTDLQPHTSINGKAINQGNFSAATMNRGEDLDYK 600  
Qy 600 TPTVGTFTPFSLDVGSTFTTIGAMNFSNGNEVYIDRIEFPVPEVTEYAEYDFEKAQEKV 659  
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Qy 660 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFVYKAKQIHIERNM 718  
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFVYKAKQIHIERNM 719

Search completed: February 14, 2005, 20:50:24  
Job time : 102.215 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005. Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2005, 17:18:14 ; Search time 23.119 Seconds  
(without alignments)  
2318.356 Million cell updates/sec

Title: US-10-019-823B-54

Perfect score: 3749

Sequence: 1 MKLKNQKHQSFSSNAKVDK.....KRELFEIVKYAKQLHIERNM 718

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pap.\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pap.\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pap.\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pap.\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pap.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3718.5	99.2	719	3	US-08-286-870A-8
2	3439	91.7	710	4	US-09-661-322A-42
3	3360.5	89.6	648	3	US-08-286-870A-4
4	3358.5	89.6	719	2	US-09-003-217-2
5	3356.5	89.5	719	3	US-09-218-942-2
6	2778.5	74.1	535	3	US-08-286-870A-6
7	2415	64.4	1229	1	US-08-100-709-4
8	2415	64.4	1229	1	US-08-176-865-4
9	2415	64.4	1229	1	US-08-474-038-4
10	2415	64.4	1229	2	US-08-779-046-4
11	2415	64.4	1229	1	US-08-881-340-4
12	2319	61.9	488	1	US-08-448-170-10
13	2319	61.9	488	3	US-08-961-803-10
14	2236	59.6	1207	1	US-07-951-715A-7
15	2236	59.6	1207	2	US-08-459-448A-7
16	2236	59.6	1207	3	US-08-459-595A-7
17	2236	59.6	1207	3	US-08-459-504B-7
18	2236	59.6	1207	3	US-08-459-444-7
19	2236	59.6	1207	3	US-09-053-549-8
20	2236	59.6	1207	3	US-09-547-422-7
21	2236	59.6	1207	4	US-09-988-462-7
22	2235	59.6	1227	3	US-09-053-549-2
23	2165	57.7	1227	1	US-08-448-170-8
24	2165	57.7	1227	3	US-08-961-803-9
25	2156	57.5	1227	4	US-09-661-322A-63
26	2141	57.1	1186	3	US-09-178-252-23
27	2141	57.1	1186	4	US-09-826-660-23

28	2085.5	55.6	1228	4	US-09-661-322A-38
29	1902	50.7	643	3	US-09-178-252-25
30	1902	50.7	643	4	US-09-826-660-25
31	1891	50.4	380	5	PCT-US91-02560-4
32	1658	44.2	653	4	US-09-661-322A-6
33	1652	44.1	1157	1	US-07-876-280-30
34	1652	44.1	1157	1	US-07-812-180A-2
35	1652	44.1	1157	1	US-08-315-468-2
36	1652	44.1	1157	3	US-07-941-650A-2
37	1482	39.5	1176	1	US-08-257-999-2
38	1480.5	39.5	1157	2	US-08-532-547-5
39	1480.5	39.5	1157	2	US-08-379-656B-5
40	1480.5	39.5	1157	3	US-08-455-838-5
41	1480.5	39.5	1157	3	US-09-019-809-5
42	1480.5	39.5	1157	4	US-09-471-177-5
43	1480.5	39.5	1157	4	US-09-220-806-5
44	1474	39.3	1156	3	US-09-002-285-72
45	1474	39.3	1156	4	US-09-589-477-72

#### ALIGNMENTS

#### RESULT 1

US-08-286-870A-8

; Sequence 8, Application US/08286870A

; Patent No. 6063605

; GENERAL INFORMATION:

; APPLICANT: ELY, S

; APPLICANT: TAILOR, RH

; APPLICANT: TIPPETT, JM

; APPLICANT: BLENN, RG

; TITLE OF INVENTION: BACTERIAL GENES

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

; ADDRESSEE: Intellectual Property Group of

; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP

; STREET: 1100 New York Avenue, N.W.

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3918

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/286,870A

; FILING DATE: 05-AUG-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/520228

; FILING DATE: 09-MAY-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 8910624.9

; FILING DATE: 09-MAY-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: PAUL N. KOKULIS

; REGISTRATION NUMBER: 16,773

; REFERENCE/DOCKET NUMBER: 70608/220720

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 861-3000

; TELEFAX: (202) 822-0944

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 719 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-286-870A-8

Thu Mar 10 14:26:03 2005

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Best Local Similarity 99.3%; Pred. No. 0;  
Matches 714; Conservative 1; Mismatches 3; Indels 1; Gaps 1;  
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DB 1 M K L K N Q D K H Q S F S S N A K V D K I S T S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60  
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DB 121 R N K A L T D L K G L D A L A V V H S L E S W G N R N N T R A S V V K S Q Y I A L E L M F V K L P S F A V S G 180  
QY 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F N R Q V E R A G D Y S H C V K W Y S 240  
DB 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F N R Q V E R A G D Y S H C V K W Y S 240  
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QY 480 A S H V K A L V S W T H R S A D R N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 539  
DB 481 A S H V K A L V S W T H R S A D R N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540  
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RESULT 2  
US-09-661-322A-42  
; Sequence 42 Application US/09661322A  
; Patent No. 6593293  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chin-Rel  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Rugar, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos  
; TITLE OF INVENTION: and Methods of Use  
; FILE REFERENCE: MECO201  
; CURRENT APPLICATION NUMBER: US/09/661,322A  
; CURRENT FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 42  
; LENGTH: 710  
; TYPE: PRN

ORGANISM: Bacillus thuringiensis  
FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2007..(200)  
; OTHER INFORMATION: No. 6593293-Coding  
US-09-661-322A-42  
Query Match 91.7%; Score 3439; DB 4; Length 710;  
Best Local Similarity 91.9%; Pred. No. 1.2e-299;  
Matches 661; Conservative 15; Mismatches 33; Indels 10; Gaps 2;  
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DB 52 Q T G I G I A G K I L G N L G V P F A G Q V A S L Y S F I L G E L W P K G S Q W E I F M E H V E E I I N K I S T Y A 111  
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DB 172 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K X W G L S D S E I S T F Y N R Q S G K S E Y S H D C V K W Y N 231  
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QY 540 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 599  
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RESULT 3  
US-08-286-870A-4  
; Sequence 4 Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: Ely, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABY & CUSHMAN



```

; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286.870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-870A-4

Query Match      89.6%; Score 3360.5; DB 3; Length 648;
Best Local Similarity 99.4%; Pred. No. 1.1e-292;
Matches 644; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy      1 M L K N Q D K H Q S F S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60
Db      1 M L K N Q D K H Q S F S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60

Qy      61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120
Db      61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120

Qy      121 R N K A L T D L K G L G D A L A V Y H D S L E S W G V G N R N N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180
Db      121 R N K A L T D L K G L G D A L A V Y H D S L E S W G V G N R N N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180

Qy      181 E E V P L L P T Y A A A N L H L L L D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S H C V K W Y S 240
Db      181 E E V P L L P T Y A A A N L H L L L D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S H C V K W Y S 240

Qy      241 T G L A N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300
Db      241 T G L A N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300

Qy      301 G T V H P H S F T T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T Y I S L L S R W S N T Q Y M N W 360
Db      301 G T V H P H S F T T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T Y I S L L S R W S N T Q Y M N W 360

Qy      361 G G H K L E P R T I G G T L N I S T Q S T N T S I N P V T L P P T S R D V Y R T E S L A G L N L F L T Q P V N V P R 419
Db      361 G G H K L E P R T I G G T L N I S T Q S T N T S I N P V T L P P T S R D V Y R T E S L A G L N L F L T Q P V N V P R 420

Qy      420 V D F H W K F V T H P I A S D N F Y P G V A G I G T Q L Q S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 479
Db      421 V D F H W K F V T H P I A S D N F Y P G V A G I G T Q L Q S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480

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RESULT 4
US-09-003-217-2
; Sequence 2, Application US/09003217
; Patent No. 5986177
; GENERAL INFORMATION:
; APPLICANT: Osman, Yehia A.
; APPLICANT: Madkour, Magdy A.
; APPLICANT: Bulla, Lee A.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
; TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
; STREET: 3605 Glenwood Ave. Suite 310
; CITY: Raleigh
; STATE: NC
; COUNTRY: US
; ZIP: 27622
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003.217
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 5718-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2202
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-003-217-2

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Query Match      89.6%; Score 3358.5; DB 2; Length 719;
Best Local Similarity 89.6%; Pred. No. 2e-292;
Matches 644; Conservative 33; Mismatches 41; Indels 1; Gaps 1;

Qy      1 M L K N Q D K H Q S F S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60
Db      1 M L K N P K H O T L S S N A K V D K I A T D S L K N E T D I E L K N M N E D Y L R M S E H S I D P F V S A S T I 60

Qy      61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120
Db      61 Q T G I G I A G K I L G T L G V P P G Q I A S L Y S F I L G E L W P K G S Q W E I P M E H V E A I I N R K I S T Y A 120

Qy      121 R N K A L T D L K G L G D A L A V Y H D S L E S W G V G N R N N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180
Db      121 R N K A L T D L K G L G D A L A V Y H S L E S W G V G N R N N T R A R S V V K N Q Y I A L E M F V Q K L P S F A V S G 180

Qy      181 E E V P L L P T Y A A A N L H L L L D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S H C V K W Y S 240

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181 EVPLPIYAQAANLHLLLDASIFKNGGLSASEISTFYNQVTRDYSYHCVKWN 240  
241 TGLNLRGTNAESWVRYNQFRDMLVALFPSYDTOMYPIKTAOLTRVYTDAL 300  
241 TGLNLRGTNAESWVRYNQFRDMLVALFPSYDTOMYPIKTAOLTRVYTDAL 300  
301 GTVHPHPTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSWSNTQYNNMW 360  
301 GTVHPHPTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSWSNTQYNNMW 360  
361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFTQPV-NVR 419  
361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFTQPV-NVR 420  
420 VDFHKKFPTLPFTSRDVRYSAGLNLFTQPV-NVR 479  
421 VDFHKKFPTLPFTSRDVRYSAGLNLFTQPV-NVR 480  
480 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGHILRTK 539  
481 GSHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGHILRTK 540  
540 TGTGDIRVNPFPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATWNGEDLDYK 599  
541 SGTGDIRVNPFPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATWNGEDLDYK 600  
600 TGTGDIRVNPFPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATWNGEDLDYK 659  
601 TGTGDIRVNPFPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATWNGEDLDYK 660  
660 TALFTSTNPRGLKTDVKDYHIDQVSNLVSDELYDEKRELFEIVKAKQIHIERNM 718  
661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSDELYDEKRELFEIVKAKQIHIERNM 719

RESULT 5  
US-09-218-942-2  
; Sequence 2, Application US/09218942  
; Patent No. 6232439  
; GENERAL INFORMATION:  
; APPLICANT: Osman, Yehia  
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum  
; FILE REFERENCE: C101  
; CURRENT FILING DATE: 1998-12-22  
; EARLIER FILING DATE: 1997-01-10  
; EARLIER FILING DATE: 1997-01-10  
; EARLIER FILING DATE: 1998-01-06  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-09-218-942-2

Query Match 89.5%; Score 3356.5; DB 3; Length 719;  
Best Local Similarity 89.6%; Pred. No. 3e-292;  
Matches 644; Conservative 33; Mismatches 41; Indels 1; Gaps 1;  
1 MKLNQDQKQSSNAKVDKISTDLSKNETDIELQNIHEDCLMKSEYENVEPVSASTI 60  
1 MKLNQDQKQSSNAKVDKISTDLSKNETDIELQNIHEDCLMKSEYENVEPVSASTI 60  
61 QTGIGIAGKILGTLGVPAGQVASYLSFILGELPKGNQWEIWEHVEILINQISTYA 120  
61 QTGIGIAGKILGTLGVPAGQVASYLSFILGELPKGNQWEIWEHVEILINQISTYA 120  
121 RNKALTDLKGLDALAVHDSLESVGNRNNTRARSVVKSOYIALELMFVKLPSPAVSG 180  
121 RNKALTDLKGLDALAVHDSLESVGNRNNTRARSVVKSOYIALELMFVKLPSPAVSG 180

191 EVPLPIYAQAANLHLLLDASIFKNGGLSASEISTFYNQVTRDYSYHCVKWN 240  
181 EVPLPIYAQAANLHLLLDASIFKNGGLSASEISTFYNQVTRDYSYHCVKWN 240  
241 TGLNLRGTNAESWVRYNQFRDMLVALFPSYDTOMYPIKTAOLTRVYTDAL 300  
241 TGLNLRGTNAESWVRYNQFRDMLVALFPSYDTOMYPIKTAOLTRVYTDAL 300  
301 GTVHPHPTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSWSNTQYNNMW 360  
301 GTVHPHPTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSWSNTQYNNMW 360  
361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFTQPV-NVR 419  
361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFTQPV-NVR 420  
420 VDFHKKFPTLPFTSRDVRYSAGLNLFTQPV-NVR 479  
421 VDFHKKFPTLPFTSRDVRYSAGLNLFTQPV-NVR 480  
480 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGHILRTK 539  
481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGHILRTK 540  
540 TGTGDIRVNPFPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATWNGEDLDYK 599  
541 SGTGDIRVNPFPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATWNGEDLDYK 600  
600 TGTGDIRVNPFPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATWNGEDLDYK 659  
601 TGTGDIRVNPFPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATWNGEDLDYK 660  
660 TALFTSTNPRGLKTDVKDYHIDQVSNLVSDELYDEKRELFEIVKAKQIHIERNM 718  
661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSDELYDEKRELFEIVKAKQIHIERNM 719

RESULT 6  
US-08-286-870A-6  
; Sequence 6, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENN, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DAREY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/286,870A  
FILING DATE: 05-AUG-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520228  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8910624.9  
FILING DATE: 09-MAY-1989

```

; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-870A-6

Query Match 74.1%; Score 2778.5; DB 3; Length 535;
Best Local Similarity 99.6%; Pred. No. 1.5e-240;
Matches 533; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 MKLNQDKHQSFNNAKVDKISTSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60
Db 1 MKLNQDKHQSFNNAKVDKISTSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60
Qy 61 QTGIGIAGKILGTIGVPPAGQVASYLFIIGELMPKGNQWEIEMFHEVEEIIINOKISTYA 120
Db 61 QTGIGIAGKILGTIGVPPAGQVASYLFIIGELMPKGNQWEIEMFHEVEEIIINOKISTYA 120
Qy 121 RNKALTDLKGDLGALAVYHDSLESWGNRNNTARSVVKSYIALELMFVQKLPFAVSG 180
Db 121 RNKALTDLKGDLGALAVYHDSLESWGNRNNTARSVVKSYIALELMFVQKLPFAVSG 180
Qy 181 EEPVLLPIYAAQANLHLLLDASIFGKEWGLSSSEISTFTNROVERAGDYSYHCVKWYS 240
Db 181 EEPVLLPIYAAQANLHLLLDASIFGKEWGLSSSEISTFTNROVERAGDYSYHCVKWYS 240
Qy 241 TGLNLGRTNAESWVRYNQFRDMLVLDLVALFPSYDTOMYPIKTTAQLTREVYTDAI 300
Db 241 TGLNLGRTNAESWVRYNQFRDMLVLDLVALFPSYDTOMYPIKTTAQLTREVYTDAI 300
Qy 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMW 360
Db 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMW 360
Qy 361 GGHKLEPRTIGTILNISTQSTNTSINPVTLPFTSRDVRYESLAGNLFUTQPVN-VPR 419
Db 361 GGHKLEPRTIGTILNISTQSTNTSINPVTLPFTSRDVRYESLAGNLFUTQPVNGVPR 420
Qy 420 VDFHKKFVTHPIASDNFYPCYAGIGTQLODSENELPEATGQPNYESYSHRLSHIGLIS 479
Db 421 VDFHKKFVTHPIASDNFYPCYAGIGTQLODSENELPEATGQPNYESYSHRLSHIGLIS 480
Qy 480 ASHKVAVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 534
Db 481 ASHKVAVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
; Sequence 4, Application US/08100709
; Patent No. 5322687
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CTYET4 AND CRYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia

```

```

; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; APPLICATION DATA:
; APPLICATION NUMBER: US/08/100.709
; FILING DATE: 19930729
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Egoif, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-100-709-4

Query Match 64.4%; Score 2415; DB 1; Length 1229;
Best Local Similarity 65.1%; Pred. No. 2.5e-207;
Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;

Qy 13 SSNAKVDKISTSLKNETDIELQNHEDCLKXSEYENVEPVSASTIQTGIGIAGKI 70
Db 7 NENIINALSPTVSNFSPQNLSPDARIEDSLCAEVNNDIPFVSASTVQTGINIAGRI 66
Qy 71 LGTVGPAGQVASYLFIIGELMPKGNQWEIEMFHEVEEIIINOKISTYARNKALTDLKG 130
Db 67 LGVLGVFPAGQVASYLFIIGELMPKGNQWEIEMFHEVEEIIINOKISTYARNKALTDLKG 126
Qy 131 LGDALAVYHDSLESWGNRNNTARSVVKSYIALELMFVQKLPFAVSGEVPVLLPIYA 190
Db 127 LGRGYSYQQALETWLDNRNDARSIIILRYVALELDITTAIPLFRIRNEEVPVLLMVA 186
Qy 191 QAANLHLLLDASIFGKEWGLSSSEISTFTNROVERAGDYSYHCVKWYSYGLNLRGTN 250
Db 187 QAANLHLLLDASIFGKEWGLSSSEISTFTNROVERAGDYSYHCVKWYSYGLNLRGTN 246
Qy 251 AESWVRYNQFRDMLVLDLVALFPSYDTOMYPIKTTAQLTREVYTDIAGTVHPHPSFT 310
Db 247 AESWVRYNQFRDMLVLDLVALFPSYDTOMYPIKTTAQLTREVYTDIAGTVHPHPSFT 306
Qy 311 STWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGHKLEPRTI 370
Db 307 STWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGHKLEPRTI 366
Qy 371 GGTILNISTQSTNTSINPVTLPFTSRDVRYESLAGNLFUTQPVN-VPRVDFHKKFVT 428
Db 367 GGTILNISTQSTNTSINPVTLPFTSRDVRYESLAGNLFUTQPVN-VPRVDFHKKFVT 422
Qy 429 HPIASDNFYPCYAGIGTQLODSENELPEATGQPNYESYSHRLSHIGLIS 481
Db 423 --INPQNIYERGATTSYQYQVGIQIFDSSTELPPTETTERPNTYESYSHRLSHIGLIS 480
Qy 482 HVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTWTG 541
Db 481 TLRAVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTWTG 540
Qy 542 TFGDIRVNINPPFAQRVRIYRISTDQLQHTSINGKAINQGNFSATMNGEDLDYKTF 601
Db 541 TFGDIRVNINPPFAQRVRIYRISTDQLQHTSINGKAINQGNFSATMNGEDLDYKTF 600
Qy 602 XTGVGFTTFFSLLDVQSTFTIGAMNFSNGEYVYIDRIEFPVPEVYEAEDFEKAQEKVTA 661
Db 601 RTAGFSTFPFNLAQSTFTLGAQFSN-OEYVIDRVEFPVPAEVTPEAEYDLERAQAVNA 659

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QY 662 LFTSTNPRGLKTDVYHIDQVSNLVESLSEDFYLDKRELFELVYKAKQLHIERNM 718  
 DB 660 LFTSTNPRRLKTDVTHIDQVSNWVACLSEDFCLDEKRELFELVYKAKQLSDERNL 716

RESULT 8  
 US-08-176-865-4  
 ; Sequence 4, Application US/08176865  
 ; Patent No. 5616319  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yiping  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; APPLICANT: Egolf, Christopher  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESS: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; FILING DATE: 30-DEC-1993  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/100,709  
 ; FILING DATE: 29-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egolf, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1229 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-176-865-4

Query Match 64.4%; Score 2415; DB 1; Length 1229;  
 Best Local Similarity 65.1%; Pred. No. 2.5e-207;  
 Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;

QY 13 SSNAKVDSKIDSLKN-ETDIEIQ-NINHEDECLKMSEYENVEPVFSASTIQTGIGIAGKI 70  
 DB 7 NENEIINALSIPVSNSTQWNLSPDARIEDSLCAEVNNDPFSASTVQTGINIAGRI 66

QY 71 LGTLGVPPAGVQASLYSIFLGELWPKGNQWEIPMEHVEIINQKISTYARKALTDLKG 130  
 DB 67 LGVLGVPPAGVQASLYSIFLGELWPKGNQWEIPMEHVEIINQKISTYARKALTDLKG 126

QY 131 LGDALVYHDSLEWGNVGNRRNTRSVVKSQYIALELMFVQKLPFSFVSGEEVPLPIYA 190  
 DB 127 LGRGVRSQQALEWLDNRNDRSIILEYVALEDDITTAIPLFRINEEVPLLMVYA 186

QY 191 QAAHLHLLLRDASIFGKWLGSSEISTFTYRQVERAGDYSYHCWYSTGLNLEGTN 250  
 DB 187 QAAHLHLLLRDASIFGKWLGSSEISTFTYRQVERAGDYSYHCWYSTGLNLEGTN 246

QY 251 AESWRYNQFRDMLVLDLVALFPSPYDTQWYPIKTTAQLTRVYTDAGTGVHPHPSFT 310

DB 247 AESMLRYNQFRDLTLGLVLDLVALFPSPYDTQWYPIKTTAQLTRVYTDAGTGVHPHPSFT 306  
 QY 311 STTWYNNAPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMGHKLFPRTI 370  
 DB 307 STNFWNNAPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMGHKLFPRTI 366

QY 371 GGTNLNISTQGST-NTSINPVTLPTSDRVYRTESLAGLNFLTOPVN-VPRVDFHWFVT 428  
 DB 367 GGTNLNISTQGST-NTSINPVTLPTSDRVYRTESLAGLNFLTOPVN-VPRVDFHWFVT 422

QY 429 HPIASDNFYPG-----YAGIGTQLODSENELPPEATGPNYSEYSHRLSHGLISAS 481  
 DB 423 --INPQNIYERGATTYSQYQGVGLDFDSELPPEATGPNYSEYSHRLSHGLISAS 480

QY 482 HYKALVYVSWTHRSADRTNTIENPNSITQIPLVKAFNLSSGAAVVRPGPTGDDILRRNTG 541  
 DB 481 TURAPVSWTHRSADRTNTIENPNSITQIPLVKAFNLSSGAAVVRPGPTGDDILRRNTG 540

QY 542 TFGDIRVNNIPPAQRYRVIRYASTTLOFHTSINGKAINQGNFSAATMNRGDDLYKTF 601  
 DB 541 TFGDIRLNNVPLSQRYRVIRYASTTLOFHTSINGKAINQGNFSAATMNRGDDLYKTF 600

QY 602 XTVGFTTSPSLDVQSTFTIGAWNFSSGNEVVIDRIEFVPEVVEVYEAEDYFEKAQKVTA 661  
 DB 601 RTAGSTPPFNLAQSTFTLGAQSFN-QEVVIDRVEFVPAEVTFEAEYDLERAQKAVNA 659

QY 662 LFTSTNPRGLKTDVYHIDQVSNLVESLSEDFYLDKRELFELVYKAKQLHIERNM 718  
 DB 660 LFTSTNPRRLKTDVTHIDQVSNWVACLSEDFCLDEKRELFELVYKAKQLSDERNL 716

RESULT 9  
 US-08-474-038-4  
 ; Sequence 4, Application US/08474038  
 ; Patent No. 5679343  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yiping  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESS: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/474,038  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/176,865  
 ; FILING DATE: 30-DEC-1993  
 ; APPLICATION NUMBER: US 08/100,709  
 ; FILING DATE: 29-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egolf, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:



Thu Mar 10 14:26:03 2005

QY 542 TFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFATMNRGCDLKYTF 601  
DB 541 TFGDIRLNLNPLSQRYRVRIRYASTTDLQFHTSINGKAINQGNFATMNRGCDLKYTF 600  
QY 602 XTGVGFTTFFSLDDVOSTFTTIGAMNFFSGNEVYIDRIEFVPEVYEAEDYFKAQKAVTA 661  
DB 601 RTAGFSTFPNPLNAQSTFTTIGAQFSN-QEYVIDRVEFVPAEVTFEAYDLERAKAVNA 659  
QY 662 LFTSTNPRGLKTDVKDHYDIDQVSNVLSLSDDEFYLDKRELFELVYKAKOLHIERNM 718  
DB 660 LFTSTNPRGLKTDVTDYHIDQVSNVACLSDDEFCLDKRELFELVYKAKOLHIERNM 716  
RESULT 11  
US-08-881-340-4  
; Sequence 4, Application US/08881340  
; Patent No. 5942658  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yiping  
; APPLICANT: Jany, Christine S.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
; ADDRESS: Nadel  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,340  
; FILING DATE: 24-JUN-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/100,709  
; FILING DATE: 29-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Egolf, Christopher  
; REGISTRATION NUMBER: 27633  
; REFERENCE/DOCKET NUMBER: 7205-49  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-757-1590  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1229 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-881-340-4  
Query Match 64.4%; Score 2415; DB 2; Length 1229;  
Best Local Similarity 65.1%; Pred. No. 2.5e-207;  
Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;  
QY 13 SSNAKVKIDSLKN-ETDIELQ-NINHEDCLMSEYNEVPEFVASTTQTGTIGIAGKI 70  
DB 7 NENEIINALSIPTVSNSTQNLSPDARIEDSLCAEVNNDIPVSAVSTQTGTINAGRI 66  
QY 71 LGTLGVPPAGVAVSLYFELGELWPKGNQWEIFMEHVVEILNQIKISTYARNKALDTLKG 130  
DB 67 LGVLGVPPAGVAVSLYFELGELWPKGNQWEIFMEHVVEILNQIKISTYARNKALDTLKG 126  
QY 131 LGDALAVTHDSLESWGNRNTRARSVVKVSYIALELMFVQKLPSPAVSGEVPPLPIYA 190

DB 127 LGRGYSYQQALETWLDNRDARSRIILERYVALELDITTAIPLFRIRNEEVPLMVA 186  
QY 191 QAAHLHLLLDASIFGKEWGLSSSEISTFYNRQVERAGDYSHVCWKYSTGLNLRGNT 250  
DB 187 QAAHLHLLLDASIFGKEWGLSSSEISTFYNRQVERAGDYSHVCWKYSTGLNLRGNT 246  
QY 251 AESWRYNQFRDMLVLDLVALFPSPDYTDQYPIKITAOLTRVYTDATGTVHPHPSFT 310  
DB 247 AESWRYNQFRDMLVLDLVALFPSPDYTDQYPIKITAOLTRVYTDATGTVHPHPSFT 306  
QY 311 STTWNNAPSAEAAVVRNPHLLDLEOVYIYSLLSRWSNTOYMMWGGHKLLEFTTI 370  
DB 307 STTWNNAPSAEAAVVRNPHLLDLEOVYIYSLLSRWSNTOYMMWGGHKLLEFTTI 366  
QY 371 GGTNLNISTQGST-NTSINPVTLPFTSRDYRTESLAGNLFLTQPVN-VPRVDFHFKVFT 428  
DB 367 GGTNLNISTQGST-NTSINPVTLPFTSRDYRTESLAGNLFLTQPVN-VPRVDFHFKVFT 422  
QY 429 HPIASDNFYPG-----YAGITQLODSENELPEATQOPNYESYSHRSLHIGLISAS 481  
DB 423 --INPQNIYERGATTSYQPYQGVGILQFSELTPEPETERENYESYSHRSLHIGLIG 480  
QY 482 HVKALVYSWTHRSADRTNITPNSITQIPLVKAFLNSGAAVVRGPGFTGGDILRTNTG 541  
DB 481 TLRAPVSWTHRSADRTNITPNSITQIPLVKAFLNSGAAVVRGPGFTGGDILRTNTG 540  
QY 542 TFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFATMNRGCDLKYTF 601  
DB 541 TFGDIRLNLNPLSQRYRVRIRYASTTDLQFHTSINGKAINQGNFATMNRGCDLKYTF 600  
QY 602 XTGVGFTTFFSLDDVOSTFTTIGAMNFFSGNEVYIDRIEFVPEVYEAEDYFKAQKAVTA 661  
DB 601 RTAGFSTFPNPLNAQSTFTTIGAQFSN-QEYVIDRVEFVPAEVTFEAYDLERAKAVNA 659  
QY 662 LFTSTNPRGLKTDVKDHYDIDQVSNVLSLSDDEFYLDKRELFELVYKAKOLHIERNM 718  
DB 660 LFTSTNPRGLKTDVTDYHIDQVSNVACLSDDEFCLDKRELFELVYKAKOLHIERNM 716  
RESULT 12  
US-08-448-170-10  
; Sequence 10, Application US/08448170  
; Patent No. 5723758  
; GENERAL INFORMATION:  
; APPLICANT: Payne, Jewel  
; APPLICANT: Cummings, David A.  
; APPLICANT: Cannon, Raymond J.C.  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Stelman, Steve  
; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted  
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes  
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/448,170  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/069,902  
; FILING DATE: 01-JUNE-1993  
; CLASSIFICATION: 424

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-448-170-10

Query Match 61.9%; Score 2319; DB 1; Length 488;
Best Local Similarity 89.3%; Pred. No. 2.3e-199;
Matches 444; Conservative 13; Mismatches 30; Indels 10; Gaps 2;

QY 1 MKLKNQDKHQSFSNAKVDKISTSLKNETDIELQNIHEDCLKMSYENVEPPFVSASTI 60
DB 1 MMSKNQNHQSLSNNAATVDKNFTGSLNNTTELQNFH-----EGIEPPFVSASTI 51

QY 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEELINQKISTYA 120
DB 52 QTGIGIVGKILGNLGVPPAGQVASYLSFILGELWPKGKSQWEIFMEHVEELINQKISTYA 111

QY 121 RNKALTDLKGDLAVYHDSLESWGNNRNRTRRSVVKSOYIAELMFPVKLPSPFVSG 180
DB 112 RNKALADLKGDLAVYHDSLESWNIENRNRTRRSVVKSOYITLMLFVQSLPSPFVSG 171

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNNRQVERAGDYSYHCWKYS 240
DB 172 EEPVLLPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNNRQSGKSKYSYDHCWKYN 231

QY 241 TGLNLRGTNAESWRYNQFRDMLMVLDLVALPSPDYDTQMYPIKTTAQLTREVYTDAT 300
DB 232 TGLNLRGNNAESWRYNQFRDMLMVLDLVALPSPDYDTQMYPIKTTAQLTREVYTDAT 291

QY 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRMSNTQYMMNW 360
DB 292 GTVHPHPSFTTWTNNNAPSFTIEAAVVRNPHLLDFLEQVTIYSLSRMSNTQYMMNW 351

QY 361 GGHKLEPRTIGTLNISTQSTNTSINPVTLPFTSRDYRTESLAGINLFLTPQVNV-VP 419
DB 352 GGHKLEPRTIGTLNISTQSTNTSINPVTLPFTSRDYRTESLAGINLFLTPQVNGVPR 411

QY 420 VDFHWKFTVTHPIASDNFYYPGAGIGTOLQDSNELPPEATGQPNYESYSHRLSHIGLIS 479
DB 412 VDFHWKFTVTHPIASDNFYYPGAGIGTOLQDSNELPPEATGQPNYESYSHRLSHIGLIS 471

QY 480 ASHVKALVYSWTHRSAD 496
DB 472 ASHVKALVYSWTHRSAD 488

RESULT 13
US-08-961-803-10
; Sequence 10, Application US/08961803
; Patent No. 6150589
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
; ; TITLE OF INVENTION: B.C. PS158C2, Active Against Lepidopteran Pests, and Genes

```

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; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961.803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,170
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: M/S 102DCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-961-803-10

Query Match 61.9%; Score 2319; DB 3; Length 488;
Best Local Similarity 89.3%; Pred. No. 2.3e-199;
Matches 444; Conservative 13; Mismatches 30; Indels 10; Gaps 2;

QY 1 MKLKNQDKHQSFSNAKVDKISTSLKNETDIELQNIHEDCLKMSYENVEPPFVSASTI 60
DB 1 MMSKNQNHQSLSNNAATVDKNFTGSLNNTTELQNFH-----EGIEPPFVSASTI 51

QY 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEELINQKISTYA 120
DB 52 QTGIGIVGKILGNLGVPPAGQVASYLSFILGELWPKGKSQWEIFMEHVEELINQKISTYA 111

QY 121 RNKALTDLKGDLAVYHDSLESWGNNRNRTRRSVVKSOYIAELMFPVKLPSPFVSG 180
DB 112 RNKALADLKGDLAVYHDSLESWNIENRNRTRRSVVKSOYITLMLFVQSLPSPFVSG 171

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNNRQVERAGDYSYHCWKYS 240
DB 172 EEPVLLPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNNRQSGKSKYSYDHCWKYN 231

QY 241 TGLNLRGTNAESWRYNQFRDMLMVLDLVALPSPDYDTQMYPIKTTAQLTREVYTDAT 300
DB 232 TGLNLRGNNAESWRYNQFRDMLMVLDLVALPSPDYDTQMYPIKTTAQLTREVYTDAT 291

QY 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRMSNTQYMMNW 360
DB 292 GTVHPHPSFTTWTNNNAPSFTIEAAVVRNPHLLDFLEQVTIYSLSRMSNTQYMMNW 351

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Best Local Similarity 63.9%; Pred. No. 2.8e-191; Indels 14; Gaps 6;  
Matches 439; Conservative 78; Mismatches 156;  
40 EDCLKMEYENVEPVASSTIQTGIGIAGKILGTGVFPAGQVASYFSLGELWPKGN 99  
10 EDSICIAEGNNIDPFVASSTVQIGINAGILGVLPVFPAGQLASFVSLVGLWPRGRD 69  
100 QWEIFMEHVEEIIINQKISTVARNKALDGLKGLDALAVYHDSLESWGVNRRNTRASVVK 159  
70 QWEIFLEHVEQLINQITENARTALRLOGLQSFAYQOQSLDMLNEDDDARTSVLY 129  
160 SOYIALELMFVKQLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSIST 219  
130 TOYIALELDFLNPMLFAIRNQEVPLLMVTAQAANLHLLLRDASLFGSEGLTSQSIQR 189  
220 FYNROVERAGDYSYHCVKWTGYSTGLNNLRGTNAESWRYNQPRRMTLMULDVALFESYD 279  
190 YIERQVETRDYSDYCVEMWNTGLNLRGTNAESWRYNQPRRDLTGLVDLVALFESYD 249  
280 TQMPYIKTTAQLTRVYTDALGTGHPHPSFTSTTWNNAFSAIEAAVVRNPHLLDFL 339  
250 TRTPINTSAQLTRVYTDALGTGAT--GVNMMWNNNNNAFSAIEAAVVRNPHLLDFL 307  
340 EQVTIYSLLSRWSNTQYMMWGGHKLFRITIGTILNISTOGSTNTSINPVTLPFTRSDVY 399  
308 EQLTIFSASSRWSNTRHMTYWGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTRSDVY 367  
400 RTELASGLNLF--LTOPVN--VPRVDFHVKFVTHP-----IASDNFYYPGAGIGTLOQDS 451  
368 RTELASGLNLF--LTOPVN--VPRVDFHVKFVTHP-----IASDNFYYPGAGIGTLOQDS 423  
452 ENELPPEATCOPNYESYSHRLSHIGLISASHVKALVSWTHRSADRTNTIENSTIQLPL 511  
424 ETELPPETTERPNYESYSHRLSHIGLISASHVKALVSWTHRSADRTNTIENSTIQLPM 483  
512 VKAFNLSSGAAVVRGEGFTGGDILRNTTGTGDIRVNIINPPFAORYRIRYASTDLQ 571  
484 VKASELPQGTTVVRGEGFTGGDILRNTTGTGDIRVNIINPPFAORYRIRYASTDLQ 543  
572 PHTSINKAINQGNFSAWNRGDLDTXVTGFTTFFSLDLDVQSTFTTIGAWNFSSGNE 631  
544 FVSRGGTTVNFRFLKTMNGSDGLKYNFVRAFTTFTTQIIDIIRTSIQGLSGNGE 603  
632 VYIDRIEFVPEVTEAEYDFEKAQEKVATLFTSTPRGLKTDVKKYHIDVSNLVESLS 691  
604 VYIDKIELIPVATFTEAEYDLERAQEAVALFTNTNPRKLTDTVDYHIDQVSNLVACLS 663  
692 DEFYLDKRELFELVYKAKQLHIERNM 718  
664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 15  
US-08-459-448A-7  
; Sequence 7, Application US/08459448A  
; Patent No. 5859336  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.

361 GGHLKERTTGGTINISTQSTNTSINPVTLPFTRSDVYRTESLAGLNLFLTOPVN--VPR 419  
352 GGHLKERTTGGTINISTQSTNTSINPVTLPFTRSDVYRTESLAGLNLFLTOPVNGVPR 411  
420 VDFHKKFVTHPIASDNFYYPGAGIGTLOQDSNELPPEATGQPNYESYSHRLSHIGLIS 479  
412 VDFHKKFVTHPIASDNFYYPGAGIGTLOQDSNELPPEATGQPNYESYSHRLSHIGLIS 471  
480 ASHKALVYSWTHRSAD 496  
472 ASHKALVYSWTHRSAD 488

RESULT 14  
US-07-951-715A-7  
; Sequence 7, Application US/07951715A  
; Patent No. 5625136  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/951,715A  
; FILING DATE: 25-SEP-1992  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8615  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1207 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-951-715A-7

Query Match 59.6%; Score 2236; DB 1; Length 1207;





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 9, 2005, 17:22:50 ; Search time 70.5047 Seconds  
(without alignments)  
3350.901 Million cell updates/sec

Title: US-10-019-823B-54  
Perfect score: 3749  
Sequence: 1 MLLKNQKHQSFSSNAKVDK.....KRELFEIVKYAKQLHIERNM 718

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3722.5	99.3	719	16	US-10-782-020-10
2	3722.5	99.3	719	16	US-10-782-141-8
3	3439	91.7	710	15	US-10-428-961-42
4	2249	60.0	1228	16	US-10-809-953-10
5	2236	59.6	1207	10	US-09-988-462-7
6	2156	57.5	1227	15	US-10-428-961-63
7	2141	57.1	1186	9	US-09-826-660-23
8	2085.5	55.6	1228	15	US-10-428-961-38
9	2085.5	55.6	1228	15	US-10-614-524-2
10	1902	50.7	643	9	US-09-826-660-25
11	1708	45.6	1167	14	US-10-089-678-1
12	1658	44.2	653	15	US-10-428-961-6
13	1652	44.1	1157	16	US-10-782-141-16

14	1500.5	40.0	1206	13	US-10-032-717-2	Sequence 2, Appli
15	1500.5	40.0	1206	14	US-10-414-637-2	Sequence 2, Appli
16	1500.5	40.0	1206	15	US-10-606-320-2	Sequence 2, Appli
17	1477.5	39.4	1210	13	US-10-032-717-4	Sequence 4, Appli
18	1477.5	39.4	1210	14	US-10-414-637-4	Sequence 4, Appli
19	1477.5	39.4	1210	15	US-10-606-320-4	Sequence 4, Appli
20	1474	39.3	1156	14	US-10-099-285-72	Sequence 72, Appli
21	1474	39.3	1156	15	US-10-428-961-28	Sequence 28, Appli
22	1441.5	38.5	1155	9	US-09-756-643-2	Sequence 2, Appli
23	1441.5	38.5	1155	10	US-09-988-462-9	Sequence 9, Appli
24	1441.5	38.5	1155	15	US-10-136-998A-2	Sequence 6, Appli
25	1441.5	38.5	1177	14	US-10-035-060-6	Sequence 6, Appli
26	1441.5	38.5	1181	10	US-09-988-462-11	Sequence 11, Appli
27	1441.5	38.5	1181	10	US-09-988-462-13	Sequence 13, Appli
28	1441.5	38.5	1181	10	US-09-988-462-15	Sequence 15, Appli
29	1441.5	38.5	1181	10	US-09-988-462-17	Sequence 17, Appli
30	1441.5	38.5	1181	10	US-09-988-462-28	Sequence 28, Appli
31	1441.5	38.5	1181	15	US-10-136-998A-4	Sequence 4, Appli
32	1441.5	38.5	1181	15	US-10-136-998A-8	Sequence 8, Appli
33	1441.5	38.5	1181	15	US-10-136-998A-10	Sequence 10, Appli
34	1441.5	38.5	1181	15	US-10-136-998A-12	Sequence 12, Appli
35	1436.5	38.3	1177	14	US-10-035-060-2	Sequence 2, Appli
36	1434.5	38.3	1177	14	US-10-035-060-8	Sequence 8, Appli
37	1433.5	38.2	1177	14	US-10-102-469-24	Sequence 24, Appli
38	1422	37.9	1176	16	US-10-782-141-6	Sequence 6, Appli
39	1400	37.3	1176	11	US-09-837-961-2	Sequence 2, Appli
40	1400	37.3	1176	16	US-10-825-751-2	Sequence 2, Appli
41	1380.5	36.8	1167	15	US-10-428-961-40	Sequence 40, Appli
42	1360.5	36.3	1177	9	US-09-873-873-26	Sequence 26, Appli
43	1360.5	36.3	1177	10	US-09-916-956A-26	Sequence 26, Appli
44	1360.5	36.3	1177	10	US-09-997-314-26	Sequence 26, Appli
45	1360.5	36.3	1177	14	US-10-365-645-26	Sequence 26, Appli

## ALIGNMENTS

RESULT 1  
US-10-782-020-10  
; Sequence 10, Application US/10782020  
; Publication No. US20040197916A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargies, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and  
; FILE REFERENCE: Methods for Its Use  
; CURRENT APPLICATION NUMBER: US/10/782.020  
; PRIOR FILING DATE: 2004-02-19  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-020-10

Query Match 99.3%; Score 3722.5; DB 16; Length 719;  
Best Local Similarity 99.4%; Pred. No. 3.4e-303;  
Matches 715; Conservative 0; Mismatches 3; Indels. 1; Gaps 1;  
Qy 1 MLLKNQKHQSFSSNAKVDKISTSLKNETDIELQINHHEDCLKMEYENVEPFSASTI 60  
Db 1 MLLKNQKHQSFSSNAKVDKISTSLKNETDIELQINHHEDCLKMEYENVEPFSASTI 60  
Qy 61 QTGGIAGKILGTGVFPAGQVASIYSPILGELPKGNQWEIFMEHVEEIIINQKISTYA 120  
Db 61 QTGGIAGKILGTGVFPAGQVASIYSPILGELPKGNQWEIFMEHVEEIIINQKISTYA 120

QY	121	RNKALTDLKGDLALAVYHDSLESWGNRNTRARSVVKQYIALELMFVKQLPSPAVSG	180
DB	121	RNKALTDLKGDLALAVYHDSLESWGNRNTRARSVVKQYIALELMFVKQLPSPAVSG	180
QY	181	EEVPLPIYAQAANLHLLLRDASI FGKEWGLSSSEISTFYNROVERAGDYSVHCVKWYS	240
DB	181	EEVPLPIYAQAANLHLLLRDASI FGKEWGLSSSEISTFYNROVERAGDYSVHCVKWYS	240
QY	241	TGLNNLRGTNAESWRYNQFRDMTLMVLDLVALFPSTQMYPIKTTAQLTREVTYDAI	300
DB	241	TGLNNLRGTNAESWRYNQFRDMTLMVLDLVALFPSTQMYPIKTTAQLTREVTYDAI	300
QY	301	GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW	360
DB	301	GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW	360
QY	361	GGHKLPERFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVN-VPR	419
DB	361	GGHKLPERFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVN-VPR	420
QY	420	VDFHMKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS	479
DB	421	VDFHMKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS	480
QY	480	ASHVKALVSWTHRSADRTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN	539
DB	481	ASHVKALVSWTHRSADRTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN	540
QY	540	TGTFGDIRVINPPEAQRVRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK	599
DB	541	TGTFGDIRVINPPEAQRVRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK	600
QY	600	TFXTVGFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQSKV	659
DB	601	TFRTVGFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQSKV	660
QY	660	TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM	718
DB	661	TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM	719
RESULT 2			
US-10-782-141-8			
; Sequence 8, Application US/10782141			
; Publication No. US20040197917A1			
; GENERAL INFORMATION:			
; APPLICANT: Carozzi, Nadine			
; APPLICANT: Hargiss, Tracy			
; APPLICANT: Koziel, Michael G.			
; APPLICANT: Duck, Nicholas B.			
; APPLICANT: Carr, Brian			
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and			
; TITLE OF INVENTION: Methods for Its Use			
; FILE REFERENCE: 045600/274143			
; CURRENT APPLICATION NUMBER: US/10/782,141			
; CURRENT FILING DATE: 2004-02-20			
; PRIOR APPLICATION NUMBER: 60/448,632			
; PRIOR FILING DATE: 2003-02-20			
; NUMBER OF SEQ ID NOS: 23			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 8			
; LENGTH: 719			
; TYPE: PRT			
; ORGANISM: Bacillus thuringiensis			
US-10-782-141-8			
Query Match 99.3%; Score 3722.5; DB 16; Length 719;			
Best Local Similarity 99.4%; Pred. No. 3.4e-303;			
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;			
QY	1	MKLKNDKQHSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPFSASTI	60

NAME/KEY: misc\_feature  
LOCATION: (200)..(200)  
OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid  
US-10-428-961-42

Query Match 91.7%; Score 3439; DB 15; Length 710;  
Best Local Similarity 91.9%; Pred. No. 2.1e-279; Indels 10; Gaps 2;  
Matches 661; Conservative 15; Mismatches 33;

QY 1 MKLNQDQHQSSNAKVDKISTDLKNETDIELQNHEDCLKMSSEYENVEPFFVASTI 60  
DB 1 MKSKNQNHQSLSNNATVDKNTGSLNNTTQLQNFH-----EGIEPFFVSSTI 51  
QY 61 QTGIGIAGKIIGTGVPPAGVASYLSFILGELWPKGNQWEIEMHVEEIIINOKISTYA 120  
DB 52 QTGIGIAGKIIGTGVPPAGVASYLSFILGELWPKGNQWEIEMHVEEIIINOKISTYA 111  
QY 121 RNKALTDLKIGDGLAVVHDSLESVGNRNTRRSVVKSOYIALELMFVQKLSFAVSG 180  
DB 112 RNKALADLKGGLDALAVVHDSLESVGNRNTRRSVVKSOYITLELMFVQKLSFAVSG 171  
QY 181 BEVPLLPYIAQAANLHLLLDASIFGKXWGLSSEISTFFYNQVERAGDYSYHCVKWS 240  
DB 172 BEVPLLPYIAQAANLHLLLDASIFGKXWGLSSEISTFFYNQSGKSEYSDHCWKYN 231  
QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPPSYDTQMPYIKTTAQTREVTYDAI 300  
DB 232 TGLNLRGMNAESWVRYNQFRDMLVLDLVALPPSYDTQMPYIKTTAQTREVTYDAI 291  
QY 301 GTVHPHPSFTSTWYNNNAPSFAIAEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYNNMW 360  
DB 292 GTVHPHPSFTSTWYNNNAPSFTIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYNNMW 351  
QY 361 GGHKLEFRTIGTLNISTQSTNTSINPVTLPFTSRDVRTESLAGNLFITQPNV-VPR 419  
DB 352 GGHKLEFRTIGTLNISTQSTNTSINPVTLPFTSRDVRTESLAGNLFITQPNVGVR 411  
QY 420 VDFHFWKVTPIASDNFFYPYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 479  
DB 412 VDFHFWKVTPIASDNFFYPYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 471  
QY 480 ASHKALVYSWTHRSADRTNIENPSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539  
DB 472 ASHKALVYSWTHRSADRTNIENPSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRKN 531  
QY 540 TGTGDIRVNIPLPPPAQRYRIRYASTTDLQFHTSINGKAINQGNFATMNRGEDLDYK 599  
DB 532 TGTGDIRVNIPLPPPAQRYRIRYASTTDLQFHTSINGKAINQGNFATMNRGEDLDYK 591  
QY 600 TFXTVGFTTTPFSLLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDYDFAQAEKV 659  
DB 592 TFXTVGFTTTPFSDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDYDFAQAEKV 651  
QY 660 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDFYLDKEKRELFEIVKYAKQLHIERNM 718  
DB 652 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDFYLDKEKRELFEIVKYAKQLHIERNM 710

RESULT 4  
US-10-809-953-10  
Sequence 10, Application US/10809953  
Publication No. US20040181825A1  
GENERAL INFORMATION:  
APPLICANT: Van Mellaert, Herman  
APPLICANT: Boterman, Johan  
APPLICANT: Van Rie, Jeroen  
APPLICANT: Joos, Henk  
TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTICIDAL PROTEINS  
FILE REFERENCE: 021565-078  
CURRENT APPLICATION NUMBER: US/10/809,953  
CURRENT FILING DATE: 2004-03-26  
PRIOR APPLICATION NUMBER: US/09/661,016

PRIOR FILING DATE: 2000-09-13  
PRIOR APPLICATION NUMBER: PCT/EP90/00905  
PRIOR FILING DATE: 1990-05-30  
PRIOR APPLICATION NUMBER: GB 89401499.2  
PRIOR FILING DATE: 1989-05-31  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 1228  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis  
US-10-809-953-10

Query Match 60.0%; Score 2249; DB 16; Length 1228;  
Best Local Similarity 62.3%; Pred. No. 3.8e-179;  
Matches 446; Conservative 80; Mismatches 164; Indels 26; Gaps 7;  
QY 23 TDSLKNETDIELQNH-----EDCLKMSSEYENVEPFFVASTIOTGIGIAGKI 70  
DB 2 TSNKKNENEINAVNSNAQMDLLPDARIEDSLCIAEGNIDPPVFASTVQTGNIAGRI 61  
QY 71 LGTLGVPPAGVASYLSFILGELWPKGNQWEIEMHVEEIIINOKISTYARNKALTDLKG 130  
DB 62 LGVLGVPPAGVASYLSFILGELWPKGNQWEIEMHVEEIIINOKISTYARNKALTDLKG 121  
QY 131 LGDLAVYHDSLESVGNRNTRRSVVKSOYIALELMFVQKLSFAVSGBEVPLLPYIA 190  
DB 122 LGDSFRAYQQSLEDWLENRDDARTSVLHTQYIALELDLFLNAMPFLAIRNQEVPLLMVYA 181  
QY 191 QAANLHLLLDASIFGKXWGLSSEISTFFYNQVERAGDYSYHCVKWSYGLNLRGTN 250  
DB 182 QAANLHLLLDASIFGKXWGLSSEISTFFYNQVERAGDYSYHCVKWSYGLNLRGTN 241  
QY 251 AESWVRYNQFRDMLVLDLVALPPSYDTQMPYIKTTAQTREVTYDAITGVHPHPSFT 310  
DB 242 AESWVRYNQFRDMLVLDLVALPPSYDTQMPYIKTTAQTREVTYDAITGVHPHPSFT 299  
QY 311 STTWYNNNAPSFAIAEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYNNMWGKHLFRTI 370  
DB 300 STTWYNNNAPSFAIAEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYNNMWGKHLFRTI 359  
QY 371 GGTNLNISTQSTNTSINPVTLPFTSRDVRTESLAGNLFITQPNV-VPRVDPHFWK 427  
DB 360 GGTNLNISTQSTNTSINPVTLPFTSRDVRTESLAGNLFITQPNV-VPRVDPHFWK 416  
QY 428 THP-----IASDNFFYPYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLISASH 482  
DB 417 TNPNQISDRGTANYSQP-YESPGQLQDSETELPEPETERPNYESYSHRLSHIGLISASH 475  
QY 483 VKALVYSWTHRSADRTNIENPSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 542  
DB 476 VNPVYSWTHRSADRTNIENPSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 535  
QY 543 FGDTRVNIPLPPPAQRYRIRYASTTDLQFHTSINGKAINQGNFATMNRGEDLDYK 602  
DB 536 FGDTRVNIPLPPPAQRYRIRYASTTDLQFHTSINGKAINQGNFATMNRGEDLDYK 595  
QY 603 TVGFTTTPFSLLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDYDFAQAEKV 662  
DB 596 RRAFTTTPFSLLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDYDFAQAEKV 655  
QY 663 FTSTNPRGLKTDVVDYHIDQVSNLVESLSDFYLDKEKRELFEIVKYAKQLHIERNM 718  
DB 656 FTSTNPRGLKTDVVDYHIDQVSNLVESLSDFYLDKEKRELFEIVKYAKQLHIERNM 711

RESULT 5  
US-09-988-462-7  
Sequence 7, Application US/09988462  
Publication No. US20030046726A1  
GENERAL INFORMATION:  
APPLICANT: Kozziel, Michael G.  
Desai, Nalini M.

Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Launis, Karen L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Syngenta Biotechnology, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 09/988,462  
FILING DATE: 20-NO. US20030046726A1-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/547,422  
FILING DATE: 11-APR-2000  
APPLICATION NUMBER: US 08/459,504  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-188051  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7  
Query Match 59.6%; Score 2236; DB 10; Length 1207;  
Best Local Similarity 63.9%; Pred. No. 4.6e-178;  
Matches 439; Conservative 78; Mismatches 156; Indels 14; Gaps 6;  
QY 40 EDCLKMSEYENPEPVSASTIOTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGN 99  
DB 10 EDSLCTAEGNNDPVSASTVGTGINIAGRIILGVLPAGQLASFYSLVGLWPRGRD 69  
QY 100 QWEIFMEHVEEIIINOKISTYARKALTDLKGIDALAVTHDSLEWVGNNRTRRSVUK 159  
DB 70 QWEIFLHEVQLINQITENARTALRLQGLGDSFRAYQOSLDWLENRDDARTSVLY 129  
QY 160 SQVIALELWFVQKLPSFVSGSEVPLPIYQAQANLHLLLRDASTFGKEWGLSSSEIST 219  
DB 130 TQVIALELDFLNAFLPFAIRNOQVPLLMVYAQANLHLLLRDASTFGSEFGLTQOEIOR 189  
QY 220 FYNRQVERAGDYSYHCWKYSTGLNNLRGTNAESWRYNQFRDMLVLDLVALFPSSYD 279  
DB 190 YYERQVEREDYSYCVEMWNTGLNSLRGTNAESWRYNQFRDMLVLDLVALFPSSYD 249  
QY 280 TOMYPIKTTAQLTREYVYDAIGTVHPHPSFTSTTTWNNAPSFSALEAAVVRNPHLLDPL 339

Db 250 TRTYPINTSAQLTREYVYDAIGAT--GVNMAWNTNNNAPSFSALEAAAIKSPHLLDPL 307  
QY 340 EQVTIYSLLRWSNTOYNNMWGKHLEFRITIGTGLNISTQGSNTNTSINPVTLPFTSRDYY 399  
Db 308 EQUTIFSSASRWSNTRHMTYWRGHTIOSRPISGGLNTSTHGATNTSINPVTLPFRASRDYV 367  
QY 400 RTESLAGLNLF--LTQPVN-VPRVDPHMKFVTHP-----IASDNFYPGYAGIGTQLODS 451  
Db 368 RTESYAGVLLWGIYLEPIHGVPTRFNF---TNPQNISDRGTANYGQP-YESFGLQKDS 423  
QY 452 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTEPNSITQIPL 511  
Db 424 ETELPPETTERPNYESYSHRLSHIGLISOSRVNVPYVSWTHRSADRTNIGPNRIQIPM 493  
QY 512 VKAFNLSSGAAVVRGPGFTGGDILRRTNTGTGDIRVNNPPPAQRYRVRIRYASTTDQ 571  
Db 484 VKASELPQGTTVVRGPGFTGGDILRRTNTGGFGPIRVTVNGPLTQRYGRIGRYASTVDFD 543  
QY 572 FHTSINGKAINQGNFSATMNRGDLDYKFTXVTGVFTTPPSLLDVQSTFTIGAWNFSSGNE 631  
Db 544 FVVSRGTTVNNFRFLRTMNSGDELKYGNFVREAFTPFTTQIQDIIRTSIQGLSGNGE 603  
QY 632 VIIDRIEFVPEVTEYAEYDFEKAQKVTAFTSTNPRGLKTDVKDVIDQVSNLVESLS 691  
Db 604 VYIDKIBIIPVTATFEAEYDLERAQAVNALFTNPRRLKTDVTYHIDQVSNLVACLS 663  
QY 692 DEFYLDKRELFELVYKAKOLHIERNM 718  
Db 664 DEFCLDEKRELLKVKYAKELSDERNL 690

RESULT 6

US-10-428-961-63  
Sequence 63, Application US/10428961  
Publication No. US20030237111A1  
GENERAL INFORMATION:  
APPLICANT: Baum, James A.  
APPLICANT: Chu, Chih-Rei  
APPLICANT: Donovan, William P.  
APPLICANT: Gilmer, Amy J.  
APPLICANT: Rupar, Mark J.  
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
FILE REFERENCE: Polynucleotides, Compositions, and Methods of Use (Amended)  
CURRENT APPLICATION NUMBER: US/10/428,961  
CURRENT FILING DATE: 2003-05-02  
PRIOR APPLICATION NUMBER: 09/661,322  
PRIOR FILING DATE: 2000-09-13  
PRIOR APPLICATION NUMBER: 60/153,995  
PRIOR FILING DATE: 1999-09-15  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 63  
LENGTH: 1227  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis  
US-10-428-961-63

Query Match 57.5%; Score 2156; DB 15; Length 1227;  
Best Local Similarity 58.8%; Pred. No. 2.5e-171;  
Matches 420; Conservative 105; Mismatches 175; Indels 14; Gaps 4;  
QY 13 SSNAKVQKISTDSLKN-----ETDIELQINIHEDCLKMSEYENPEPVSASTIOTGIG 65  
DB 7 NENEIINALSIPAVSNHSAQNLSTDAI-----EDSLCIAEGNNDPVSASTVGTGIN 61  
QY 66 TAGKITGLGVPPAGQVASYLSFILGELWPKGNWEIFMEHVEEIIINOKISTYARKAL 125  
DB 62 IAGRIILGVLPAGQIASFISFLVGLWPRGRDPWEIFLHEVHLIRQQVTENTRDTAL 121  
QY 126 TDLKGLGDALAVTHDSLEWVGNNRTRRSVKSQYIALEIMFVQKLPSFVSGSEVPL 185



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; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-614-524-2

Query Match      55.6%; Score 2085.5; DB 15; Length 1228;
Best Local Similarity 59.0%; Pred. No. 2e-165;
Matches 421; Conservative 98; Mismatches 183; Indels 11; Gaps 8;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPVFSASTIQTGIGIAGKI 70
Db 7 NENEIINALSPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66
QY 71 LGTGVPPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKG 130
Db 67 LGVLGVPPAGQIASFYSLVGLWPRGRDOWEIFLEHVEQLINQOITENARNATALARLQ 126
QY 131 LGDALAVYHDSLESWGNRNTRARSVKSQYIALELMFVOKLPSFAVSGEEVPLPIYA 190
Db 127 LGDSFRAYQQSLEDWLENRDDARTSRVLYTQYIALELDPLNAMPFAIRNOEVPMLMVA 186
QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRGTN 250
Db 187 QAAHLHLLLRDASIFGSEFGLTSQEIQRYVERQVQTRDYSYCVWEYNTGLNSLRGTN 246
QY 251 AESWVRYNQFRDRLTMVLVDFVALFPSYDTOMYPIKTTAQLTREVVYDAIGTVHPHPSFT 310
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QY 311 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLSLRSWNTQYMMNGGHKLEPRTI 370
Db 305 SNWYNNNAPSFAIETAVIRSPHLLDFLEQLTIFSTSSRSATRHMTYWRGHTIQSRPI 364
QY 371 GGTNLISQTGSTNTSINPVLTPFTSRDYYRTESLAGLNF--LTQPVN-VRPVDVHMKFV 427
Db 365 GGLNTSTHGSTNTSINPVLSPFSDRVVYTESYAGVLLWGLIYLEPIHGVTVRFRNRP 424
QY 428 --THPIASDNFYPCYAGIGTQDSENELPPEATGQPNYESYSHRSLSHGLISASHVKA 485
Db 425 QNTFERGTANYSQP--YESPGLQKDSLETLPPEPPERPNYESYSHRSLSHGLISQSRVHV 483
QY 486 LVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGTGFD 545
Db 484 PVSWSHRSADRTNTISSDSITQIPLVKSFLNSGSTSVSGPGFTGGDIIRTNVNGSVLS 543
QY 546 IRVINPFPQAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSAWNRGEDIIDYKFTXTVG 605
Db 544 MGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGPSTMSANESLTSQSRFAE 603
QY 606 FTTPFSLDQVSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQKVTAFTS 665
Db 604 FVPGISAGSQ--TAGISISNNAGRTQTHFDKIEFIPITATPEAYDLERAQEAVALFTN 662
QY 666 TNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFELVYKAKOLHIERNM 718
Db 663 TNPRRLKTDVTDYHIDQVSNLVACLSDFECLDEKRELEKVKYAKRSDERNL 715

RESULT 10
US-10-614-524-2
; Sequence 2, Application US/10614524
; Publication No. US20040016020A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva
; APPLICANT: Vanneste, Strijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
; FILE REFERENCE: NEWTSUS2
; CURRENT APPLICATION NUMBER: US/10/614,524
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/739,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28
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Db 523 SDKITQIPAVKCDMLYLGSSVVOGPGFTGGDILKXNTNPSILGTFAVTNGSLSQRYRVI 582  
Qy 563 RYASTDLDQFHTSINGKAINQGNFATMNRGEBLDYKFTXVGTTPFSLDLDVQSTFTIG 622  
Db 583 RYASTTDFEF-TLYLGDITIEKNRNFKNWDNGASLTETFKFASFTDFQFRETQDKILLS 641  
Qy 623 ANWFSSGNEVYDRIEFVPEVVEYAEVDYFEKAQEKVTALTSTNPRGLKTDVQDHYHQ 682  
Db 642 MGDFFSGGEVYDRIEFVPEVVEYAEQDLEAAKAVNALFTNTKD-GLRPGVTDYEVNQ 700  
Qy 683 VSNLVESLSDYFYLDEKELFEIVKYAKOLHIERNM 718  
Db 701 AANLVECLSDLLYPNEKRLLFDAVREAKRLSGARNL 736  
  
RESULT 14  
US-10-032-717-2  
; Sequence 2, Application US/10032717  
; Publication No. US20020151709A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/032,717  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR FILING DATE: 2001-10-23  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1206  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-032-717-2  
  
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Best Local Similarity 44.2%; Pred. No. 2.5e-116;  
Matches 336; Conservative 129; Mismatches 230; Indels 65; Gaps 22;  
  
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Db 1 MSPNNQNEYEIIDATPST-SVSNDSNRYPPFANEPTNALQNDYKDYLKQNSAGNASEYPGS 59  
  
Qy 51 VEPFVSA-STTQTGIGIAGKILGTLPVPFAGQVASLYSFILGELWPKG-KNQWEIFMEHV 108  
Db 60 PEVLVSGQDAKAAIDIVGKLLSGLVFPVGPVIVSLYTLQILDILWPSEKQWEIFMEQV 119  
  
Qy 109 BEINQKISTYARNKALTDLKGLDALAVYHDSLESWGNRNTRARVSVKSYQIALELM 168  
Db 120 BELINQKIAEYARNKALSELEGLNNYQLYLTALFEWENPNNGSRALDRVNRFEILSL 179  
  
Qy 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTFYRQVERA 228  
Db 180 FTQMPSPRVNFEVFTVTYAMAANLHLLLRDASIFGEEWGWSTTTINNYYDQMKLT 239  
  
Qy 229 GDYSYHCVKYSTGLNNLRGTNAESWRYNFRDMTLMVLDLVALFPSYDTOMYPIKTT 288  
Db 240 AEYSDHCVKWYETGLAKLGISAKQWYDYNQFRREMTLAVLDVVALFNYDTRYPMETK 299  
  
Qy 289 AOLREVTYDAIGTVHPHPSFTSTWYNNNAPSFAIEAAVVRPHLLDFLEQVITYSL 348  
Db 300 AOLREVTYDPLGAVNV---SIGSWY-DKAPSFQVIESSVIRPHVFDYITGLTVYVTS 355  
  
Qy 349 SRWNTQYMMWGGHKLFRITGTLNISTOGSTNTSINPV-TLPFTSRDYVRYTESLAGL 407  
Db 356 RSISARVIRHWAGHQISYHRVSRGSLNQYMGYGTNQNLHSTSTFDFTNYDIKTLKSDAV 415

Qy 408 NLFLTQTP-----VNVPRVDFHWKVFVTHPIASDN---FYFYCYAGIGTQLOQDSENELPPE 458  
Db 416 LLDIVYFGYTYIFFGMEVEF---FMVQLNNTKRLKYNPVPVKDIIAISTRDSELELPPE 472  
Qy 459 ATGQPNYESYSHRLSHIGLISAS-HVKAL--VYSWTHESADRTNTIENSITQIPLVKAF 515  
Db 473 TSDQPNYESYSHRLCHITSIPATGNTGLVPVFSWTHRSADLNNNTIYSDKKTQIPAVKWC 532  
Qy 516 NLSSGAAVVRGPGFTGGDILR-RTNTGTFGDI---RVNINPFPFAQRYVRIRYASTTDLQ 571  
Db 533 DNLFPVPVVGPGHTGGDILQYNRSTGSGVTLFLARYGLALEKAGKYRVRURYATDADIV 592  
Qy 572 FHTSINGKAINQGNFATMNRGEBLDYKTF-----XTVGTTPPSLL-----DVQST 618  
Db 593 LH--VNDAAQI---QMPKTMNPGEDLTSTKTFVADAITTLNLATDSSLKALHNLGDPNST 647  
Qy 619 FTIGAWNFSSGNEVYDRIEFVPEVVEYAEVDYFEKAQEKVTALTSTNPRGLKTDVQDY 678  
Db 648 LS-----GIVYDRIEFVPEVVEYAEQDLEAAKAVNALFTNTKD-GLRPGVTDY 697  
Qy 679 HIDQVSNLVESLSDYFYLDEKELFEIVKYAKOLHIERNM 718  
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RESULT 15  
US-10-414-637-2  
; Sequence 2, Application US/10414637  
; Publication No. US20030177528A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1 Proteins With  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/414,637  
; PRIOR FILING DATE: 2003-04-15  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR FILING DATE: 2001-10-23  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1206  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-414-637-2  
  
Query Match 40.0%; Score 1500.5; DB 14; Length 1206;  
Best Local Similarity 44.2%; Pred. No. 2.5e-116;  
Matches 336; Conservative 129; Mismatches 230; Indels 65; Gaps 22;  
  
Qy 1 MKLKNQDKHQSFSSNAKVVDKISTDS---LKNETDIELQINHEDECLW-----SEYE-N 50  
Db 1 MSPNNQNEYEIIDATPST-SVSNDSNRYPPFANEPTNALQNDYKDYLKQNSAGNASEYPGS 59  
  
Qy 51 VEPFVSA-STTQTGIGIAGKILGTLPVPFAGQVASLYSFILGELWPKG-KNQWEIFMEHV 108  
Db 60 PEVLVSGQDAKAAIDIVGKLLSGLVFPVGPVIVSLYTLQILDILWPSEKQWEIFMEQV 119  
  
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Db 120 BELINQKIAEYARNKALSELEGLNNYQLYLTALFEWENPNNGSRALDRVNRFEILSL 179  
  
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Db 180 FTQMPSPRVNFEVFTVTYAMAANLHLLLRDASIFGEEWGWSTTTINNYYDQMKLT 239



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:32:21 ; Search time 16.5835 Seconds  
(without alignments)  
4171.616 Million cell updates/sec

Title: US-10-019-823B-55  
Perfect score: 3760  
Sequence: 1 MKLNQDKHQSFSSNAKVDK.....KRELFEIVKAKOLHIERNM 719  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3760	100.0	719	2 I39815	insecticidal prote
2	3751	99.8	719	2 S25383	paraasporal crystal
3	3743	99.5	719	2 I39814	insecticidal prote
4	3520	93.6	719	2 I40590	cryv465 protein -
5	2277.5	60.6	1228	2 S00873	paraasporal crystal
6	1900	50.5	380	2 B42459	hypothetical prote
7	1492	39.7	1157	1 S49247	paraasporal crystal
8	1482.5	39.4	1166	2 S32645	paraasporal crystal
9	1474	39.2	1155	2 A26513	paraasporal crystal
10	1471	39.1	1174	2 S32649	paraasporal crystal
11	1467	39.0	1155	2 JD0002	paraasporal crystal
12	1467	39.0	1156	2 A29125	paraasporal crystal
13	1454.5	38.7	934	2 A22798	paraasporal crystal
14	1453.5	38.7	1176	2 JT0241	paraasporal crystal
15	1450	38.6	1155	2 S02134	paraasporal crystal
16	1449.5	38.6	1181	2 A41052	paraasporal crystal
17	1447.5	38.5	1176	2 JC2219	paraasporal crystal
18	1446	38.5	1155	2 I39838	paraasporal crystal
19	1443.5	38.4	1176	2 A22617	paraasporal crystal
20	1443.5	38.4	1176	2 S02215	paraasporal crystal
21	1360	36.2	1174	2 A42459	paraasporal crystal
22	1353	36.0	1138	2 A48944	paraasporal crystal
23	1339.5	35.6	1156	2 A29838	paraasporal crystal
24	1331.5	35.4	823	2 S04181	paraasporal crystal
25	1322.5	35.2	1189	2 S00944	paraasporal crystal
26	1310	34.8	1154	2 S39536	paraasporal crystal
27	1272	33.8	1171	2 I40572	paraasporal crystal
28	1272	33.8	1171	2 A37829	paraasporal crystal
29	1263	33.6	1176	2 A48970	paraasporal crystal

30 1234 32.8 1160 2 S32647 paraasporal crystal  
31 1219.5 32.4 1165 2 S11446 paraasporal crystal  
32 1209.5 32.2 655 2 JC7140 protoxin - Bacilli  
33 1196 31.8 1172 2 S32689 paraasporal crystal  
34 1186 31.5 1160 2 I40589 paraasporal crystal  
35 1163.5 30.9 1178 1 USBSXH paraasporal crystal  
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37 1156 30.7 652 2 A27323 paraasporal crystal  
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39 1100.5 29.3 652 2 I39811 paraasporal crystal  
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43 828 22.0 1136 1 USBS81 paraasporal crystal  
44 694.5 18.5 934 2 B29838 paraasporal crystal  
45 667 17.7 1180 2 I39870 paraasporal crystal

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C:Species: Bacillus thuringiensis  
C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I39815  
R:Gleave, A.P.; Williams, R.; Hedges, R.J.  
Appl. Environ. Microbiol. 59, 1683-1687, 1993  
A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for t  
iensis subsp. kurstaki.  
A:Reference number: I39815; MUID:93298009; PMID:8517758  
A:Accession: I39815  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:Cross-references: UNIPROT:Q45752; GB:M98544; NID:G142767; PIDN:AAA22354.1; PID:G142768  
C:Genetics:  
A:Gene: cryV  
C:Superfamily: paraasporal crystal protein

Query Match	100.0%;	Score 3760;	DB 2;	Length 719;
Best Local Similarity	100.0%;	Fred. No. 2.9e-256;	Mismatches 0;	Indels 0;
Matches 719;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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QY	301	GTVHPHPSSTSTWYNNNAPSFAEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW	360	
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DB	361	GGHKLFEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRTSLAGNLFLTOPVNGVPR	420	

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421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNVESYSHRLSHIGLIS 480  
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Qy |||||  
541 TGTGDIIRVNPPPAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
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661 TALFTSTNPRGLTKDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
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661 TALFTSTNPRGLTKDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
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RESULT 2  
S25383  
parasporal crystal protein cryIIal - Bacillus thuringiensis  
N;Alternate names: delta-endotoxin; parasporal crystal protein cryV  
C;Species: Bacillus thuringiensis  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C;Accession: S25383  
R;Tailor, R.; Tippet, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.  
Mol. Microbiol. 6, 1211-1217, 1992  
A;Title: Identification and characterization of a novel Bacillus thuringiensis delta-end  
A;Reference number: S25383; MUID:92269582; PMID:1588820  
A;Accession: S25383  
A;Molecule type: DNA  
A;Residues: 1-719 <TAI>  
A;Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:G40289; PIDN:CAA44633.1; PID:G40290  
C;Genetics:  
A;Gene: cryV  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 99.8%; Score 3751; DB 2; Length 719;  
Best Local Similarity 99.9%; Pred. No. 1.3e-255;  
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MKLNQDKHQSFSNNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
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Db 61 QTGIGIAGKILGTLGVPPAGQVSLYSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120  
Qy 121 RNKALTDLKGIGDALAYVHDLSLSWGNRNNTARSVVKSQYIALELMFVKLPSPAVSG 180  
Db 121 RNKALTDLKGIGDALAYVHDLSLSWGNRNNTARSVVKSQYIALELMFVKLPSPAVSG 180  
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Db 181 BEVPLLPYIAQAANLHLLLRDASI FCKEWGLSSSEISTFYNQVERAGDYSYHCVKWYS 240  
Qy 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAL 300  
Db 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAL 300  
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Qy 361 GGHKLEPFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
Db 361 GGHKLEPFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420

421 VDEHMKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNVESYSHRLSHIGLIS 480  
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421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNVESYSHRLSHIGLIS 480  
Qy |||||  
481 ASHKVYVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
Db |||||  
481 ASHKVYVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
Qy |||||  
541 TGTGDIIRVNPPPAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
Db |||||  
541 TGTGDIIRVNPPPAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
Qy |||||  
601 TPTVGTFTPTPSFLDVQSTFTIGAWNFSSGNEVYDRIEFVPEVTVYEAEDFEKAQEKV 660  
Db |||||  
601 TPTVGTFTPTPSFLDVQSTFTIGAWNFSSGNEVYDRIEFVPEVTVYEAEDFEKAQEKV 660  
Qy |||||  
661 TALFTSTNPRGLTKDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
Db |||||  
661 TALFTSTNPRGLTKDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
Qy |||||

RESULT 3  
I39814  
insecticidal protein cryVI - Bacillus thuringiensis  
C;Species: Bacillus thuringiensis  
C;Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 26-Aug-1999  
C;Accession: I39814  
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A;Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis  
tomocidus.  
A;Reference number: I39814; MUID:95314293; PMID:7793960  
A;Accession: I39814  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-719 <RES>  
A;Cross-references: GB:L36338; NID:G540281; PIDN:AAC36999.1; PID:G540282  
C;Genetics:  
A;Gene: cryVI  
C;Superfamily: parasporal crystal protein

Query Match 99.5%; Score 3743; DB 2; Length 719;  
Best Local Similarity 99.6%; Pred. No. 4.6e-255;  
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKLNQDKHQSFSNNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
Db 1 MKLNQDKHQSFSNNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
Qy 61 QTGIGIAGKILGTLGVPPAGQVSLYSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120  
Db 61 QTGIGIAGKILGTLGVPPAGQVSLYSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120  
Qy 121 RNKALTDLKGIGDALAYVHDLSLSWGNRNNTARSVVKSQYIALELMFVKLPSPAVSG 180  
Db 121 RNKALTDLKGIGDALAYVHDLSLSWGNRNNTARSVVKSQYIALELMFVKLPSPAVSG 180  
Qy 181 BEVPLLPYIAQAANLHLLLRDASI FCKEWGLSSSEISTFYNQVERAGDYSYHCVKWYS 240  
Db 181 BEVPLLPYIAQAANLHLLLRDASI FCKEWGLSSSEISTFYNQVERAGDYSYHCVKWYS 240  
Qy 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAL 300  
Db 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAL 300  
Qy 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLSLSWSNTQYNNMW 360  
Db 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLSLSWSNTQYNNMW 360  
Qy 361 GGHKLEPFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
Db 361 GGHKLEPFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420

QY 421 VDFHWKFTVTHPTIASDNFFYPGAGIGTQLQDSNELPPPEATQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFTVTHPTIASDNFFYPGAGIGTQLQDSNELPPPEATQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVRGPFTGCDILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVRGPFTGCDILRRTN 540  
QY 541 TGTFGDIRVINPPPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600  
DB 541 TGTFGDIRVINPPPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600  
QY 601 TPRTVGFTTTPPSFLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVYIEAYEFKAQEKV 660  
DB 601 TPRTVGFTTTPPSFLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVYIEAYEFKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDHYDOVSNLVSDEFLDEKRELFEIVKYAKOLHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDHYDOVSNLVSDEFLDEKRELFEIVKYAKOLHIERNM 719

RESULT 4  
I40590  
CryV465 protein - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text change 09-Jul-2004  
C:Accession: I40590  
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis  
tomocidus.  
A:Reference number: I39814; MUID:95314293; PMID:7793960  
A:Accession: I40590  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:g467234; PIDN:AAA82114.1; PID:g467234  
C:Genetics:  
A:Gene: cryV465  
C:Superfamily: parasporal crystal protein

Query Match 93.6%; Score 3520; DB 2; Length 719;  
Best Local Similarity 92.9%; Pred. No. 2.2e-239;  
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDTELQNIHEDCLKMEYENVEPFSASTI 60  
DB 1 MKLKNPDKKQSLSSNAKVDKIATDSLKNETDTELKNNEDYLRSEHESIDPFSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVHEIINQKISTYA 120  
DB 61 QTGIGIAGKILGTGVPFAGQIASYLSFILGELWPKGQWEIFMEHVHEIINQKILTYA 120  
QY 121 RNKALTDLGLDALAYHDSLESWGNRNTRARSVVKSVQIALBLMFQKLPSPAVSG 180  
DB 121 RNKALSDLGLDALAYHDSLESWYENRNTRARSVWKNQYIALBLMFQKLPSPAVSG 180  
QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSCHCVKWS 240  
DB 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSCHCVKWS 240  
QY 241 TGLNNLRGTNABSWRYNQFRDMLTDLVALFSPSYDTQMPYIKTTAQLTREVVYTDI 300  
DB 241 TGLNNLRGTNABSWRYNQFRDMLTDLVALFSPSYDTQMPYIKTTAQLTREVVYTDI 300  
QY 301 GTVHPHPSSTTWNNAAPSIAEAAVVRNPHLLDFLEQVTIYSLLSRWNTQPMNWM 360  
DB 301 GTVHPNQAPASTTWNNAAPSIAEAAVVRNPHLLDFLEQVTIYSLLSRWNTQPMNWM 360  
QY 361 GGHKLEFRITGTLNISTOGSTNTSINPVTLPFTSRDVRVTSLAGLNLFLTPQVNGVR 420  
DB 361 GGHRLSSRPIGALNTSTOGSTNTSINPVTLPFTSRDVRVTSLAGLNLFLTPQVNGVR 420

QY 421 VDFHWKFTVTHPTIASDNFFYPGAGIGTQLQDSNELPPPEATQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFTVTHPTIASDNFFYPGAGIGTQLQDSNELPPPEATQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVRGPFTGCDILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVRGPFTGCDILRRTN 540  
QY 541 TGTFGDIRVINPPPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600  
DB 541 TGTFGDIRVINPPPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600  
QY 601 TPRTVGFTTTPPSFLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVYIEAYEFKAQEKV 660  
DB 601 TPRTVGFTTTPPSFLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVYIEAYEFKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDHYDOVSNLVSDEFLDEKRELFEIVKYAKOLHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDHYDOVSNLVSDEFLDEKRELFEIVKYAKOLHIERNM 719

RESULT 5  
S00873  
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis  
N:Alternate names: parasporal crystal protein cryA4  
C:Species: Bacillus thuringiensis subsp. thuringiensis  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text change 09-Jul-2004  
C:Accession: S00873  
R:Brizzard, B.L.; Whiteley, H.R.  
Nucleic Acids Res. 16, 2723-2724, 1988  
A:Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus  
A:Reference number: S00873; MUID:88203216; PMID:3362680  
A:Accession: S00873  
A:Molecule type: DNA  
A:Residues: 1-1228 <BRI>  
A:Cross-references: UNIPROT:P05517; EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PID:g58094;  
C:Genetics:  
A:Gene: cryA4  
A:Start codon: TTG  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 60.6%; Score 2277.5; DB 2; Length 1228;  
Best Local Similarity 62.7%; Pred. No. 1.2e-151;  
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

QY 23 TDSLKNETDTELQNTNH-----EDCLKMEYENVEPFSASTIQTGIGTAGKI 70  
DB 2 TSNRRKNEEINAVSNHSAQMDLLPDARIEDSLCAEGNNIDPFVSASTVQTGINIAGRI 61  
QY 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVHEIINQKISTYARNKALTDLKG 130  
DB 62 LGVLGVPPAGQALASYLSFILGELWPKGRDOWEIFLEHVQOLINQKITENARNTALARLOG 121  
QY 131 LGDALAVYHDSLESWGNRNTRARSVVKSVQIALBLMFQKLPSPAVSGEVPPLPIYA 190  
DB 122 LGDSFRAYQOQSLDLEWLENRDDARTARSLVYQVIALELDFLNAMPLFAIRNOEVPPLLMVYA 181  
QY 191 QAAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSCHCVKWSSTGLNNLRGTN 250  
DB 182 QAAANLHLLLRDASIFGSEFGLTSOEIQRYERQVTRTSDYCVQVWNTGLNSLRGTN 241  
QY 251 ABSWRYNQFRDMLTDLVALFSPSYDTQMPYIKTTAQLTREVVYTDIAGTGVHPHPSFT 310  
DB 242 AASWRYNQFRDMLTDLVALFSPSYDTQMPYIKTTAQLTREVVYTDIAGTGVHPHPSFT 299  
QY 311 STTWYNNNAAPSIAEAAVVRNPHLLDFLEQVTIYSLLSRWNTQPMNWMGHHLEFRIT 370  
DB 300 SMWYNNNAAPSIAEAAVVRNPHLLDFLEQVTIYSLLSRWNTQPMNWMGHHLEFRIT 359  
QY 371 GGTINISTOGSTNTSINPVTLPFTSRDVRVTSLAGLNLFLTPQVNGVRPVDHFKFV 428  
DB 360 GGGLNTSTHGATNTSINPVTLPFTSRDVRVTSLAGLNLFLTPQVNGVRPVDHFKFV 416

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429 THP-----IASDPPYGVAGITGLQDSENELPPEATGQPNVESHRLSHIGLISASH 483  
 417 TNPQNTSDRGATANSOP-YESPGLQKDSSETLPPTTERPNVESHRLSHIGLILQSR 475  
 484 VKALVSWTHRSADRTNTPNPSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTNTGT 543  
 476 VNPVSVWTHRSADRTNTPNPSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTNTGT 535  
 544 FGDVRNINPFPQARVVRIRYASTTDLQPHSTINGKAINQGNFSAATMRGDDLDYKTFR 603  
 536 FGPVRVWNGPLQTRVGRYASTTVDFFVSRGGTTPVNFPLRTMNSGDELKVGNEFV 595  
 604 TVGTTTFFSLDQSTFTIGAMNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQKVTA 663  
 596 RRAFTTFFTOIQDITRTISQISGNGEVYIDKIEIIPVTATFEAYDLERAQEAVAL 655  
 664 FTSTNPRGLKTDVXDYHIDQVSNLVESLDEFYDKKELFEIVKYAKOLHIERNM 719  
 656 FTNTNPRRLKTDVYHIDQVSNLVACLSDDEFCLDEKRELLEKVKYAKRLSDERNL 711

RESULT 6  
 B42459  
 Hypothetical protein 2 (cryIF 3' region) - Bacillus thuringiensis (strain aizawai) (frag  
 C:Species: Bacillus thuringiensis  
 C:Date: 10-Jul-1992 #sequence\_revision 10-Jul-1992 #text\_change 09-Jul-2004  
 R:Chambers, J.A.; Jelen, A.; Jelen, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.  
 A:Accession: B42459  
 J. Bacteriol. 173, 3966-3976, 1991  
 A:Title: Isolation and characterization of a novel insecticidal crystal protein gene fr  
 A:Reference number: A42459; MUID:91286178; PMID:2061280  
 A:Accession: B42459  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-380 <CHA>  
 A:Cross-references: UNIPROT:Q8KV61; UNIPROT:Q45740; GB:M63897  
 C:Superfamily: parasporal crystal protein

Query Match 50.5%; Score 1900; DB 2; Length 380;  
 Best Local Similarity 95.5%; Pred. No. 6.6e-126;  
 Matches 363; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSNAKVDKISTDSLNKNTDTELQNHEDCLKMEYENVEPVSASTI 60  
 DB 1 MKLNQDKHQSFSNAKVDKISTDSLNKNTDTELQNHEDCLKMEYENVEPVSASTI 60

QY 61 QTGIGTAGKILGTLGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGTAGKILGTLGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGGLDALAVYHDSWGNRNTTRARSVKQSVIALFELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLKGGLDALAVYHDSWGNRNTTRARSVKQSVIALFELMFVQKLPFAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240  
 DB 181 EEPVLLPIYAQAANLHLLLDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240

QY 241 TGLNLRGTNAESWVRNQPRDMLTMDLVALFPSYDTOMYPIKTTAQLTRVYTDAL 300  
 DB 241 TGLNLRGTNAESWVRNQPRDMLTMDLVALFPSYDTOMYPIKTTAQLTRVYTDAL 300

QY 301 GTVHPHPSFTTWNNAFSAIEAAVVRNPHLLDLEQVITYSLLRWSNTQYNNW 360  
 DB 301 GTVHPHPSFTTWNNAFSAIEAAVVRNPHLLDLEQVITYSLLRWSNTQYNNW 360

QY 361 GGHKLEPRTIGGLTINISQ 380  
 DB 361 GGHKLEPRTIGGLTINISQ 380

RESULT 7

549247  
 parasporal crystal protein cry9CaI [validated] - Bacillus thuringiensis  
 N:Alternate names: parasporal crystal protein cryIH  
 C:Species: Bacillus thuringiensis  
 C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
 C:Accession: A59350; S49247  
 R:Lambert, B.; Buyse, L.; Decock, C.; Janssens, S.; Piens, C.; Saey, B.; Seurinck, J.; Va  
 Appl. Environ. Microbiol. 62, 80-86, 1996  
 A:Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity again  
 A:Reference number: A59350; MUID:96141404; PMID:8572715  
 A:Accession: A59350  
 A:Molecule type: DNA  
 A:Residues: 1-1157 <LAM>  
 A:Cross-references: UNIPROT:Q45733; EMBL:Z37527; NID:9547554; PIDN:CAA85764.1; PID:954755  
 A:Experimental source: serovar toIworthi  
 C:Comment: This parasporal crystal protein, active against corn borer and other insects,  
 C:Superfamily: parasporal crystal protein  
 C:Keywords: delta-endotoxin

Query Match 39.7%; Score 1492; DB 1; Length 1157;  
 Best Local Similarity 43.3%; Pred. No. 1.9e-96;  
 Matches 322; Conservative 115; Mismatches 217; Indels 90; Gaps 15;

QY 26 LKNETDIELQNHEDCLKMEYENVEPVSAS-----TIQTGIGIAGKILGTLGVFP 78  
 DB 29 LASDPNALQNNYKDYLOMTDEDYDTSINPSISISGRDAVQATLTVGRLGALGVFP 88

QY 79 AGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKGLDALAV 137  
 DB 89 SQQIVSVFQFLTLNLPVNDTALWEAFMRQVEELVNOQITBFARNQALRLQGLGDSFNV 148

QY 138 YHDSLESWGNRNTTRARSVKQSVIALFELMFVQKLPFAVSGBEVPLPTIYAQAANLHL 197  
 DB 149 YQSLQNLADNRNLNLSVWRAQFIALDLDVNAIPLFVNGQQVPLLSVYAQAANLHL 208

QY 198 LLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTNAESWVR 257  
 DB 209 LLLKDALSGEGWGTGQELISYIDYDQLTAKYNTYNTGLDRLRGNTESWLRY 268

QY 258 NQPRDMLTMDLVALFPSYDTOMYPIKTTAQLTRVYTDALIGTVHPHPSFTTWN 317  
 DB 269 HQPRREMTLVLDVALFPYDVRVLTGNSPQLTREVYTDIFVNPFPANVGLCRWGN 328

QY 318 NAFSFAIEAAVVRNPHLLDLEQVITYSLLRWS--NTQYNNWGHKLE----- 366  
 DB 329 PYNTFSELENAFIRPHLPDLNLSLTSS--NRFVSSNFMVDSGHTLRRSYLNDASVQ 386

QY 367 -----FRITGGTINISQGSTNTSINPVLPTSDYRVTESLAGLNLFLQTPVNGVPR 420  
 DB 387 EDSYGLITTTTRATINPGVDGTRN--IESTAVDFRS-----ALIG-----IYGVR 429

QY 421 VDFHWKVFTHPIASDNFYPYAGIGT-----QLQDSENELPP-BATGQPNYESVS 470  
 DB 430 ASF-----VPGGLFNGTTPANGCRDLYDNDLPPDESG-----SST 469

QY 471 HRLSHIGLIS-----ASHVKALVSWTHRSADRTNTPNPSITQIPLVKAFNLSSG 521  
 DB 470 HRLSHVTFSPQTNQAGSIANAGSVPTVYWRTRDVLNNTITNTRITQLPLVKASAPVSG 529

QY 522 AAVRGPGFTGGDILRTNTGTGDIERNINPFPQARVVRIRYASTTDLQPHSTINGKA 581  
 DB 530 TTVLKGPGFTGGDILRTNTGTGDIERNINPFPQARVVRIRYASTTDLQPHSTINGKA 589

QY 582 INQGNFSAATMRGDDLDYKTFRTVGTFT-----PFSFLDVQSTFTTGANFSSGNEVYI 635  
 DB 590 LGDVLGSLTMRGQELITYESFTREFTTGPFPNPPFTTQAEILLTVNAGSVSTGGSYII 649

QY 636 DRIEFVPEVVEYEAEDFEKAQKVTAFTSTNPRGLKTDVYHIDQVSNLVESLSD 695  
 DB 650 DRIEIVPVNPARAEEDLEAAKAVASLFTTRD-GLQVNTDYQVDAQANLVCLSD 708

QY 696 YLDEKRELFELVKKAKOLHIERNM 719  
 DB 696 YLDEKRELFELVKKAKOLHIERNM 719



709 YGDKKMLLEAVRAAKLSRRLN 732

RESULT 8  
S32645  
Parasporal crystal protein cryI Gal - Bacillus thuringiensis  
C/Species: Bacillus thuringiensis  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C/Accession: S32645  
R/Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A/Reference number: S32645  
A/Accession: S32645  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1166 <LAM>  
A/Cross-references: UNIPROT.Q45746; EMBL.Z22510; NID:g295861; PID:n295861; PID:g295861  
C/Superfamily: parasporal crystal protein  
C/Keywords: delta-endotoxin

Query Match 39.4%; Score 1482.5; DB 2; Length 1166;  
Best Local Similarity 46.1%; Pred. No. 8.9e-96;  
Matches 325; Conservative 101; Mismatches 204; Indels 75; Gaps 17;

Qy 41 DCLKMSYE---NVBPFVSGASTQTGTIGAGIKLTGLGVFPFAGQVASLYSFILGELWPK 96  
Db :  
Qy 13 NCLNNPSEIFNARNNSFGLVQSVSGL--TRFLLEAAVPEAGFALGLFDIIWGAL--- 66  
Db :  
Qy 97 GKQWEIEMEHVEEIIINOKISTYARNKALTDLKGLDALAVYHDSLESWGYNNTFARS 156  
Db :  
Qy 67 GVQWSLPLRQIEQLRIQEITELERNRATAILTGLSSYNLYVEALREWENDPNNPASQE 126  
Db :  
Qy 157 VKSQYTALSLMFWQKLPSFAVSGEEVPLPIYAQAANHLHLIRLDASIFGEKWGLSSSE 216  
Db :  
Qy 127 RVRTRFLTDADIVTGPTLAIRNLVVNLSVTQAANLHLSLRDVAVERGWLTOAN 186  
Db :  
Qy 217 ISTFYNQVERAGDYSDHCVKVKGSTGLNNLRGNNAESWRYNQFRDRMTLMVLDLVALFP 276  
Db :  
Qy 187 IEDLYRTLTSNIQEQSDHCARWYNOGLEIGISR---RVLDLFQDRLTISVLDI VALFP 242  
Db :  
Qy 277 SYDQMYPKITTAQLTREVTDAI--GTVPHPHSFTTTWYNNAPSPSAIAEA VNRPH 334  
Db :  
Qy 243 NYDIRTYPIPTQSOLTREIVTSPVAGNI-----NFGLSIANVLGRAPH 285  
Db :  
Qy 335 LLDFLEOVITYLLSRWSNTQYMMNGCHKEPRTIG-GTLN-----ISTQGSTNTS 385  
Db :  
Qy 286 LMDIFDIRVIYTNVR--STPY---WAGHEVISRRTOGGQNEIRPPPLYGVANAEPVPT 340  
Db :  
Qy 386 INPVTLPTGRDVYRTES-----LAGNLFLTPQVNGVPRVDPMHKVFTHPIASDNFY 439  
Db :  
Qy 341 IRPTGTFDEQRWYRARSRVVSFRSSGDPSLDAVG-----FLT-IFS AVSIYR 389  
Db :  
Qy 440 PGYAGIGTQODSENELPPEATGPQNYVESYSHRLSHGLISAS-----HYKALVYSWTHR 494  
Db :  
Qy 390 NGP-GFNT---DTIDEPIEGTDP--ETGYSHRLCHVGFGLASSPFISQYARAPIFSWTHR 443  
Db :  
Qy 495 SADRTNTIEPNSITQIPLVKAFNLSSGA VVRGPGTGGDI LRRTNTGTFGDIRVNINPP 554  
Db :  
Qy 444 SATLTNTIADPVIIQIPLVKAFNLHSGATVKGPGFTGGDI LRRTNVGSTGDMRWKITAP 503  
Db :  
Qy 555 PAQRYRRIYASTTDLQFHITSINGKAINOGNFSA TNRGEDLDYKTRFTVGFTTFFSPL 614  
Db :  
Qy 504 LSQRVRIYASTTDLQFYTNINGTTINIGNFSS TWD SGDDLQYGRFRVAGFTTPTPTS 563  
Db :  
Qy 615 DVQSTFTIGAWNPFSSGNEVIDRIEFVVPVEVTEAEYDFEKAQEKVTALTSTSNPGLKT 674  
Db :  
Qy 564 DANSTFTIGA FGSFPNNNEVIDRIEFVPAEVTEAEYDFEKAQKAVNALFTSSNQIGLKT 623  
Db :  
Qy 675 DVKDHYHDVSNLVESI SD EYLDEKELFEIVKYAKOLHIERNM 719  
Db :  
Qy 624 DVTDYHDKVSNLVESLSD EFCFLDEKELSEKVKHAKRLSDERNL 668

RESULT 9.  
 A26513  
 C:Species: Bacillus thuringiensis (strain aizawai)  
 C:Date: 11-Mar-1988 #sequence\_revision 11-Mar-1988 #text\_change 09-Jul-2004  
 C:Accession: A26513  
 R:Oeda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H.  
 Gene 53, 113-119, 1987  
 A:Title: Nucleotide sequence of the insecticidal protein gene of *Bacillus thuringiensis*  
 A:Reference number: A26513; MUID:87248103; PMID:3297927  
 A:Accession: A26513  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1155 <END>  
 A:Cross-references: UNIPROT:P06578; GB:M16463; NID:g143098; PIDN:AAA22551.1; PID:g143099  
 C:Superfamily: parasporal crystal protein  
 C:Keywords: delta-endotoxin

Query Match		39.2%; Score 1474; DB 2; Length 1155;	
Best Local Similarity 44.4%; Pred. No. 3.5e-95;			
Matches	315; Conservative 113; Mismatches 227; Indels 54; Gaps 12;		
Qy	36 NINHEDCLKMEYENVE-PFVSASTIQG-----IGIAGKITGLGVPPAGOVASILYS 87		
Db	4 NPNINECIPYNCLGNPEVEVLGGERIETGTPIDISLSTQFLSSEF-VPGAGFVLGLVD 62		
Qy	88 FILGELMPKGNQWEIIMEHVEEIIINQISTYARNKALTDLGLGDALAYVHDSLESWVG 147		
Db	63 IIWGIF---GPSQWDAFLVQIEQLNQRLEEFARNQAISRLEGLSNLYQIYASFRWEA 119		
Qy	148 NRNTRARSVVQSYIALELMPVKQLPSPAVSGEEVPLPIYAAQANLHLILLRDAISFG 207		
Db	120 DPTNPALREEMRIQDNMSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVG 179		
Qy	208 KEWGLSSSEISFTFYNRQVERAGDYSDHCVKYWTSTGLNLRGNTAESWVRNQPRDMLM 267		
Db	180 QRWGFDAATINSRYNDLTRLTGNITDHAVRVNTGLERVWGPDSRDWIRYNQPRRELTLT 239		
Qy	268 VLDLVALPPSYDTOMYPTKTAQLTRVYTDATGTVHPHPSFTSTTWNNNAPSFAIEA 327		
Db	240 VLDIVSLFPNVDSTYPTRTVSQLTREIYNPV-----LENFDSGFRALAQ 285		
Qy	328 AV---VRNPHLLDFLEQVITYSLLSR----WSNTQYMMN---WGHKLEFRTTGGTLNIS 377		
Db	286 GIEGSIKSPHLMIDLNSITIVTDAHREYVWSGHQIMASPVGSPGPEFTFLYGTWGNAA 345		
Qy	378 TQGSTNTSINPVTLPTSRDYYRTESLAGLNFLTPQVNGVPRVDFHWKVFTHPIADSNF 437		
Db	346 PQQRIVAGLQGGVYRTLSTLTYRRFPNIGIN---NQQLSVLDGTEFAYG-----TSSNL 396		
Qy	438 YYPGVAGITGLQDSENELPPEATGPQNYESYSHRLSHIGLI-----SASHVKALVYS 490		
Db	397 PSAYIRKSGT--VUSLDEIPQNNVPPRQGFSHRLSHVSMFRSGNSVSVSIIRAPMPS 454		
Qy	491 WTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRRTTGTGFDIRVN 550		
Db	455 WIHRSABFNIIIPSSQIIQIPLTKSTNLGSGTSVVKPGFTGGDILRRRTSPGOISTLRVN 514		
Qy	551 INPFAQRYRIRYASTDIDQFHTSINKALINQGNFSATMRGCDLDYKTPRTVGTGTTT 610		
Db	515 ITAPLSQRYRIRYASTNTLQFHTSIDGRPINQGNFSATMSSGNSLQSGSPRTVGTGTTT 574		
Qy	611 FSPLDVQSTFTIGAWNPSGNGEVYIDRIEFVPEVTEYAEYDPEKAEKYALTFTSTNPR 670		
Db	575 FNFSGNSGVFTLSAHVFNNGNEVYIDRIEFVPAEVTFEAYDLERAKQAVNEFLTSSNQI 634		
Qy	671 GLKTDVQDHYHDQVSNLVESLSDSEFYLDREKLEFVYKVAQLHIERNM 719		
Db	635 GLKTDVTDYHDQVSNLVESLSDSEFCLEDEKELSEKVKHAKRLSDERNL 683		

RESULT 10  
 S32649

paraspore crystal protein cry1Fa3 - Bacillus thuringiensis  
 C:Species: Bacillus thuringiensis  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 C:Accession: S32649  
 R:Lambert, B.  
 submitted to the EMBL Data Library, April 1993  
 A:Reference number: S32645  
 A:Accession: S32649  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1174 <LAMB>  
 A:Cross-references: UNIPROT:Q45749; EMBL:Z22512; NID:G295865; PIDN:CAA80235.1; PID:G2958  
 C:Superfamily: paraspore crystal protein  
 C:Keywords: delta-endotoxin

Query Match 39.1%; Score 1471; DB 2; Length 1174;  
 Best Local Similarity 44.8%; Pred. No. 5.8e-95;  
 Matches 325; Conservative 103; Mismatches 202; Indels 96; Gaps 17;

36 NINHE---DCLKMEYENVEFPVSASTIQTGIA-GKILGTGVFPAGQVSLYSFIL 90  
 4 NIONQVFNCLSNPEVEILSEERSTGRPLDISLSTRFLLSEFPVGVGVAFLDLIW 63  
 91 GELWPKGNQWEIFMEHVEEINQKISTYARKKALTDLGLGDALAVYHDSLSWGGRN 150  
 64 GPITP---SEWFLFLLQIEQRIETLERNRAITLRLGLADSYEVYLAERWEENPN 120  
 151 NTRARSVVKSVQYIAELMFVQKLPFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEW 210  
 121 NAQLREDVIRPANTDDALITAINFTLTSFEIPLLSVYQAANLHLLLRDASVFGQW 180  
 211 GLSSSEISFTYRQVERAGDYSDHCWKYSTGLNLRGTNAESVRYNQFERDMLAVLD 270  
 181 GLDIATVNNHYNRLINLHRYTEHCLDYNQGLENLRTNTRQSRFNQFRRETLTVLD 240  
 271 LVALPSTQYQVPIKTAQLTRVYVTDAGTVVHPHPSFTSTWYNNAPS-FSAIRAAV 329  
 241 IVALFNYPARAVPIQTSQTLREIYTSV--IEDSP-----VSANIPGNFRAEFG- 290  
 330 VRNPHLLDFLEQVITYISLRSNNTQYMMWGGHKLFRFTGTLNISTQSTNTSNPV 389  
 291 VRPPLHLMDFN-----SLFVTAETVRSQTVWGGHLV-----FVRGGFGN 331  
 390 TLPF-----TSRDVYRTESLAGLNLFLTPQVNGVPRVDFHMKFVTHPIAS 434  
 332 NFPIYGFNPGGAIWADEDPFPIKT-----LSDPV-----FVRGGFGN 371  
 435 DNFFYPGYAGIGTQLQ-----DSENELPPATQPNVYESYSHLSHI----- 476  
 372 PH-YVLGLRGVAFQQTGNHTRFRNSGTIDSLDEIPQDNGAPMNDYSHVNLHVTFR 430  
 477 --GLISASHV-KALVSWTHRSADRTNTPNSITQPLVKAPNLSSGAAVVRGPGFTGG 533  
 431 WPGIAGSDWRAPMFSWTHRSADRTNINPNITQIPAKHNLHSGSVVRGPGFTGG 490  
 534 DILARTWTGFGDIRVNIINPPFAQRYRIRYASTTDLQPHTSINKALNQGNFSATMR 593  
 491 DLLARTWTGFGDIRVNIITPLSQRYRIRYASTTDLQPHTSINKALNQGNFSATMR 550  
 594 CEDLDYKTRVGTTPFPFLDVGSTTIGANFSSGNEVYIDRIEVPVEVYEAEDF 653  
 551 GGNLESGNFRTAGFSTPFSNAOSTTTLGQAFSN-QEVIIDRIEVPVEVYEAEDF 609  
 654 EKAQEKVATLFTSNPRGLKTDVYHIDQVSNLVSLSDFVLDKRELFETVYKAKQL 713  
 610 ERAQKAVNALFTSISQLGKTNVTGYHIDQVSNLVACLSDEFCLDKRELSKVYAKRL 669  
 714 HIERNM 719  
 670 SDRKRL 675

JD0002  
 paraspore crystal protein cry1Ab3 - Bacillus thuringiensis  
 N:Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal prot  
 C:Species: Bacillus thuringiensis  
 C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 09-Jul-2004  
 C:Accession: A90025; A91560; A90955; S14555; A26461; A24172; A29043; JD0002  
 R:Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.  
 Agric. Biol. Chem. 51, 455-463, 1987  
 A>Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from  
 A:Reference number: A90025  
 A:Accession: A90025  
 A:Molecule type: mRNA  
 A:Residues: 1-1155 <KON>  
 A:Cross-references: UNIPROT:P06578  
 A:Experimental source: subsp. kurstaki  
 R:Geisler, M.; Schweitzer, S.; Grimm, C.  
 Gene 48, 109-118, 1986  
 A>Title: The hypervariable region in the genes coding for entomopathogenic crystal protei  
 A:Reference number: A91560; MUID:87163505; PMID:3557124  
 A:Accession: A91560  
 A:Molecule type: DNA  
 A:Residues: 1-1155 <GBI>  
 A:Cross-references: GB:M15271; NID:G143123; PIDN:AAA22561.1; PID:G143124  
 A:Experimental source: subsp. kurstaki  
 R:Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.  
 DNA 5, 305-314, 1986  
 A>Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product anal  
 A:Reference number: A90955; MUID:86300092; PMID:3743328  
 A:Accession: A90955  
 A:Molecule type: DNA  
 A:Residues: 1-1155 <WAB>  
 A:Cross-references: GB:M13898; NID:G142719; PIDN:AAA22330.1; PID:G142720  
 A:Experimental source: subsp. berliner  
 R:Chak, K.F.; Jen, J.C.  
 submitted to the EMBL Data Library, October 1990  
 A:Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thur  
 A:Reference number: A26461; MUID:87054026; PMID:3023091  
 A:Accession: A26461  
 A:Molecule type: DNA  
 A:Residues: 1-730, 'L', 732-784, 'R', 786-1155 <HOP>  
 A:Cross-references: GB:X04698; NID:G40254; PIDN:CAA28405.1; PID:G40255  
 A:Experimental source: strain berliner 1715  
 C:Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.  
 C:Genetics:  
 A:Gene: cry-1-2; bt2  
 C:Superfamily: parasporal crystal protein  
 C:Keywords: delta-endotoxin  
 P:82-586/Product: toxic peptide #status predicted <TXP>  
 F:82-300/Region: toxic #status predicted  
 F:300-586/Region: insecticidal #status predicted

Query Match 39.0%; Score 1467; DB 2; Length 1155;  
 Best Local Similarity 44.5%; Pred. No. 1.1e-94;  
 Matches 316; Conservative 112; Mismatches 226; Indels 56; Gaps 13;

36 NINHEDCLEMEYENVE-PFVSASTIQTG-----TGIAGKILGTGVFPAGQVSLYS 87  
 4 NFINNECIPYCNLSNPEVEVLGGRIETGYTPIDISLSTQFLLEF-VPGAGFVLGLVD 62  
 88 FILGELWPKGNQWEIFMEHVEEINQKISTYARKKALTDLGLGDALAVYHDSLSWG 147  
 63 IIWGIF--GPSQDAFLVQIEQLINQRIEFAFNQALISRLGLSNLYQIYAESFREWEA 119  
 148 NNNTRARSVVKSVQYIAELMFVQKLPFAVSGEEVPLPIYAQAANLHLLLRDASIFG 207

Db 120 DPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFVG 179  
QY 208 KEWGLSSSEISTFYNRQVERAGDYSCHCKVWYSTGLNNLRGTNAESWVRYNQPRRDWTLM 267  
Db 180 QRWGPDAAATNSRYNDLTRIGNYTHDAVRWYNTGLERVWGPDSRDWRINQPRRELTIT 239  
QY 268 VLDLVALFSDYDTOMYPIKTTAQLTREVYTDAGTVHPPHSFTSTTWYNNAPSF-----S 323  
Db 240 VLDIVSLFFNYDSRTYPIRTVSQLTREIYTNV-----LENFDGSPRGSQAQ 285  
QY 324 AIEAAVVRNPHLLDFEQVTIYSLLSR-----WSNTQYMMN---WGCHKLEFRITGTLNI 376  
Db 286 GIEGS-IRSPHLMIDLINSITIYTHAHRGEYYSGHQIMASPVGFSGPETFFPLYGTMGNA 344  
QY 377 STQGSNTSINPVTLPFTSRDVRYSLAGLNLFLTPQVNGVRVDFHMKFVTHPIASDN 436  
Db 345 APQORIVAQLGGQVYRTLSLTYRPPFNIGIN---NQQLSVLDGTEFAYG-----TSSN 395  
QY 437 FYYPGAGTQLODSENELPPEATQPNYESYSHRLSHIGLI-----SASHVKALVY 489  
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQGFHSRLSHVSPRSGFSNSSVSIIRAPMF 453  
QY 490 SWTHRSADRTNTEPNISITQIPLVAFNLSGAAVVRGPGFTGGDILRRTNTGTFGDIRV 549  
Db 454 SWTHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSPQISTLRV 513  
QY 550 NINPPPAQRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGSDLDYKTFRTVGF 609  
Db 514 NITAPLSQRVRIRYASTTNLQFHTSIDGRPINQGNFSAATMSSGNLQSGSPRTVGF 573  
QY 610 PFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQKVLTALFTSTNP 669  
Db 574 PNFNSGSSVFTLSAHVFNSEVYIDRIEFVPAEVTPEAEYDLERAQKAVNELFTSSNQ 633  
QY 670 RGLKTDVKDHYHIDQVSNLSESLDFYLDKRELFELVYKAKOLHIERNM 719  
Db 634 IGLKTDVTDYHIDQVSNLVECLSDFECLDEKSELSEKVKHAKRLSDERNL 683

RESULT 12  
A29125  
parasporal crystal protein Bt2 - *Bacillus thuringiensis* subsp. *kurstaki* (strain HD-1)  
C:Species: *Bacillus thuringiensis* subsp. *kurstaki*  
C>Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 09-Jul-2004  
C:Accession: A29125  
R:Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niedermeyer, J.; et al.  
Bio/Technology 5, 807-813, 1987  
A:Title: Insect tolerant transgenic tomato plants.  
A:Reference number: A29125  
A:Accession: A29125  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-1156 <FIS>  
A:Cross-references: UNIPROT:Q9F296; UNIPROT:Q93T21  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 39.0%; Score 1467; DB 2; Length 1156;  
Best Local Similarity 44.5%; Pred. No. 1.1e-94;  
Matches 316; Conservative 112; Mismatches 226; Indels 56; Gaps 13;

QY 36 NINHEDECLKMSYENVE-PFVSASTITQTG-----IGIAGKILGTLGVFPAGQVASLYS 87  
Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLSSEF-VPGAGFVLGLVD 62  
QY 88 FILGELWPKGKNQWEIFMEHVEEINOKISTYARNKALTDKLGCDALAVYHDSLSWVG 147  
Db 63 IINGIF---GPSQWDAFLVQIEQLINQRIEEFARNQAISRLGSLNLYQIYAESFREWEA 119  
QY 148 NRNTRARSVVKSOYTALELMFVKQLPSFAVSGEEVPLPIYQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFVG 179

QY 208 KEWGLSSSEISTFYNRQVERAGDYSCHCKVWYSTGLNNLRGTNAESWVRYNQPRRDWTLM 267  
Db 180 QRWGPDAAATNSRYNDLTRIGNYTHDAVRWYNTGLERVWGPDSRDWRINQPRRELTIT 239  
QY 268 VLDLVALFSDYDTOMYPIKTTAQLTREVYTDAGTVHPPHSFTSTTWYNNAPSF-----S 323  
Db 240 VLDIVSLFFNYDSRTYPIRTVSQLTREIYTNV-----LENFDGSPRGSQAQ 285  
QY 324 AIEAAVVRNPHLLDFEQVTIYSLLSR-----WSNTQYMMN---WGCHKLEFRITGTLNI 376  
Db 286 GIEGS-IRSPHLMIDLINSITIYTHAHRGEYYSGHQIMASPVGFSGPETFFPLYGTMGNA 344  
QY 377 STQGSNTSINPVTLPFTSRDVRYSLAGLNLFLTPQVNGVRVDFHMKFVTHPIASDN 436  
Db 345 APQORIVAQLGGQVYRTLSLTYRPPFNIGIN---NQQLSVLDGTEFAYG-----TSSN 395  
QY 437 FYYPGAGTQLODSENELPPEATQPNYESYSHRLSHIGLI-----SASHVKALVY 489  
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQGFHSRLSHVSPRSGFSNSSVSIIRAPMF 453  
QY 490 SWTHRSADRTNTEPNISITQIPLVAFNLSGAAVVRGPGFTGGDILRRTNTGTFGDIRV 549  
Db 454 SWTHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSPQISTLRV 513  
QY 550 NINPPPAQRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGSDLDYKTFRTVGF 609  
Db 514 NITAPLSQRVRIRYASTTNLQFHTSIDGRPINQGNFSAATMSSGNLQSGSPRTVGF 573  
QY 610 PFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQKVLTALFTSTNP 669  
Db 574 PNFNSGSSVFTLSAHVFNSEVYIDRIEFVPAEVTPEAEYDLERAQKAVNELFTSSNQ 633  
QY 670 RGLKTDVKDHYHIDQVSNLSESLDFYLDKRELFELVYKAKOLHIERNM 719  
Db 634 IGLKTDVTDYHIDQVSNLVECLSDFECLDEKSELSEKVKHAKRLSDERNL 683

RESULT 13  
A22798  
parasporal crystal protein - *Bacillus thuringiensis*  
C:Species: *Bacillus thuringiensis*  
C>Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 09-Jul-2004  
C:Accession: A22798  
R:Shibano, Y.; Yamagata, A.; Nakamura, N.; Iizuka, T.; Sugieaki, H.; Takanami, M.  
Gene 34, 243-251, 1985  
A:Title: Nucleotide sequence coding for the insecticidal fragment of the *Bacillus thuringiensis* delta-endotoxin.  
A:Reference number: A22798; MUID:85232070; PMID:2989108  
A:Accession: A22798  
A:Molecule type: DNA  
A:Residues: 1-934 <SHI>  
A:Cross-references: UNIPROT:Q9S5V8; GB:M10917; NID:G143100; PIDN:AAA22552.1; PID:G551713  
C:Comment: The authors translated the codon ACA for residue 264 as Ser.  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 38.7%; Score 1454.5; DB 2; Length 934;  
Best Local Similarity 43.5%; Pred. No. 5.8e-94;  
Matches 310; Conservative 119; Mismatches 222; Indels 61; Gaps 12;

QY 36 NINHEDECLKMSYENVE-PFVSASTITQTG-----IGIAGKILGTLGVFPAGQVASLYS 87  
Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLSSEF-VPGAGFVLGLVD 62  
QY 88 FILGELWPKGKNQWEIFMEHVEEINOKISTYARNKALTDKLGCDALAVYHDSLSWVG 147  
Db 63 IINGIF---GPSQWDAFLVQIEQLINQRIEEFARNQAISRLGSLNLYQIYAESFREWEA 119  
QY 148 NRNTRARSVVKSOYTALELMFVKQLPSFAVSGEEVPLPIYQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFVG 179  
QY 208 KEWGLSSSEISTFYNRQVERAGDYSCHCKVWYSTGLNNLRGTNAESWVRYNQPRRDWTLM 267

Db	180	QRMGDAATINSRYNDLTRIGNYTDYAVRWYNTGLERVWGPDSRDWVRNQFRRELTLT	239
Qy	268	VLDLVALFPSTQMYPIKTAQITREVYTDALGTVHPHPSFTSTTWYNNNAPSFAIEA	327
Db	240	VLDLVALFSNYSRRYPIRTVSQUTREIYNPV-----LENFDCSFRGMAQ	285
Qy	328	AV---VRNPHLLDFLEQVITYSLLSRMSNTQYMMWGGHKLFRITGGT---LNISTQGS	381
Db	286	RIEQNIQPHLMDLNLNITITVDVHRG-----FNWWSHQITASPVGSGPEAFPLFGN	340
Qy	382	TNTSINPVTLPTFRDVRRESL-----AGNLFLTPQVNGVPRVDFHKKFVTHPI	432
Db	341	AGNAAPPVLSLTGLIGFIRTLSSPLRYRIILGSGPN---NOELFVLDTGTEFSFASLTNL	397
Qy	433	ASDNFYPGYAGICTQLQDSENELPPEATGPNYESYSHRLSHIGLISAS-----HVKAL	487
Db	398	PSTIYRQGTV-----DSLDTVPQDNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP	450
Qy	488	VYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRITNGTGGDI	547
Db	451	TFSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVGPGFTGGDILRRITSPQISTL	510
Qy	548	RVINPPPAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDTYKTRTVGF	607
Db	511	RVNITAPUSQRYVRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRITVGF	570
Qy	608	TPPFSFLDVQSTFTTIGAMNFFSGNEVYIDRIEFVPEVVEYAEVDFEKAQKVTAFTST	667
Db	571	TPPFSNGSSVFTLSAHVFNSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSS	630
Qy	668	NPRGLKTDVKDHYHIDQVSNLVESLDEFLDEKRELFEIVKAKOLHIERNM	719
Db	631	NOIGLKTDTVTDYHIDQVSNLVESLDEFLDEKRELFEIVKAKOLHIERNM	682
RESULT 14			
JT0241			
parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)			
N/Alternate names: 135K insecticidal protein			
C/Species: Bacillus thuringiensis			
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004			
C/Accession: JT0241			
R/Shimizu, M.; Ohie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.			
Agric. Biol. Chem. 52, 1565-1573, 1988			
A/Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein			
A/Reference number: JT0241			
A/Accession: JT0241			
A/Molecule type: DNA			
A/Residues: 1-1176 <SH1>			
A/Cross-references: UNIPROT:P02965			
A/Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal protein			
C/Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae			
C/Superfamily: parasporal crystal protein			
C/Keywords: delta-endotoxin			
Query Match 38.7%; Score 1453.5; DB 2; Length 1176;			
Best Local Similarity 43.5%; Pred. No. 9.9e-94;			
Matches 310; Conservative 118; Mismatches 223; Indels 61; Gaps 12;			
Qy	36	NINHEDECLMSEYENVE-PFVSASTIQGT-----IGIAGKILGTGLVPPAGQVASYLS	87
Db	4	NPINEICIPNCLSNPEVEVLGGERIETGYPTIDISLSTQFLLSEF-VPGAGFVLGLVD	62
Qy	88	FILGELWPKGNOWELFMEHVEEINOKISTVARNKALTDLKGLDALAVYHDSLSWSVG	147
Db	63	IILGIF---GPSQMDALFVQIEQLINRIEERAPNAQISLEGLSNLYQIYAESPREWEA	119
Qy	148	NRNTRARVVVKSQYIALELMFVKQLPSFAVSGEEVPLPIPIYAQANLHLLLRDASIFG	207
Db	120	DPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLDRSVFG	179
Qy	208	KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNLRGNTAESWVRYNRPDRDWTLM	267

Db	180	QRMGDAATINSRYNDLTRIGNYTDYAVRWYNTGLERVWGPDSRDWVRNQFRRELTLT	239
Qy	268	VLDLVALFPSTQMYPIKTAQITREVYTDALGTVHPHPSFTSTTWYNNNAPSFAIEA	327
Db	240	VLDLVALFSNYSRRYPIRTVSQUTREIYNPV-----LENFDCSFRGMAQ	285
Qy	328	AV---VRNPHLLDFLEQVITYSLLSRMSNTQYMMWGGHKLFRITGGT---LNISTQGS	381
Db	286	RIEQNIQPHLMDLNLNITITVDVHRG-----FNWWSHQITASPVGSGPEAFPLFGN	340
Qy	382	TNTSINPVTLPTFRDVRRESL-----AGNLFLTPQVNGVPRVDFHKKFVTHPI	432
Db	341	AGNAAPPVLSLTGLIGFIRTLSSPLRYRIILGSGPN---NOELFVLDTGTEFSFASLTNL	397
Qy	433	ASDNFYPGYAGICTQLQDSENELPPEATGPNYESYSHRLSHIGLISAS-----HVKAL	487
Db	398	PSTIYRQGTV-----DSLDTVPQDNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP	450
Qy	488	VYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRITNGTGGDI	547
Db	451	TFSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVGPGFTGGDILRRITSPQISTL	510
Qy	548	RVINPPPAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDTYKTRTVGF	607
Db	511	RVNITAPUSQRYVRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRITVGF	570
Qy	608	TPPFSFLDVQSTFTTIGAMNFFSGNEVYIDRIEFVPEVVEYAEVDFEKAQKVTAFTST	667
Db	571	TPPFSNGSSVFTLSAHVFNSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSS	630
Qy	668	NPRGLKTDVKDHYHIDQVSNLVESLDEFLDEKRELFEIVKAKOLHIERNM	719
Db	631	NOIGLKTDTVTDYHIDQVSNLVESLDEFLDEKRELFEIVKAKOLHIERNM	682
RESULT 15			
S02134			
parasporal crystal protein cryIC1 - Bacillus thuringiensis (strain aizawai IC1)			
N/Alternate names: delta-endotoxin IC1; entomocidal crystal protein			
C/Species: Bacillus thuringiensis			
A/Variety: strain aizawai IC1			
C/Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004			
C/Accession: S02134; S04994			
R/Haider, M.Z.; Ellar, D.J.			
Nucleic Acids Res. 16, 10927, 1988			
A/Title: Nucleotide sequence of a Bacillus thuringiensis aizawai IC1 entomocidal crystal			
A/Reference number: S02134; MUID:89083518; PMID:3205732			
A/Accession: S02134			
A/Status: translation not shown			
A/Molecule type: DNA			
A/Residues: 1-1155 <HA1>			
A/Cross-references: UNIPROT:P06578; EMBL:X13233; NID:g40277; PIDN:CAA31620.1; PID:g40278			
A/Experimental source: strain aizawai IC1			
R/Haider, M.Z.; Ellar, D.J.			
J. Mol. Biol. 208, 183-194, 1989			
A/Title: Functional mapping of an entomocidal delta-endotoxin. Single amino acid changes			
A/Reference number: S04994; MUID:89362455; PMID:2769751			
A/Accession: S04994			
A/Molecule type: DNA			
A/Residues: 429-449, 'A', 451-724 <HAW>			
A/Cross-references: EMBL:X16315			
A/Experimental source: strain aizawai IC1			
C/Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.			
C/Superfamily: parasporal crystal protein			
C/Keywords: delta-endotoxin			
Query Match 38.6%; Score 1450; DB 2; Length 1155;			
Best Local Similarity 44.1%; Pred. No. 1.7e-93;			
Matches 313; Conservative 112; Mismatches 229; Indels 56; Gaps 13;			
Qy	36	NINHEDECLMSEYENVE-PFVSASTIQGT-----IGIAGKILGTGLVPPAGQVASYLS	87

Db 4 NPNINECIPYNCLSNPEVEVLGGRIETGYTPIDISLSLTQFLLSBP-VPGAGFVLGLVD 62

Qy 88 FILGELWPKGNQWEIFMEHVEBIIINQKISTYARNKALTDLKGGLDALAVYHDSLESWVG 147

Db 63 IIWGIPI---GPSQWDAFLVQIEQLINQRIEFPARNQAISRLGLESLNYQIYAESPWEA 119

Qy 148 NRNNTARSVVVKSOYTALELMFVKLPSFAVSSEVEPLPIYAQAANLHLLLRDASIFG 207

Db 120 DPTNPALREEMRIQFNDMSALTTPALFPAVQNYQVPLLSVYVQAANLHLSVLRDVSVEG 179

Qy 208 KEWGLSSSEISTEYRQVERAGYSCHVKWYSTGLNNLRGTNAESWRYNQFRDWTLM 267

Db 180 QRWGPDAAATINSYNDLIRLIGNYTHAVRWYTGLERWGPDSDRWIRYINQFRRELTLT 239

Qy 268 VLDLVALFSDYDQMPYIKTTAQLTREVYDAIGTVHPPSPFTSTTYNNNAESP----S 323

Db 240 VLDIVSLFPNYSRTYPIRTVSQLTREIYNPV-----LENFDCGSPRGSQAQ 285

Qy 324 AIEAAVVRNPHLLDFLEQVTIYISLSR-----WNTQYMMN---WGGHKLEFRITIGTLNI 376

Db 286 GIEGS-IRSPHLMIDILNSITITDAHRGEYYSGHQIMASPVGSGPEFTFPLYGTMGNA 344

Qy 377 STQGSTNTSINPVTLPTSRDVTRESLACNLFLTPQVNGVPRVDFHMKFVTHPIASDN 436

Db 345 APOQRIVAQCGGVYRTLSTLRRFPNIGIN---NQQLSVLDGTEFAYG-----TSSN 395

Qy 437 FYYPGYAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLI-----SASHVKALVY 489

Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRPPMF 453

Qy 490 SWTHRSADRNTIEPNSITQIPLVKAPNLSSGAAVRGPFGTCGDILRRNTGTGDIRV 549

Db 454 SWTHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVVKGPFGTCGDILRRTPSQI1STLRV 513

Qy 550 NINPPPAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAFMNRGDLDYKTFRTVGFTT 609

Db 514 NITAPLSQRYVRIRYASTTNLQHTSIDGRIINQGNFSAFMNRGDLDYKTFRTVGFTT 573

Qy 610 PFSFLDVQSTFTTIGAWNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKVTAFTSTNP 669

Db 574 PFNFSNGSVFTLSAHVFNNGNEVYIDRIEFVPEVTEAEYDFEKAQEKVTAFTSTNP 633

Qy 670 RGLKTDVKYHIDQVSNLVSLSDEFLDEKRELFEIVYAKOLHIERNM 719

Db 634 IGLKTDVTDYHIDQVSNLVSLSDEFLDEKRELFEIVYAKOLHIERNM 683

Search completed: February 14, 2005, 21:00:47  
Job time : 18.5835 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:11:42 ; Search time 81.1112 Seconds  
(without alignments)  
4539.261 Million cell updates/sec

Title: US-10-019-823B-55  
Perfect score: 3760  
Sequence: 1 MKLKNQKHQSFSNAKVDK.....KRELFEIVKAKQLHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3760	100.0	719	1 C1IA BACTK	Q45752 bacillus th
2	3760	100.0	719	2 Q6X181	Q6x181 bacillus th
3	3755	99.9	719	2 Q93NJ5	Q93nj5 bacillus th
4	3754	99.8	719	2 Q85796	Q85796 bacillus th
5	3625	96.4	719	2 Q8KY61	Q8ky61 bacillus th
6	3531	94.4	719	2 Q9F0P8	Q9f0p8 bacillus th
7	3520	93.6	719	1 C1IB BACTE	Q45709 bacillus th
8	3377	89.8	719	1 C1IC BACTU	Q9xd11 bacillus th
9	3377	89.8	719	1 C1IB BACTU	Q87404 bacillus th
10	2446.5	65.1	1329	1 C1BB BACTU	Q45739 bacillus th
11	2446.5	65.1	1323	1 C1BC BACTM	Q45774 bacillus th
12	2278.5	60.6	1228	2 Q93T75	Q93t75 bacillus th
13	2277.5	60.6	1228	1 C1BA BACTK	P05517 bacillus th
14	2269.5	60.4	1228	2 Q93NM5	Q93nm5 bacillus th
15	2195.5	58.4	849	2 Q6PYW8	Q6pyw8 bacillus th
16	2195.5	58.4	1327	1 C1BE BACTU	Q85805 bacillus th
17	2112.5	56.2	1231	2 Q8KNV2	Q8kny2 bacillus th
18	2107.5	56.1	1231	1 C1BD BACTZ	Q9zaz5 bacillus th
19	1988.5	52.9	1215	1 C1KA BACTM	Q45715 bacillus th
20	1904	50.6	381	2 Q45740	Q45740 bacillus th
21	1670.5	44.4	1157	1 C8AA BACUK	Q45704 bacillus th
22	1658	44.1	1144	2 Q8KZL7	Q8kz17 bacillus th
23	1492	39.7	1157	1 C9CA BACTO	Q45733 bacillus th
24	1486.5	39.5	1169	1 C8BA BACUK	Q45705 bacillus th
25	1482.5	39.4	1166	1 C1GA BACTU	Q45746 bacillus th
26	1478	39.3	1167	1 C1VA BACTU	Q45738 bacillus th
27	1477	39.3	1169	1 C1FB BACTM	Q66377 bacillus th
28	1471	39.1	1174	2 Q45749	Q45749 bacillus th
29	1467	39.0	1155	1 C1AB BACTK	P06578 bacillus th
30	1467	39.0	1155	2 Q7BE98	Q7be98 bacillus th
31	1467	39.0	1155	2 Q9F296	Q9f296 bacillus th

32	1465	39.0	1118	2 Q9AM83	Q9am83 bacillus th
33	1462	38.9	1156	2 Q6GUA7	Q6gua7 bacillus th
34	1457	38.8	1177	2 Q6EIX3	Q6eix3 bacillus th
35	1455	38.7	1155	2 Q9T21	Q9t21 bacillus th
36	1454.5	38.7	793	2 Q6PYW7	Q6pyw7 bacillus th
37	1454.5	38.7	1180	2 Q9S5V8	Q9s5v8 bacillus th
38	1453.5	38.7	1176	2 Q7WZT9	Q7wzt9 bacillus th
39	1449.5	38.6	1181	1 C1AE BACTL	Q03748 bacillus th
40	1447.5	38.5	1176	2 Q45736	Q45736 bacillus th
41	1443.5	38.4	1176	1 C1AA BACTK	P02965 bacillus th
42	1443.5	38.4	1176	2 Q9RC30	Q9rc30 bacillus th
43	1437.5	38.2	1169	2 Q8GHE8	Q8ghe8 bacillus th
44	1430.5	38.0	1169	1 C1GB BACTZ	Q9zaz6 bacillus th
45	1420.5	37.8	1179	1 C1AD BACTA	Q03744 bacillus th

ALIGNMENTS

RESULT 1:  
C1IA BACTK  
ID C1IA BACTK STANDARD; PRT; 719 AA.  
AC Q45752: P71092; Q45750; Q45751; Q45756;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DE Pesticidial crystal protein cryIIa (Insecticidal delta-endotoxin)  
DE CryII(a) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
GN Name=cryIIa; Synonyms=CGCryV, cryII(a), cryV, cryVI;  
OS Bacillus thuringiensis (subsp. kurstaki).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=29339;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSIR732;  
RX MEDLINE=93298009; PubMed=8517758;  
RA Gleave A.P., Williams R., Hedges R.J.;  
RT "Screening by polymerase chain reaction of Bacillus thuringiensis  
RT serotypes for the presence of cryV-like insecticidal protein genes and  
RT characterization of a cryV gene cloned from B. thuringiensis subsp.  
RT kurstaki";  
RL Appl. Environ. Microbiol. 59:1683-1687(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JHCC4835;  
RX MEDLINE=92269582; PubMed=1588820;  
RA Taylor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;  
RT "Identification and characterization of a novel Bacillus thuringiensis  
RT delta-endotoxin entomocidal to coleopteran and lepidopteran larvae";  
RL Mol. Microbiol. 6:1211-1217(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HD-1;  
RX MEDLINE=95314293; PubMed=7793960;  
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;  
RT "Distribution of cryV-type insecticidal protein genes in Bacillus  
RT thuringiensis and cloning of cryV-type genes from Bacillus  
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.  
RT entomocidus";  
RL Appl. Environ. Microbiol. 61:2402-2407(1995).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AB88;  
RX MEDLINE=96178985; PubMed=8606196;  
RA Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,  
RA Craig J.A., Koziel M.G., Satruch J.J.;  
RT "Cloning of a cryV-type insecticidal protein gene from Bacillus  
RT thuringiensis: the cryV-encoded protein is expressed early in  
RT stationary phase";  
RL J. Bacteriol. 178:2141-2144(1996).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=61;

RA Selvapandian A., Bhatnagar R.K.;  
RT "Isolation, cloning and expression of cryV gene.";  
RL SUBMITTED (OCT-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut  
CC epithelial cells of certain coleopteran and lepidopteran species.  
CC Active on Plutella xylostella and Bombyx mori.  
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
CC sporulation and is accumulated both as an inclusion and as part of  
CC the spore coat.  
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
CC terminus.  
CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; M98544; AAA22354.1; -;  
CC EMBL; X62821; CAA44633.1; -;  
CC EMBL; L36338; AAC36999.1; -;  
CC EMBL; L49391; AAB00958.1; -;  
CC EMBL; X08920; CAA70124.1; -;  
CC PIR; I39815; I39815.  
CC PIR; S25383; S25383.  
CC HSSP; P02965; 1CIY.  
CC InterPro; IPR001178; Endotoxin.  
CC InterPro; IPR005638; endotoxin\_C.  
CC InterPro; IPR005639; endotoxin\_N.  
CC InterPro; IPR008979; Gal\_bind\_like.  
CC Pfam; PF03944; Endotoxin\_C; 1.  
CC Pfam; PF00555; Endotoxin\_M; 1.  
CC Pfam; PF03945; Endotoxin\_N; 1.  
CC Sporulation; Toxin.  
KW VARIANT 159 159 K -> R (in strain JHCC4835 and strain HD-  
FT VARIANT 233 233 1).  
FT VARIANT 443 443 A -> V (in strain AB88).  
FT VARIANT 711 712 KQ -> NE (in strain HD-1 and strain 61).  
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;  
  
Query Match 100.0%; Score 3760; DB 1; Length 719;  
Best Local Similarity 100.0%; Pred. No. 3e-251;  
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPFSASTI 60  
DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPFSASTI 60  
  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFTLGLWPKGNQWEIFMEHVEEIIINOKISTYA 120  
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFTLGLWPKGNQWEIFMEHVEEIIINOKISTYA 120  
  
QY 121 RNKALTDLKGIDALAVYHDSLESWGNNRNNRARSVVKQSYIALELMFVKLPSPFVSG 180  
DB 121 RNKALTDLKGIDALAVYHDSLESWGNNRNNRARSVVKQSYIALELMFVKLPSPFVSG 180  
  
QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDSDHCWKYS 240  
DB 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDSDHCWKYS 240  
  
QY 241 TGLNLRGNASWRYNFRDMLTWLDLVALPSTDTOMYPKTTAQLTREYVTDAL 300  
DB 241 TGLNLRGNASWRYNFRDMLTWLDLVALPSTDTOMYPKTTAQLTREYVTDAL 300  
  
QY 301 GTVHPHPSFTTWTNNNAPSFAEAAVVRNPHLLDFLEQVTIYSLLSRWSTNTQYMNW 360  
DB 301 GTVHPHPSFTTWTNNNAPSFAEAAVVRNPHLLDFLEQVTIYSLLSRWSTNTQYMNW 360  
  
QY 361 GGKLEFRITGTLNISTQGSINTSINPVLPTSTRDYRTESLAGLNLFLTPQVNGVPR 420

DB 361 GGKLEFRITGTLNISTQGSINTSINPVLPTSTRDYRTESLAGLNLFLTPQVNGVPR 420  
QY 421 VDFHKKFVTHPTASDNFYYPGAGIGTQLODSENELPPEATGQPNYESVSHRLSHIGLIS 480  
DB 421 VDFHKKFVTHPTASDNFYYPGAGIGTQLODSENELPPEATGQPNYESVSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNINPPFAQRYVRIRVASTTDLQFHTSINGKAINQGNFSATNMRGSDLDYK 600  
DB 541 TGTFGDIRVNINPPFAQRYVRIRVASTTDLQFHTSINGKAINQGNFSATNMRGSDLDYK 600  
QY 601 TFRVTGFTTPFGLDQVSTFTIGANNFSSGNVWIDRIEFVPEVVEYEAEDYFEKAQEKV 660  
DB 601 TFRVTGFTTPFGLDQVSTFTIGANNFSSGNVWIDRIEFVPEVVEYEAEDYFEKAQEKV 660  
QY 661 TALFTSTNPRGLTKVDKYHIDQVSNLVSLSDEPFYLDKRELFELIVKAKOLHIERNM 719  
DB 661 TALFTSTNPRGLTKVDKYHIDQVSNLVSLSDEPFYLDKRELFELIVKAKOLHIERNM 719

RESULT 2

Q6X181 PRELIMINARY; PRT; 719 AA.  
ID AC Q6X181;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE CryII.  
DE Names=CryII;  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AV262167; AAP86782.1; -;  
DR GO; GO:0005102; F:receptor binding; IEA.  
DR GO; GO:0006952; P:defense response; IEA.  
DR GO; GO:0009405; P:pathogenesis; IEA.  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR008979; Gal\_bind\_like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;

Query Match 100.0%; Score 3760; DB 2; Length 719;  
Best Local Similarity 100.0%; Pred. No. 3e-251;  
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPFSASTI 60  
DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPFSASTI 60  
  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFTLGLWPKGNQWEIFMEHVEEIIINOKISTYA 120  
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFTLGLWPKGNQWEIFMEHVEEIIINOKISTYA 120  
  
QY 121 RNKALTDLKGIDALAVYHDSLESWGNNRNNRARSVVKQSYIALELMFVKLPSPFVSG 180  
DB 121 RNKALTDLKGIDALAVYHDSLESWGNNRNNRARSVVKQSYIALELMFVKLPSPFVSG 180  
  
QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDSDHCWKYS 240  
DB 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDSDHCWKYS 240



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QY 241 TGLNLRGNTNAESWVRYNQFRDMLTMDLVALFPSYDTQMPYPIKTTAQLTREVTYDAI 300
DB 241 TGLNLRGNTNAESWVRYNQFRDMLTMDLVALFPSYDTQMPYPIKTTAQLTREVTYDAI 300
QY 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDLEQVTTIYSLLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDLEQVTTIYSLLSRWSNTQYNNMW 360
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLOTPVNGVPR 420
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLOTPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
DB 541 TGTFGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 601 TFRVTGFTTFFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660
DB 601 TFRVTGFTTFFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYDOVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDHYDOVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 3
Q93NUS PRELIMINARY; PRT; 719 AA.
AC Q93NUS;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Crylia.
GN Names-crylia;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Song F., Zhang J., Gu A., Huang D., Li G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF373207; AAK66742.1; -.
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;

Query Match 99.98; Score 3755; DB 2; Length 719;
Best Local Similarity 99.98; Pred. No. 6.6e-251;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLNQDKHOSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEFPVSASTI 60
DB 1 MKLNQDKHOSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEFPVSASTI 60
QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKQKQWEIFMESHVEEIIINQKISTYA 120

```

```

DB 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKQKQWEIFMESHVEEIIINQKISTYA 120
QY 121 RNKALTDLXGLGDALAVYHDSLESWVGNRNNTARSQVIALELMFVQKLPSPFAVSG 180
DB 121 RNKALTDLXGLGDALAVYHDSLESWVGNRNNTARSQVIALELMFVQKLPSPFAVSG 180
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISITFYNRQVRAGDYSCHCKWYS 240
DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISITFYNRQVRAGDYSCHCKWYS 240
QY 241 TGLNLRGNTNAESWVRYNQFRDMLTMDLVALFPSYDTQMPYPIKTTAQLTREVTYDAI 300
DB 241 TGLNLRGNTNAESWVRYNQFRDMLTMDLVALFPSYDTQMPYPIKTTAQLTREVTYDAI 300
QY 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDLEQVTTIYSLLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDLEQVTTIYSLLSRWSNTQYNNMW 360
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLOTPVNGVPR 420
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLOTPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
DB 541 TGTFGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 601 TFRVTGFTTFFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660
DB 601 TFRVTGFTTFFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYDOVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDHYDOVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 4
O85796 PRELIMINARY; PRT; 719 AA.
AC O85796;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Insecticidal protein.
GN Names-cryV101;
OS Bacillus thuringiensis (subsp. kurstaki).
OG Plasmid large plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SI01;
RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076953; AAC26910.1; -.
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.

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KW Plasmid. 719 AA; 81230 MW; 42746D478359BBA7 CRC64;  
SQ SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;  
Query Match 99.8%; Score 3754; DB 2; Length 719;  
Best Local Similarity 99.9%; Pred. No. 7,7e-251;  
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSYEYENVEPVSASTI 60  
Db 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSYEYENVEPVSASTI 60  
Qy 61 QTGIGIAGKILGTLGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
Db 61 QTGIGIAGKILGTLGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
Qy 121 RNKALTDLKGGLDALAVYHDSLESWGNRNNTARSVVKSYQYIALELMFVKQLPSFAVSG 180  
Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNNTARSVVKSYQYIALELMFVKQLPSFAVSG 180  
Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNQVERAGDYSDHCVKWS 240  
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNQVERAGDYSDHCVKWS 240  
Qy 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300  
Db 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300  
Qy 301 GTVHPHPSFTSTWYNNAPSFSAIAEAAVVRNPHLLDLEQVITYSLLSRWSNTQYNNMW 360  
Db 301 GTVHPHPSFTSTWYNNAPSFSAIAEAAVVRNPHLLDLEQVITYSLLSRWSNTQYNNMW 360  
Qy 361 GGHKLEERTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFITQPVNGVPR 420  
Db 361 GGHKLEERTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFITQPVNGVPR 420  
Qy 421 VDFHMKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
Db 421 VDFHMKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
Qy 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRTN 540  
Db 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRTN 540  
Qy 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600  
Db 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600  
Qy 601 TFRVTGFTTTPPSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660  
Db 601 TFRVTGFTTTPPSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660  
Qy 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFLDEKRELFEIVKYAKQLHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFLDEKRELFEIVKYAKQLHIERNM 719

RESULT 5  
Q8KY61 ID Q8KY61 PRELIMINARY; PRT; 719 AA.  
AC Q8KY61  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE CRY  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP Porcar M., Martinez C., Caballero P.;  
RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AF278797; AM73516.1; -  
DR PIR; B42459; B42459.

DR HSP; P02965; 1CIY.  
DR GO:0005102; F:receptor binding; IEA.  
DR GO:0006952; P:defense response; IEA.  
DR GO:0009405; P:pathogenesis; IEA.  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR008979; Gal bind\_like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
SQ SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;  
Query Match 96.4%; Score 3625; DB 2; Length 719;  
Best Local Similarity 96.2%; Pred. No. 6.4e-242;  
Matches 692; Conservative 12; Mismatches 15; Indels 0; Gaps 0;  
Qy 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSYEYENVEPVSASTI 60  
Db 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSYEYENVEPVSASTI 60  
Qy 61 QTGIGIAGKILGTLGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
Db 61 QTGIGIAGKILGTLGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
Qy 121 RNKALTDLKGGLDALAVYHDSLESWGNRNNTARSVVKSYQYIALELMFVKQLPSFAVSG 180  
Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNNTARSVVKSYQYIALELMFVKQLPSFAVSG 180  
Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNQVERAGDYSDHCVKWS 240  
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNQVERAGDYSDHCVKWS 240  
Qy 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300  
Db 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300  
Qy 301 GTVHPHPSFTSTWYNNAPSFSAIAEAAVVRNPHLLDLEQVITYSLLSRWSNTQYNNMW 360  
Db 301 GTVHPHPSFTSTWYNNAPSFSAIAEAAVVRNPHLLDLEQVITYSLLSRWSNTQYNNMW 360  
Qy 361 GGHKLEERTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFITQPVNGVPR 420  
Db 361 GGHKLEERTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFITQPVNGVPR 420  
Qy 421 VDFHMKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
Db 421 VDFHMKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
Qy 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRTN 540  
Db 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRTN 540  
Qy 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600  
Db 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600  
Qy 601 TFRVTGFTTTPPSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660  
Db 601 TFRVTGFTTTPPSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660  
Qy 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFLDEKRELFEIVKYAKQLHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFLDEKRELFEIVKYAKQLHIERNM 719  
RESULT 6  
Q9F0P8 ID Q9F0P8 PRELIMINARY; PRT; 719 AA.  
AC Q9F0P8  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

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DE Name=cryII;
GN Bacillus thuringiensis.
OS Plasmid pBTc19.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BTC007;
RX DOI=10.1128/AEM.69.9.5207-5211.2003;
RA Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,
HU Hu Y., Li G., Huang D.;
RT "Identification of cryII-type genes from Bacillus thuringiensis
RL Appl. Environ. Microbiol. 69:5207-5211(2003).
DR EMBL: AF211190; AAG43526.1; -.
DR HSP; P02965; ICIY.
DR GO: 0005102; P: receptor binding; IEA.
DR GO: 0006952; P: defense response; IEA.
DR GO: 0009405; P: pathogenesis; IEA.
DR InterPro: IPR001178; Endotoxin.
DR InterPro: IPR005638; endotoxin_C.
DR InterPro: IPR005639; endotoxin_N.
DR Pfam: PF03944; Endotoxin_C; 1.
DR Pfam: PF00555; Endotoxin_M; 1.
DR Pfam: PF03945; Endotoxin_N; 1.
DR Plasmid.
KW Plasmid.
SQ SEQUENCE 719 AA; 81024 MW; 7E17481922C435B6 CRC64;

Query Match 94.4%; Score 3551; DB 2; Length 719;
Best Local Similarity 93.6%; Pred. No. 8.5e-237;
Matches 673; Conservative 26; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MCLKNQKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYEYENVEPVSASTI 60
Db |||||
Qy 1 MCLKNPKDQKHSLSNAKVDKIATDSLKNETDIELKNIHEDFLRMSHESIDPVSASTI 60
Db |||||

Qy 61 QTGIGTAGKLTGLVGFAGQASVLSYFILGELWPKGKQWEIFMEHVEBIIQKISTYA 120
Db |||||

Qy 61 QTGIGTAGKLTGLVGFAGQIASVLSYFILGELWPKGKQWEIFMEHVEBIIQKISTYA 120
Db |||||

Qy 121 RNKALTDKLGDALAYVHDSLSVGNRNNTARSVVKVQYIALELMFVKLPSPAVSG 180
Db |||||

Qy 121 RNIALADKLGDALAYVHDSLSVGNRNNTARSVVKVQYIALELMFVKLPSPAVSG 180
Db |||||

Qy 181 EYVPLPIYQAANLHLLLRDASIFGKENGLSSEISTYFNQVERAGYSYDHCVKWYS 240
Db |||||

Qy 181 EYVPLPIYQAANLHLLLRDASVFGKENGLSQISTYFNQVERTSDYSYDHCVKWYS 240
Db |||||

Qy 241 TGLNNLRGTNAESVVRVYQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTRVYTDI 300
Db |||||

Qy 241 TGLNNLRGTNAESVVRVYQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTRVYTDI 300
Db |||||

Qy 301 GTVHPHPSFTSTWYNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMW 360
Db |||||

Qy 301 GTVHPNASFASTWYNNAPSFAIESAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMW 360
Db |||||

Qy 361 GGHKLEPRTTGGTLNISTQSTNTSINPVLPTFSRDVYRTESLAGLNLFLOTQVNGVPR 420
Db |||||

Qy 361 GGHKLEPRTTGGVLTNTQSTNTSINPVLPTFSRDVYRTESLAGLNLFLOTQVNGVPR 420
Db |||||

Qy 421 VDFHKKVPTHPIASDNFPYPCYAGIGTQLODSENLPEATGQPNVYESYSHRSLHGLIS 480
Db |||||

Qy 421 VDFHKKVPTHPIASDNFPYPCYAGIGTQLODSENLPEATGQPNVYESYSHRSLHGLIS 480
Db |||||

Qy 481 ASHVKALVYSWTHRSADRTNTIENSITQIPLVKAFNLSSGAAVVRPGTGGDILRRTN 540
Db |||||

Qy 481 ASHVKALVYSWTHRSADRTNTIENSITQIPLVKAFNLSSGAAVVRPGTGGDILRRTN 540
Db |||||

Qy 541 TGTFGDIRVINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMNGEDLDYK 600
Db |||||

Db 541 TGTFGDIRVINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMNGEDLDYK 600
Qy 601 TFRVTGFTTFFSFLDVQSTFTTGAMNFFSGNEVYIDRIEFVPEVTEYAEYDFEKAQKV 660
Db |||||
Qy 601 TFRVTGFTTFFSFLDVQSTFTTGAMNFFSGNEVYIDRIEFVPEVTEYAEYDFEKAQKV 660
Db |||||
Qy 661 TALFTSTNPRGLTKDVKDHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQKHIERNM 719
Db |||||
Qy 661 TALFTSTNPRGLTKDVKDHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQKHIERNM 719
Db |||||

RESULT 7
CLIB_BACTE STANDARD; PRT; 719 AA.
AC Q45709;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIB (insecticidal delta-endotoxin)
DE CryII(b) (crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Names=cryIIB; Synonyms=cryII(b), cryV, cryV465;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP465;
RX MEDLINE=95314293; PubMed=7793960;
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;
RT Distribution of cryV-type insecticidal protein genes in Bacillus
RT thuringiensis and cloning of cryV-type genes from Bacillus
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
RT entomocidus."
RL Appl. Environ. Microbiol. 61:2402-2407(1995).
CC -1- FUNCTION: Promotes colloidal lysis by binding to the midgut
CC epithelial cells of certain coleopteran and lepidopteran species.
CC Active on Plutella xylostella but not on Bombyx mori.
CC -1- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -1- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -1- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC ENBL: U07642; AAA82114.1; -.
CC PIR: I40590; I40590.
CC HSP; P02965; ICIY.
CC InterPro: IPR001178; Endotoxin.
CC InterPro: IPR005638; endotoxin_C.
CC InterPro: IPR005639; endotoxin_N.
CC InterPro: IPR008979; Gal_bind_like.
CC Pfam: PF03944; Endotoxin_C; 1.
CC Pfam: PF00555; Endotoxin_M; 1.
CC Pfam: PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81295 MW; E8210ABEA97688E CRC64;

Query Match 93.6%; Score 3520; DB 1; Length 719;
Best Local Similarity 92.9%; Pred. No. 1.2e-234;
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MCLKNQKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYEYENVEPVSASTI 60
Db |||||
Qy 1 MCLKNPKDQKHSLSNAKVDKIATDSLKNETDIELKNIHEDFLRMSHESIDPVSASTI 60
Db |||||
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QY 61 QTGIGIAGKILGTLGVPPAGQVASYLFGELWPKGNQWEIFMEHVEIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTLGVPPAGQVASYLFGELWPKGNQWEIFMEHVEIINQKISTYA 120  
 QY 121 RNKALTDLKGGLDALAVYHDSLEWGNRNNTARSVVKQYIALELMFVKQLPSPFAVSG 180  
 DB 121 RNKALSDRLGGLDALAVYHDSLEWGNRNNTARSVVKQYIALELMFVKQLPSPFAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLDASIFGKWLSSSEISTFYNROVERAGYSDHCVKWS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLDASIFGKWLSSSEISTFYNROVERAGYSDHCVKWS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSPYDTOMYPIKTAQTALREVYTDAL 300  
 DB 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSPYDTOMYPIKTAQTALREVYTDAL 300  
 QY 301 GTVHPHPSFTTWTNNNAPSFAIAEAAVVRNPHLLDPLEQVITYSLLSRWSTQYNNMW 360  
 DB 301 GTVHPHPSFTTWTNNNAPSFAIAEAAVVRNPHLLDPLEQVITYSLLSRWSTQYNNMW 360  
 QY 361 GGHKLEFRTIGTLNISTQSTNTSINPVTLPFTSRDVRTESLAGNLFITQPVNGVPR 420  
 DB 361 GGHKLEFRTIGTLNISTQSTNTSINPVTLPFTSRDVRTESLAGNLFITQPVNGVPR 420  
 QY 421 VDFHKKFVTHPIASDNFYYPGAGIGITQDSENELPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHKKFVTHPIASDNFYYPGAGIGITQDSENELPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHKVAVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHKVAVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTGDIRVNTNPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATNMGEDLDYK 600  
 DB 541 TGTGDIRVNTNPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATNMGEDLDYK 600  
 QY 601 TERTVGTFTTTPFDVQSTFTTCAMNFSNGEVIYDRIEFVPEVTEYAEYDFEKAQEKV 660  
 DB 601 TERTVGTFTTTPFDVQSTFTTCAMNFSNGEVIYDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKYHIDQVNLVESLDEFLDEKELFEIVKAYQOLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKYHIDQVNLVESLDEFLDEKELFEIVKAYQOLHIERNM 719

RESULT 8  
 CLID\_BACTU STANDARD; PRT; 719 AA.  
 ID CLID\_BACTU  
 AC Q9XDL1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryII (Insecticidal delta-endotoxin  
 DE CryII(d)) (crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Names=cryII(d); Synonyms=cryII(d), NRCryV;  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BR30;  
 RA MEDLINE=20374042; PubMed=10919402;  
 RX Choi S.-K., Shin B.-S., Kong E.-M., Rho H.-M., Park S.-H.;  
 RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein  
 RT gene.";  
 RL Curr. Microbiol. 41:65-69(2000).  
 CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut  
 CC epithelial cells of many lepidopteran larvae. Active on Plutella  
 CC xylostella and on Bombyx mori.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-

terminus.  
 -!- SIMILARITY: Belongs to the delta endotoxin family.  
 -----  
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 -----  
 EMBL; AF047579; AD44366.1; -;  
 HSSP; P02965; 1CIY.  
 InterPro; IPR001178; Endotoxin.  
 InterPro; IPR005638; endotoxin\_C.  
 InterPro; IPR005639; endotoxin\_N.  
 InterPro; IPR008979; Gal\_bind\_Like.  
 Pfam; PF03944; Endotoxin\_C; 1.  
 Pfam; PF00555; Endotoxin\_M; 1.  
 Pfam; PF03945; Endotoxin\_N; 1.  
 Sporulation; Toxin.  
 SQU SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;

Query Match 90.3%; Score 3397; DB 1; Length 719;  
 Best Local Similarity 89.8%; Pred. No. 3.8e-226;  
 Matches 646; Conservative 35; Mismatches 38; Indels 0; Gaps 0;  
 QY 1 MKLNQDQKHSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMESEYENVEPVSASTI 60  
 DB 1 MKSNQMYRFSFSNATVDKSFDDPLEHNTNMLQNSHEDCLKMESEYEVFVSSTI 60  
 QY 61 QTGIGIAGKILGTLGVPPAGQVASYLFGELWPKGNQWEIFMEHVEIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTLGVPPAGQVASYLFGELWPKGNQWEIFMEHVEIINQKISTYA 120  
 QY 121 RNKALTDLKGGLDALAVYHDSLEWGNRNNTARSVVKQYIALELMFVKQLPSPFAVSG 180  
 DB 121 RNKALADLKGGLDALAVYHDSLEWGNRNNTARSVVKQYIALELMFVKQLPSPFAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLDASIFGKWLSSSEISTFYNROVERAGYSDHCVKWS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLDASIFGKWLSSSEISTFYNROVERAGYSDHCVKWS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSPYDTOMYPIKTAQTALREVYTDAL 300  
 DB 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSPYDTOMYPIKTAQTALREVYTDAL 300  
 QY 301 GTVHPHPSFTTWTNNNAPSFAIAEAAVVRNPHLLDPLEQVITYSLLSRWSTQYNNMW 360  
 DB 301 GTVHPHPSFTTWTNNNAPSFAIAEAAVVRNPHLLDPLEQVITYSLLSRWSTQYNNMW 360  
 QY 361 GGHKLEFRTIGTLNISTQSTNTSINPVTLPFTSRDVRTESLAGNLFITQPVNGVPR 420  
 DB 361 GGHKLEFRTIGTLNISTQSTNTSINPVTLPFTSRDVRTESLAGNLFITQPVNGVPR 420  
 QY 421 VDFHKKFVTHPIASDNFYYPGAGIGITQDSENELPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHKKFVTHPIASDNFYYPGAGIGITQDSENELPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHKVAVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHKVAVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTGDIRVNTNPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATNMGEDLDYK 600  
 DB 541 TGTGDIRVNTNPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATNMGEDLDYK 600  
 QY 601 TERTVGTFTTTPFDVQSTFTTCAMNFSNGEVIYDRIEFVPEVTEYAEYDFEKAQEKV 660  
 DB 601 TERTVGTFTTTPFDVQSTFTTCAMNFSNGEVIYDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKYHIDQVNLVESLDEFLDEKELFEIVKAYQOLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKYHIDQVNLVESLDEFLDEKELFEIVKAYQOLHIERNM 719

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Db      661 TAMPTSTNLRRLKNTVTDCHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLNIERNM 719
RESULT 9
C11C_BACTU STANDARD; PRT; 719 AA.
ID      C11C_BACTU STANDARD; PRT; 719 AA.
AC      O87404;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Pesticidal crystal protein cryIIc (Insecticidal delta-endotoxin
DE      CryII(c)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN      Name=cryIIC; Synonyms=cryII(c);
OS      Bacillus thuringiensis.
OG      Plasmid.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=1426;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C18 / Egypt;
RA      Osman Y.A., Makkour M.A., Bulla L.A. Jr.;
RL      Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC      -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC      epithelial cells of insects.
CC      -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC      sporulation and is accumulated both as an inclusion and as part of
CC      the spore coat.
CC      -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC      terminus.
CC      -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL; AF056933; AAC62933.1; -.
DR      HSSP; P02965; 1C1Y.
DR      InterPro; IPR001178; Endotoxin.
DR      InterPro; IPR005638; endotoxin_C.
DR      InterPro; IPR008979; Gal_bind_like.
DR      Pfam; PF03944; Endotoxin_C; 1.
DR      Pfam; PF00555; Endotoxin_M; 1.
DR      Pfam; PF03945; Endotoxin_N; 1.
KW      Plasmid; Sporulation; Toxin.
SQ      SEQUENCE 719 AA; 81210 MW; 837083F06B905DFF CRC64;

Query Match      89.8%; Score 3377; DB 1; Length 719;
Best Local Similarity 89.8%; Pred. No. 9.1e-225;
Matches 646; Conservative 33; Mismatches 40; Indels 0; Gaps 0;

QY      1 MKLKNQDKHQSFSNNKVDKISTDSLKNTDIELQNIHEDCLKMSEYENVPFVSASTI 60
Db      1 MKLKNPKDKHTLSSNAKVDKIATDSLKNETIELKNMNNEDYLRNSESIDPFVSASTI 60
QY      61 QTGIGTAGILGTGVPFAGQVASYLSFTLGLMPPKGNQWEIFMEHVHEIINOKISTYA 120
Db      61 QTGIGTAGIKLGTGVPFPGQASLSYFTLGLMPPKGSQWEIFMEHVHEIINRKISTYA 120
QY      121 RNKALTDLKGLDALAVYHDSLESVGNRNNTARRSVKVSQVIALELMFVQKLPGFVAVSG 180
Db      121 RNKALTDLKGLDALAVHESLESVGNRNNTARRSVKVNQVIALELMFVQKLPGFVAVSG 180
QY      181 BEVPLLPPIYAQANLHLLLRDASIFGKEWGLSSSEISITFYNRQVERAGDSDHCWKVYS 240
Db      181 BEVPLLPPIYAQANLHLLLRDASIFPKNGGLSASEISITFYNRQVERTRDYSVHCWKVNN 240
QY      241 TGLNLRGCTNARSWRYNQFRDMTLMVLVDLVALPFSYDTQMPYIKTTAQLTREVYTDAI 300
Db      241 TGLNLRGCTNARSWRYNQFRDKIELMVLVDLVRVFPFSDYDTLVYPIKTTQLTREVYTDAI 300
QY      301 GTVHPHPSPSTTWTYNNNAPSFSAIEAAVVRNPHLLDFLEQVTFIYLSLSRWSNTQYNNMW 360
Db      301 GTVDPNQALRSTTWTYNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYLSLSRWSNTQYNNMW 360
QY      361 GGHKLEFRITGGTILNISTOGSNTSINPVTLSRSDVTRTESLAGLNFLTOPVNGVPR 420
Db      361 GGHRLSERPIGGALNTSTOGSNTSINPVTLOFTSRDFYRTESWAGLNFLTOPVNGVPR 420
QY      421 VDFHMKFVTHPTASDNFYVPGVAGTGLQDSENELPPEATGPNPVSYSRLSHLGLIS 480
Db      421 VDFHMKFPTLPASDNFYVGLVAGTGLQDSENELPPTTGPPTYESYSHRLSHLGLIS 480
QY      481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDIILRTN 540
Db      481 GSHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTK 540
QY      541 TGTGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db      541 SGTFGHIRVINPPFAQRYRVRMSYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY      601 TERTVGFTTPPSFLDVQSTFTIGANFSSGNEVYIDRIEFVPEVTVTEAEYDFEKAQEKV 660
Db      601 TERTVGFTTPPSFLDVQSTFTIGANFSSGNEVYIGRIEFVPEVTVTEAEYDFEKAQEKV 660
QY      661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLNIERNM 719
Db      661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDELVDKRELFEIVKYAKQLNIERNM 719

RESULT 10
C11B_BACTU STANDARD; PRT; 1229 AA.
ID      C11B_BACTU STANDARD; PRT; 1229 AA.
AC      Q45739;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Pesticidal crystal protein cryIIB (Insecticidal delta-endotoxin
DE      CryIIB(b)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN      Name=cryIIB; Synonyms=cryET5, cryIIB(b);
OS      Bacillus thuringiensis.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=1428;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=NRRL B-21110 / EG5847;
RA      Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
RT      Toxic to lepidopteran insects.
RL      Patent number US5322687, 21-JUN-1994.
CC      -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC      epithelial cells of many lepidopteran larvae.
CC      -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC      sporulation and is accumulated both as an inclusion and as part of
CC      the spore coat.
CC      -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC      terminus.
CC      -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL; L32020; AAA22344.1; -.
DR      HSSP; P02965; 1C1Y.
DR      InterPro; IPR001178; Endotoxin.
DR      InterPro; IPR005638; endotoxin_C.
DR      InterPro; IPR005639; endotoxin_N.

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DR	InterPro; IPR008979; Gal bind like.	DR	InterPro; IPR008979; Gal bind like.
DR	Pfam; PF03944; Endotoxin_C; 1.	DR	Bishop A.H., Bone E.J., Ellar D.J.;
DR	Pfam; PF00555; Endotoxin_M; 1.	RT	"Cloning of novel Bacillus thuringiensis delta-endotoxin.";
DR	Pfam; PF03945; Endotoxin_N; 1.	RL	Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
DR	Spurulation; Toxin.	CC	-I- FUNCTION: Promotes colloidemetic lysis by binding to the midgut
DR	SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;	CC	epithelial cells of insects.
DR		CC	-I- DEVELOPMENTAL STAGE: The crystal protein is produced during
DR		CC	sporulation and is accumulated both as an inclusion and as part of
DR		CC	the spore coat.
DR		CC	-I- MISCELLANEOUS: Toxin segment of the protein is located in the N-
DR		CC	terminus.
DR		CC	-I- SIMILARITY: Belongs to the delta endotoxin family.
DR		CC	-----
DR		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR		CC	the European Bioinformatics Institute. There are no restrictions on its
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DR		CC	modified and this statement is not removed. Usage by and for commercial
DR		CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
DR		CC	or send an email to license@isb-sib.ch).
DR		CC	-----
DR		CC	EMBL; Z46442; CAA86568.1; --
DR		CC	HSP; P02965; ICY.
DR		CC	InterPro; IPR001178; Endotoxin.
DR		CC	InterPro; IPR005638; endotoxin_C.
DR		CC	InterPro; IPR005639; endotoxin_N.
DR		CC	InterPro; IPR008979; Gal bind like.
DR		CC	Pfam; PF03944; Endotoxin_C; 1.
DR		CC	Pfam; PF00555; Endotoxin_M; 1.
DR		CC	Pfam; PF03945; Endotoxin_N; 1.
DR		CC	Sporulation; Toxin.
DR		CC	SEQUENCE 1233 AA; 140451 MW; 7318382413529F21 CRC64;
DR		CC	-----
DR		CC	Query Match 65.1%; Score 2446.5; DB 1; Length 1233;
DR		CC	Best Local Similarity 65.6%; Pred. No. 4.4e-160;
DR		CC	Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;
DR		CC	-----
DR		CC	13 SSNAKVDKISTDSLKN-ETDIELO-NINHEDECKMSEYENVEPVFVSASTTGTGIGIAGKI 70
DR		CC	7 NENEIINALSIPTVSNPSTQMLSPDARIEDSLCAEVNNDIPFVSASTVQTGINIAGRI 66
DR		CC	-----
DR		CC	71 LGTLGVFPAGOVASLYSFLIGELWPKGNOWEIPMEHVEIINOKISTYARNKALTDLKG 130
DR		CC	67 LGVLGVFPAGOLASFSYFLVGLWPSGRDPWEIHEVQLIRQOVVTRNTAIALEG 126
DR		CC	131 LGDALAVVHDSLSWGNRNTRARSVVKSOYIALELMFVQKLPSPFVSGEVEPLPIYA 190
DR		CC	127 LGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEEVELLMVYA 186
DR		CC	191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSDHCVKWYSTGLNLRGTN 250
DR		CC	187 QAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEYSNHCVCQWYNTGLNLRGTN 246
DR		CC	251 AESWVRNQFRDMLVLDLVALPSPYDTOMYPIKTTAOLTRVYTDATGTVHPHPSFT 310
DR		CC	247 AESWLRNQFRDMLVLDLVALPSPYDTOMYPIKTTAOLTRVYTDATGTVHPHPSFT 306
DR		CC	311 STTWNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMMNGHKLFRPTI 370
DR		CC	307 STWNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMMNGHKLFRPTI 366
DR		CC	371 GGTINISTQGST-NTSINPVTLPSTSDVTRTESLAGNLFLTOPVNGVPRVDFHWKFTV 429
DR		CC	367 GGTINTSTQGLTNTSINPVTLPSTSDVTRTESLAGNLFLTOPVNGVPRVDFHWKFTV 422
DR		CC	430 HPIASDNFYYPG-----YAGIGTQODSENEUPPEATGQPNYVESYSHRSLHGLISAS 482
DR		CC	423 --INPQNIYERGATTYQPGVGIQFDSSTELPPTTERPNVYESYSHRSLHGLIIGN 480
DR		CC	483 HVKALVSWTHRSADRTNTIENPSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTG 542
DR		CC	481 TLRAPVYSWTHRSADRTNTIGPNRITQIPLVKALNLSGVTGVGPGFTGGDILRRNTG 540
DR		CC	-----
DR		CC	543 TFGDIRVNINPFPAPQRYRIRYASTTDLPQHTSINKAINGKSNFATMNGEDLDYKTF 602
DR		CC	541 TFGDIRVNINPFPAPQRYRIRYASTTDLPQHTSINKAINGKSNFATMNGEDLDYKTF 600
DR		CC	603 RTVGFTTTPFLDVGSTFTIGAMFNSGNEVVIDRIEVPVEVVEYAEYDPEKAEKVTA 662
DR		CC	601 RTAGFTSTPFLNLAQSTFTLGAQSFN-QEYVIDRVEFVPAEVEYAEYDPEKAEKVTA 659
DR		CC	663 LFTSTNPRGLKTDVNDKHIDQVSNLVSDEFVLDEKRELFEIVKAKQHLIERNM 719
DR		CC	660 LFTSTNPRGLKTDVNDKHIDQVSNLVSDEFVLDEKRELFEIVKAKQHLIERNM 716
DR		CC	-----
DR		CC	RESULT 11
DR		CC	C1BC BACTM STANDARD; PRT; 1233 AA.
DR		CC	AC C45774;
DR		CC	DT 30-MAY-2000 (Rel. 39, Created)
DR		CC	DT 30-MAY-2000 (Rel. 39, Last sequence update)
DR		CC	DT 05-JUL-2004 (Rel. 44, Last annotation update)
DR		CC	DE Pesticidal crystal protein cryIbC (insecticidal delta-endotoxin
DR		CC	DE CryIb(c)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
DR		CC	GN Name=cryIbC; Synonyms=cryIb(C), cryIbC;
DR		CC	OS Bacillus thuringiensis (subsp. morrisoni).
DR		CC	OC Bacteria; Firmicutes, Bacillales; Bacillaceae; Bacillus.
DR		CC	OX NCBI_taxid=1441;

```
QY 543 TFGDIRVNWPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYKTF 602
Db 541 TFGDIRLNVPLSQRYRVRIRYASTTDLQFTRINGTWNIGNFSRTWNRGNLEYRSF 600
QY 603 RTVGFTTPEFLDVOSTFTTIGAWNFGSSGNEVYIDRIEFVPUVYVEAEVDFEKAQEKVTA 662
Db 601 RTAGSTPPEFLNAQSTFTTIGAQSFN-QEVYIDRIEFVPAEYVDFEAEYDLERAQKAVNA 659
QY 663 LFTSTNPRGLKTDVYDHYDQVSNLVESLSDFYLDKEKELFEIVKYAKQLHIERNM 719
Db 660 LFTSTNPRKLTVDYDHYDQVSNLVACLSDFCLDEKELFEKVKYAKLSDERNL 716

RESULT 12
Q93T75 PRELIMINARY; PRT; 1228 AA.
AC Q93T75; STRAIN=HD-9;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-WAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Delta-endotoxin Cry1Ba2.
GN Name=Cry1Ba2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAK51084.1; -.
DR HSSP; P07130; 1DLC.
DR GO; GO:005102; F:receptor binding; IEA.
DR GO; GO:006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;
SQ
Query Match 60.6%; Score 2278.5; DB 2; Length 1228;
Best Local Similarity 62.7%; Pred. No. 1.8e-148;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;
QY 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEFPFVSASTIQTGIGIAGKI 70
Db 2 TSNRKNEEIIINAVSNHSAQMDLLDPARTEDSLCIAEGNIDPFVVSASTVQTGINIAGRI 61
QY 71 LGTLGVPPAGQVAVSLYSPILGELWPKGKQWEIFMEHVEEINQKISTYARNKALTDLKG 130
Db 62 LGVLGVPPAGQVAVSLYSPILGELWPKGKQWEIFMEHVEEINQKISTYARNKALTDLKG 121
QY 131 LGDALAVYHDSLESWNGNNTFRASVVKSOYTALELMPVQKLPSPAVSGEEVPLPIYA 190
Db 122 LGDSFRAYQOQLEDWLENDKDATRSVLHTQYTALELDFINAMPLFAIRNQEVPPLMVA 181
QY 191 QAANLHLLLRDASIFGKEWGLSSSISFYNRQVRAGDYSDHCYVKWYSTGLNLRGYN 250
Db 182 QAANLHLLLRDASLFGSEFGLTSQEIQRYERQVTRDYSDYCVWEYNTGLSLRGYN 241
QY 251 ASWRYNQFRDRTMLVLDLVALPSPYDTQMPYIKTTAQLREVYDTAIGTVHPHPSFT 310
Db 242 AASWRYNQFRDRLTGLVDLVALPSPYDTQMPYIKTTAQLREVYDTAIGAT--GVNNA 299
QY 311 STTWYNNAPSFAIAEAAVVRNPHLDLEQVITYSLRSWNTQYMNWVGKHLFRTI 370
Db 300 SMWYNNAPSFAIAEAAIRSPHLLDFLEQLTIFSSASRWSNTRHWTYWRGHTIOSRPI 359
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QY 371 GGTINISTOGSTNTSINPVTLPFTSRDVRVYRTESLAGLMLF--LTOPVNGVPRVDFHWKEV 428
Db 360 GGGTLTTHGATNTSINPVTLPFTSRDVRVYRTESLAGLMLF--LTOPVNGVPRVDFHWKEV 416
QY 429 THP-----IASDNFYVPGVAGTGLQDSENELPPEATGQPNVYESVSHRLSHIGLISASH 483
Db 417 TNPQNISRGATANYSQP-YESPGQLQKSETELPETTERPNVYESVSHRLSHIGLILQSR 475
QY 484 VKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGCDILRRTNCT 543
Db 476 VNVVYVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGCDILRRTNCT 535
QY 544 FGDIRVNWPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYKTF 603
Db 536 FGPDIRVNWPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDLDYKTF 595
QY 604 TVGFTTPEFLDVOSTFTTIGAWNFGSSGNEVYIDRIEFVPUVYVEAEVDFEKAQEKVTA 663
Db 596 RRAFTTPTFTTQIIDIIRTSQGLSGEVIYDKLEIIPVTATFAEYDLERAQKAVNAL 655
QY 664 FTSTNPRGLKTDVYDHYDQVSNLVESLSDFYLDKEKELFEIVKYAKQLHIERNM 719
Db 656 FTNTNPRKLTVDYDHYDQVSNLVACLSDFCLDEKELFEKVKYAKLSDERNL 711

RESULT 13
C1BA_BACTK STANDARD; PRT; 1228 AA.
AC P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cry1Ba (insecticidal delta-endotoxin Cry1B(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cry1Ba; Synonyms=cryA4, cry1B(a);
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1436;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
RX MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from Bacillus thuringiensis subsp. thuringiensis.";
RL Nucleic Acids Res. 16:2723-2723(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC
CC EMBL; X06711; CAA29898.1; -.
CC EMBL; X95704; CAA65003.1; -.
CC FIR; S00873; S00873.
CC HSSP; P07130; 1DLC.
```



DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR008979; Gal\_bind\_Like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
KW Sporulation; Toxin.  
FT VARIANT 150 150 Y -> H (in strain HD-110).  
SQ SEQUENCE 1228 AA; 139647 MW; C8E3A19FBD98575 CRC64;

Query Match 60.6%; Score 2277.5; DB 1; Length 1228;  
Best Local Similarity 62.7%; Pred. No. 2.1e-148;  
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQINH-----EDCLKMSEYENVEPVFVSASTIQTGIGIAGKI 70  
DB 2 TSNRKNENEIINAVNSHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61  
QY 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130  
DB 62 LGVLGVPPAGQLASFSYFLVGLWPRGRDQWEIFLEHVEQLINQOITENARTALARLQ 121  
QY 131 LGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVOKLPSFAVSGEEVPLPIYA 190  
DB 122 LGDSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYA 181  
QY 191 QAAHLHLLLDASIFGKEMGLSSEISTFYNRQVERAGDYSDHCVKWYSTGLNLRGNTN 250  
DB 182 QAAHLHLLLDASIFGSEFGLTSQEIQRYYEYERQVTRDYSDYCVENYNTGLNLRGNTN 241  
QY 251 AESWVRVYQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVYDAITGVVHPHSFT 310  
DB 242 AASWVRVYQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVYDAITGVVHPHSFT 299  
QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYLSLSRWSNTQYVNMWGGHKLERTI 370  
DB 300 SMWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYLSLSRWSNTQYVNMWGGHKLERTI 359  
QY 371 GGTINISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLF--LTQPVNGVPRVDFHMKFV 428  
DB 360 GGLTSTHGTATNTSINPVTLPFTSRDVRVYTESLAGNLF--LTQPVNGVPRVDFHMKFV 416  
QY 429 THP-----IASDNFYPGYAGIGTQDSENELPPEATQPNYESYSHRISHIGLISASH 483  
DB 417 TNPQNISDRGTANYSQP--YESPGQLKDSLETPEPPERPEPPERPEPPERPEPPERPEPPER 475  
QY 484 VKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTGT 543  
DB 476 VNPVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTGT 535  
QY 544 FGDIRVNNPPPAQRYVRIRYASTDLOPHTSINGKAINQGNFSATNMNAGEDLDYKTFR 603  
DB 536 FGPIRVTVNGPLTQRYRIGFYASTVDFPFVSRGGTTVNNFRFLRTMNSGDELKYNFV 595  
QY 604 TVGFTTPFSLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTVYEAEDFEKAQKVTAL 663  
DB 596 RRAFTTPTFTQIQDIIRTSIQGLSGNGEVYIDKIEIIPVTATFEAYDLERAQEAVAL 655  
QY 664 FTSTNPRGLKTDVKDHYIDQVSNLVESLSDPFYLDKRELFELVYKAKQLHIERNM 719  
DB 656 FTNTNPRLKTVDVTDHYIDQVSNLVESLSDPFYLDKRELFELVYKAKQLHIERNM 711

RESULT 14

Q93NM5 PRELIMINARY; PRT; 1228 AA.  
ID Q93NM5  
AC Q93NM5;  
DT 01-DEC-2001 (TremBrel. 19, Created)  
DT 01-DEC-2001 (TremBrel. 19, Last sequence update)  
DT 01-MAR-2004 (TremBrel. 26, Last annotation update)  
DE CrylBa.  
GN Name=crylBa;

OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zhang J., Song F., Huang D.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF368257; AAK63251.1; -.  
DR HSSP; P07130; IDLC.  
DR GO; GO:0005102; P:receptor binding; IEA.  
DR GO; GO:0006952; P:defense response; IEA.  
DR GO; GO:0009405; P:pathogenesis; IEA.  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR008979; Gal\_bind\_Like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
SQ SEQUENCE 1228 AA; 139665 MW; E86D9842341FB439 CRC64;

Query Match 60.4%; Score 2269.5; DB 2; Length 1228;  
Best Local Similarity 62.6%; Pred. No. 7.7e-148;  
Matches 448; Conservative 80; Mismatches 163; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQINH-----EDCLKMSEYENVEPVFVSASTIQTGIGIAGKI 70  
DB 2 TSNRKNENEIINAVNSHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61  
QY 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130  
DB 62 LGVLGVPPAGQLASFSYFLVGLWPRGRDQWEIFLEHVEQLINQOITENARTALARLQ 121  
QY 131 LGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVOKLPSFAVSGEEVPLPIYA 190  
DB 122 LGDSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYA 181  
QY 191 QAAHLHLLLDASIFGKEMGLSSEISTFYNRQVERAGDYSDHCVKWYSTGLNLRGNTN 250  
DB 182 QAAHLHLLLDASIFGSEFGLTSQEIQRYYEYERQVTRDYSDYCVENYNTGLNLRGNTN 241  
QY 251 AESWVRVYQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVYDAITGVVHPHSFT 310  
DB 242 AASWVRVYQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVYDAITGVVHPHSFT 299  
QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYLSLSRWSNTQYVNMWGGHKLERTI 370  
DB 300 SMWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYLSLSRWSNTQYVNMWGGHKLERTI 359  
QY 371 GGTINISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLF--LTQPVNGVPRVDFHMKFV 428  
DB 360 GGLTSTHGTATNTSINPVTLPFTSRDVRVYTESLAGNLF--LTQPVNGVPRVDFHMKFV 416  
QY 429 THP-----IASDNFYPGYAGIGTQDSENELPPEATQPNYESYSHRISHIGLISASH 483  
DB 417 TNPQNISDRGTANYSQP--YESPGQLKDSLETPEPPERPEPPERPEPPERPEPPERPEPPER 475  
QY 484 VKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTGT 543  
DB 476 VNPVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTGT 535  
QY 544 FGDIRVNNPPPAQRYVRIRYASTDLOPHTSINGKAINQGNFSATNMNAGEDLDYKTFR 603  
DB 536 FGPIRVTVNGPLTQRYRIGFYASTVDFPFVSRGGTTVNNFRFLRTMNSGDELKYNFV 595  
QY 604 TVGFTTPFSLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTVYEAEDFEKAQKVTAL 663  
DB 596 RRAFTTPTFTQIQDIIRTSIQGLSGNGEVYIDKIEIIPVTATFEAYDLERAQEAVAL 655  
QY 664 FTSTNPRGLKTDVKDHYIDQVSNLVESLSDPFYLDKRELFELVYKAKQLHIERNM 719  
DB 656 FTNTNPRLKTVDVTDHYIDQVSNLVESLSDPFYLDKRELFELVYKAKQLHIERNM 711



**RESULT 15**

Q6PYW8	PRELIMINARY;	PRT;	849 AA.
1D	Q6PYW8		
2C	Q6PYW8;		
3D	05-JUL-2004 (TrEMBLrel. 27, Created)		
4D	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
5D	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
6D	CryIb type crystal protein (Fragment).		
7D	Bacillus thuringiensis (subsp. kurstaki).		
8D	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
9D	NCBI_TaxID=29339;		
10D	[1]		
11D	SEQUENCE FROM N.A.		
12D	RP		
13D	STRAIN=KI;		
14D	Li M.S., Choi J.Y., Roh J.Y., Shim H.J., Boo K.S., Je Y.H. ;		
15D	Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.		
16D	ENBL; AY570734; AAC93737.1; . . .		
17D	GO; GO:0005102; F:receptor binding; IEA.		
18D	GO; GO:0006952; P:defense response; IEA.		
19D	GO; GO:0009405; P:pathogenesis; IEA.		
20D	InterPro; IPR001178; Endotoxin.		
21D	InterPro; IPR005638; endotoxin_C.		
22D	InterPro; IPR005639; endotoxin_N.		
23D	InterPro; IPR008979; Gal bind like.		
24D	Pfam; PF031944; Endotoxin_C; 1.		
25D	Pfam; PF00555; Endotoxin_M; 1.		
26D	Pfam; PF03945; Endotoxin_N; 1.		
27D	NON TER	849	849
28D	SEQUENCE	849 AA;	95886 MW; FCB98495787CF763 CRC64;
29D	FT		

Query Match	58.4%	Score	2195.5	DB 2	Length	849			
Best Local Similarity	59.4%	Pred. No.	5.9e-143						
Matches	424	Conservative	106	Mismatches	171	Indels	13	Gaps	3

  

QY	13	SSNAKVDKISTDSLKN-----ETDLELQMINHEDCLKMSEYENVPFPVSASTIQIGIG	65
DB	7	NENEIINALSIPAVNSHSAQNLSTDARI-----EDSLCIAEGNNIDPFPVASIVQTGIN	61
QY	66	IAGKILGTIGVPFAGQVASYLSYFILGBELWPKGNQWEI FMEHVEEII NOKISTVARKAL	125
DB	62	IAGRIILGVLPFAGQIASPYSLFVGLBMLPRGDPWEIFLEHVBLQIRQQVTTERTDAL	121
QY	126	TDLKGGLDALAVYHDSLESWGNRRNNTRASVVKSQVIALELMFVQKLPSFAVSGEEVPL	185
DB	122	ARLQGLGNSFRAYQOOSLEDWLENRDDARTSVLYTQYIALELDFLNAMPLFAIRNQEVPL	181
QY	186	LPYIAQAANLHLLLRDASITPGKEWGLSSSEISTFFYNRQVERAGDYSDHCVKWYSTGLNN	245
DB	182	LMYIAQAANLHLLLRDASITFGSEFGTISOBIIQRYRYERQVEKTEYSYDCARWNTZGLNN	241
QY	246	LRGTNAESVRYNQPRRDMTLMWLDLVALPSPYDTOMYPIKTTAQLTRFVVYTDAGTVHP	305
DB	242	LRGTNAESWRYNQFRDDLTLGLVDLVALPSPYDTRVYPMNTSQAQLTRFYYTDPGRNA	301
QY	306	HPSTSTTYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQPMNMGGHL	365
DB	302	PSGFASNTWNNNAPSFAIEAAVIRPHLLDFPEQLTIFSVLSRWSTQTMNVAVGHL	361
QY	366	EFTIGTGLNISTOGSNTSINPVTLPSTRDVVYRTESLAGNLFLQTPVNGVPRVDFHW	425
DB	362	ESTIRGLSTSTHGNTSINPVTLPSTRDVVYRTESFAGINLLTTPVNGVPAWFENW	421
QY	426	KFVTHPIASDNFYYPGYAGITQLQDSENELPPEATQOPNYESYSHRLSHITGLISASHVK	485
DB	422	RNPLNSLRGSLLYTIGYTGVTQLQFDSETELPETTERPNYESSYSHRLSNIRLISGNTLR	481
QY	486	ALVYSWTHRSADRTNTEPNSITQIPLVKAENLSSGAAVRGPGFTGCDILRRNTNTGFG	545
DB	482	APVYSWTHRSADRTNLTSSSITQIPLVKSFNLNSGTSVVSGPGFTGCDIIRTNVNGSVL	541
QY	546	DIRVNIINPPFAQRYVRIRVASTTDLQFHTSINGKAINQGNFSANMARGEDLDYKTRTV	605

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542 542 SMLGNFNNTSLORYVRVRYAASQTMWLRVTVGGSTTFDQGFSTWMCANESLTSQSFRFA 601
Db

606 606 GETTFPSFLDVQSTTFIGAMNFSNGNEYYIIDRIEFVPVEVTEAYEYDFEKAQEKVTALFT 665
Qy

602 602 EFPVGISASGSG-TAGISISNNAQRQTHFDKIEFIPITATFEAYEYDLERAQVNALFT 660
Db

666 666 STNPRGLKTDVKDYYHIDQVSNLVLSLSDSEFYLDKRELFEIVVYAKOLHIERNM 719
Qy

661 661 NTNPRRLKTVTDYHIDEVSNLVACLSDSEFYLDKRELLEKVKYAKRLSDERNL 714
Db

Search completed: February 14, 2005, 20:40:24
Job time : 85.1112 secs

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Search completed: February 14, 2005, 20:40:24  
Job time : 85.1112 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:22:09 ; Search time 60.0945 Seconds  
(without alignments)  
3909.384 Million cell updates/sec

Title: US-10-019-823B-55  
Perfect score: 3760  
Sequence: 1 MKLKNQDKHQSFSNAKVDK.....KRELFEIVKYAKOLHIERN 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
1: /cgn2\_6/prodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/prodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/prodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
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15: /cgn2\_6/prodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
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18: /cgn2\_6/prodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3760	100.0	719	16	US-10-782-020-10 Sequence 10, Appl
2	3760	100.0	719	16	US-10-782-141-8 Sequence 8, Appl
3	3476.5	92.5	710	15	US-10-428-961-42 Sequence 42, Appl
4	2278.5	60.6	1228	16	US-10-809-953-10 Sequence 10, Appl
5	2265.5	60.3	1207	10	US-09-988-462-7 Sequence 7, Appl
6	2186.5	58.2	1227	15	US-10-428-961-63 Sequence 63, Appl
7	2171.5	57.8	1186	9	US-09-826-660-23 Sequence 23, Appl
8	2116	56.3	1228	15	US-10-428-961-38 Sequence 38, Appl
9	2116	56.3	1228	15	US-10-614-524-2 Sequence 2, Appl
10	1932.5	51.4	643	9	US-09-826-660-25 Sequence 25, Appl
11	1722.5	45.8	1167	14	US-10-089-678-1 Sequence 1, Appl
12	1681.5	44.7	653	15	US-10-428-961-6 Sequence 6, Appl
13	1670.5	44.4	1157	16	US-10-782-141-16 Sequence 16, Appl

14	1511	40.2	1206	13	US-10-032-717-2	Sequence 2, Appl
15	1511	40.2	1206	14	US-10-414-637-2	Sequence 2, Appl
16	1511	40.2	1206	15	US-10-606-320-2	Sequence 2, Appl
17	1495	39.8	1210	13	US-10-032-717-4	Sequence 4, Appl
18	1495	39.8	1210	14	US-10-414-637-4	Sequence 4, Appl
19	1495	39.8	1210	15	US-10-606-320-4	Sequence 4, Appl
20	1485.5	39.5	1156	14	US-10-093-285-72	Sequence 72, Appl
21	1485.5	39.5	1156	15	US-10-428-961-28	Sequence 28, Appl
22	1467	39.0	1155	9	US-09-756-643-2	Sequence 2, Appl
23	1467	39.0	1155	10	US-09-988-462-9	Sequence 9, Appl
24	1467	39.0	1155	15	US-10-136-998A-2	Sequence 2, Appl
25	1467	39.0	1177	14	US-10-035-060-6	Sequence 6, Appl
26	1467	39.0	1181	10	US-09-988-462-11	Sequence 11, Appl
27	1467	39.0	1181	10	US-09-988-462-13	Sequence 13, Appl
28	1467	39.0	1181	10	US-09-988-462-15	Sequence 15, Appl
29	1467	39.0	1181	10	US-09-988-462-17	Sequence 17, Appl
30	1467	39.0	1181	10	US-09-988-462-28	Sequence 28, Appl
31	1467	39.0	1181	15	US-10-136-998A-4	Sequence 4, Appl
32	1467	39.0	1181	15	US-10-136-998A-8	Sequence 8, Appl
33	1467	39.0	1181	15	US-10-136-998A-10	Sequence 10, Appl
34	1467	39.0	1181	15	US-10-136-998A-12	Sequence 12, Appl
35	1462	38.9	1177	14	US-10-035-060-2	Sequence 2, Appl
36	1460	38.8	1177	14	US-10-035-060-8	Sequence 8, Appl
37	1459	38.8	1177	14	US-10-102-469-24	Sequence 24, Appl
38	1443.5	38.4	1176	16	US-10-782-141-6	Sequence 6, Appl
39	1420.5	37.8	1176	11	US-09-837-961-2	Sequence 2, Appl
40	1420.5	37.8	1176	16	US-10-825-751-2	Sequence 2, Appl
41	1400	37.2	1167	15	US-10-428-961-40	Sequence 40, Appl
42	1379	36.7	1177	9	US-09-873-873-26	Sequence 26, Appl
43	1379	36.7	1177	10	US-09-916-956A-26	Sequence 26, Appl
44	1379	36.7	1177	10	US-09-997-914-26	Sequence 26, Appl
45	1379	36.7	1177	14	US-10-365-645-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1

US-10-782-020-10  
; Sequence 10, Application US/10782020  
; Publication No. US20040197916A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for its Use  
; FILE REFERENCE: 045600/274139  
; CURRENT APPLICATION NUMBER: US/10/782,020  
; PRIOR FILING DATE: 2004-02-19  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-020-10

Query Match 100.0%; Score 3760; DB 16; Length 719;  
Best Local Similarity 100.0%; Pred. No. 7, 2e-310;  
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLKKNQDKHQSFSNAKVDKISTDSLKNETDELQINHEDCLKMGEYENVEFVASTI	60
Db	1	MLKKNQDKHQSFSNAKVDKISTDSLKNETDELQINHEDCLKMGEYENVEFVASTI	60
QY	61	QTGIGTAGKILCTGLGVPPFAGQVASYLSFILGELWPKGKQWEIFMEHVEIINQKISTYA	120
Db	61	QTGIGTAGKILCTGLGVPPFAGQVASYLSFILGELWPKGKQWEIFMEHVEIINQKISTYA	120

121 RNKALTDLKGGLDALAVYHDSLESVWGNRNNTARSVVKSYIALELMFVKQLPSFAVSG 180  
121 RNKALTDLKGGLDALAVYHDSLESVWGNRNNTARSVVKSYIALELMFVKQLPSFAVSG 180  
181 BEVPLLPYIAQAANLHLLLDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCVKWS 240  
181 BEVPLLPYIAQAANLHLLLDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCVKWS 240  
241 TGLNLRGTNAESVWRVYNQFRDMLVLDLVALFPYSYDTQMPYIKTTAQLTREVTDAI 300  
241 TGLNLRGTNAESVWRVYNQFRDMLVLDLVALFPYSYDTQMPYIKTTAQLTREVTDAI 300  
301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
361 GGHKLEFRTIGTTLNISTOGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420  
361 GGHKLEFRTIGTTLNISTOGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420  
421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
541 TGTGDIRVNIAPPFAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
541 TGTGDIRVNIAPPFAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
601 TFRVTGFTTFFSFLDVQSTFTTGANFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660  
601 TFRVTGFTTFFSFLDVQSTFTTGANFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660  
661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 719  
661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 719

RESULT 2  
US-10-782-141-8  
; Sequence 8, Application US/10782141  
; Publication No. US20040197917A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274143  
; CURRENT APPLICATION NUMBER: US/10782,141  
; CURRENT FILING DATE: 2004-02-20  
; PRIOR APPLICATION NUMBER: 60/448,632  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-141-8

Query Match 100.0%; Score 3760; DB 16; Length 719;  
Best Local Similarity 100.0%; Pred. No. 7.2e-310;  
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MCLKNQKHQSFSSNAKVDKISTDLSKNETDIELQNIHEDCLKMSEYENVEPFSASTI 60  
121 RNKALTDLKGGLDALAVYHDSLESVWGNRNNTARSVVKSYIALELMFVKQLPSFAVSG 180  
121 RNKALTDLKGGLDALAVYHDSLESVWGNRNNTARSVVKSYIALELMFVKQLPSFAVSG 180  
181 BEVPLLPYIAQAANLHLLLDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCVKWS 240  
181 BEVPLLPYIAQAANLHLLLDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCVKWS 240  
241 TGLNLRGTNAESVWRVYNQFRDMLVLDLVALFPYSYDTQMPYIKTTAQLTREVTDAI 300  
241 TGLNLRGTNAESVWRVYNQFRDMLVLDLVALFPYSYDTQMPYIKTTAQLTREVTDAI 300  
301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
361 GGHKLEFRTIGTTLNISTOGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420  
361 GGHKLEFRTIGTTLNISTOGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420  
421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
541 TGTGDIRVNIAPPFAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
541 TGTGDIRVNIAPPFAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
601 TFRVTGFTTFFSFLDVQSTFTTGANFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660  
601 TFRVTGFTTFFSFLDVQSTFTTGANFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660  
661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 719  
661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 719

1 MCLKNQKHQSFSSNAKVDKISTDLSKNETDIELQNIHEDCLKMSEYENVEPFSASTI 60  
61 QTGIGACKILGTLPAGQVASYLSFILGELWPKGNQWEIIFWEHVEEIIINOKISTYA 120  
61 QTGIGACKILGTLPAGQVASYLSFILGELWPKGNQWEIIFWEHVEEIIINOKISTYA 120  
121 RNKALTDLKGGLDALAVYHDSLESVWGNRNNTARSVVKSYIALELMFVKQLPSFAVSG 180  
121 RNKALTDLKGGLDALAVYHDSLESVWGNRNNTARSVVKSYIALELMFVKQLPSFAVSG 180  
181 BEVPLLPYIAQAANLHLLLDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCVKWS 240  
181 BEVPLLPYIAQAANLHLLLDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCVKWS 240  
241 TGLNLRGTNAESVWRVYNQFRDMLVLDLVALFPYSYDTQMPYIKTTAQLTREVTDAI 300  
241 TGLNLRGTNAESVWRVYNQFRDMLVLDLVALFPYSYDTQMPYIKTTAQLTREVTDAI 300  
301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
361 GGHKLEFRTIGTTLNISTOGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420  
361 GGHKLEFRTIGTTLNISTOGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420  
421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
541 TGTGDIRVNIAPPFAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
541 TGTGDIRVNIAPPFAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
601 TFRVTGFTTFFSFLDVQSTFTTGANFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660  
601 TFRVTGFTTFFSFLDVQSTFTTGANFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660  
661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 719  
661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 719

RESULT 3  
US-10-428-961-42  
; Sequence 42, Application US/10428961  
; Publication No. US20030237111A1  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Rupaar, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)  
; FILE REFERENCE: MECO201--1  
; CURRENT APPLICATION NUMBER: US/10/428,961  
; CURRENT FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: 09/661,322  
; PRIOR FILING DATE: 2000-09-13  
; PRIOR APPLICATION NUMBER: 60/153,995  
; PRIOR FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 42  
; LENGTH: 710  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
; FEATURE:

```
; NAME/KEY: misc feature
; LOCATION: (200)..(200)
; OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid
US-10-428-961-42

Query Match      92.58; Score 3476.5; DB 15; Length 710;
Best Local Similarity 92.58; Pred. No. 8.3e-286;
Matches 665; Conservative 15; Mismatches 30; Indels 9; Gaps 1;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIEQLQNHEDCLKMEYENVEPVFASSTI 60
Db 1 MKSKQNMHQSLENNATVDKNFTGSLNNTNTELOQFNH-----EGIEFVSVSTI 51

Qy 61 QTGIGIAGKILGTGVPPAGQASLYSFILGELWPKGNQWEIFMEHVEEIIINOKISTVA 120
Db 52 QTGIGIAGKILGNLGVPPAGQASLYSFILGELWPKGQWEIFMEHVEEIIINOKISTVA 111

Qy 121 RNKALDALKGLDALAVYHDSLESWGNRNNTARSVKVSOYIALHLMFVKQLPSFAVSG 180
Db 112 RNKALADLKLGLDALAVYHDSLESWGNRNNTARSVKVSOYITLBMFVQSLPSFAVSG 171

Qy 181 EYVPLPIYAAQANLHLLLRDASIFGKEWGLSSSEISTEYNQVERAGDYSDHCKWYS 240
Db 172 EYVPLPIYAAQANLHLLLRDASIFGKEWGLSDSEISTEYNQSGKSEYSDHCKWYN 231

Qy 241 TGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPSTQYPIKTTAQLTREVTDAI 300
Db 232 TGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPSTQYPIKTTAQLTREVTDAI 291

Qy 301 GTVHPHPSFTTWNANNAPSAIEAAVVRNPHLLDLEQVITYLLSRWSNTQNMNW 360
Db 292 GTVHPHPSFTTWNANNAPSAIEAAVVRNPHLLDLEQVITYLLSRWSNTQNMNW 351

Qy 361 GGHKLFRITGLTNTSTQSTNTSINPVTLPFTSRDVRTESLAGNLFLTOPVNGVPR 420
Db 352 GGHKLFRITGLTNTSTQSTNTSINPVTLPFTSRDVRTESLAGNLFLTOPVNGVPR 411

Qy 421 VDPHMKFVTHPIASDNFFYPGYAGIGTQLQDSNELPPEATGPNYESYSHRLSHGLIS 480
Db 412 VDPHMKFVTHPIASDNFFYPGYAGIGTQLQDSNELPPEATGPNYESYSHRLSHGLIS 471

Qy 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDIIRTN 540
Db 472 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDIIRTN 531

Qy 541 TGTFGDIRVNINPPFAQRYVRIRYASTTDLOFHTSINGKAINQGNFSAATMNGEDLDYK 600
Db 532 TGTFGDIRVNINPPFAQRYVRIRYASTTDLOFHTSINGKAINQGNFSAATMNGEDLDYK 591

Qy 601 TFRVTGFTTTPFSFLDQSTFTTIGAMNPFSSGNEVYIDRIEFPVVEVTEAYEYDPEKAQEV 660
Db 592 TFRVTGFTTTPFSFLDQSTFTTIGAMNPFSSGNEVYIDRIEFPVVEVTEAYEYDPEKAQEV 651

Qy 661 TALFTSTNPRGLTKTDVKYHIDQVSNLVESLSDEFYLDKRELFETVVKAKQLHIERNM 719
Db 652 TALFTSTNPRGLTKTDVKYHIDQVSNLVESLSDEFYLDKRELFETVVKAKQLHIERNM 710

RESULT 4
US-10-809-953-10
; Sequence 10, Application US/10809953
; Publication No. US2004018125A1
; GENERAL INFORMATION:
; APPLICANT: Van Mellaert, Herman
; APPLICANT: Botterman, Johan
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Joos, Henk
; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTICIDAL PROTEINS
; FILE REFERENCE: 021565-078
; CURRENT APPLICATION NUMBER: US/10/809,953
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/09/661,016
```

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; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: PCT/EP90/00905
; PRIOR FILING DATE: 1990-05-30
; PRIOR APPLICATION NUMBER: GB 89401499.2
; PRIOR FILING DATE: 1989-05-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; US-10-809-953-10

Query Match      60.6%; Score 2278.5; DB 16; Length 1228;
Best Local Similarity 62.7%; Pred. No. 9.7e-184;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

Qy 23 TUSLKNETDIEQLQNH-----EDCLKMEYENVEPVFASSTIQTGIGIAGKI 70
Db 2 TSNRKNENIEINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVASTVQTGINIAGRI 61

Qy 71 LGTLGVPPAGQASLYSFILGELWPKGNQWEIFMEHVEEIIINOKISTVARNKALDCLKG 130
Db 62 LGVLGVPPAGQASLYSFILGELWPKGRQWEIFLEHVEQLINQQTENARNNTALARLOG 121

Qy 131 LGDALAVYHDSLESWGNRNNTARSVKVSOYIALHLMFVKQLPSFAVSGEYVPLPIYA 190
Db 122 LGDSPRAYQOSLEDWLENRDDARTSRVLHTQVIALELDPLNAMPLFAIRNOEVPPLMVA 181

Qy 191 QAAHLHLLLRDASIFGKEWGLSSSEISTEYNQVERAGDYSDHCKWYSTGLNLRGTN 250
Db 182 QAAHLHLLLRDASLYFSEFGLTQSIQRYERYQVERTRDSDYCVQEWYNTGLNLRGTN 241

Qy 251 ASWRYNQFRDMTLMVLDLVALFPSTQYPIKTTAQLTREVTDAITGVHPHPSFT 310
Db 242 ASWRYNQFRDMLTGLVLDLVALFPSTQYPIKTTAQLTREVTDAIGAT--GVNMA 239

Qy 311 STTWNNNAPSAIEAAVVRNPHLLDLEQVITYLLSRWSNTQNMNWGGHKLFRIT 370
Db 300 SMWYNNNAPSAIEAAVVRNPHLLDLEQVITYLLSRWSNTRHMTYWRGHTIQSRPI 359

Qy 371 GGTNLNSTQSTNTSINPVTLPFTSRDVRTESLAGNLFL--LTQPNVGVPRVDFHWKFV 428
Db 360 GGTNLNSTHGATNTSINPVTLPFTSRDVRTESLAGNLFL--LTQPNVGVPRVDFHWKFV 416

Qy 429 THP-----IASDNFFYPGYAGIGTQLQDSNELPPEATGPNYESYSHRLSHGLISASH 483
Db 417 THPQNSIDRGTYNSOP--YESPLQKQSELTLPPTETTERPNYESYSHRLSHGLISLQSR 475

Qy 484 VKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDIIRNTGT 543
Db 476 VNPVYVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDIIRNTGT 535

Qy 544 FDIRVNINPPFAQRYVRIRYASTTDLOFHTSINGKAINQGNFSAATMNGEDLDYK 603
Db 536 FDIRVNINPPFAQRYVRIRYASTTDLOFHTSINGKAINQGNFSAATMNGEDLDYK 595

Qy 604 TVGFTTTPFSFLDQSTFTTIGAMNPFSSGNEVYIDRIEFPVVEVTEAYEYDPEKAQEV 663
Db 596 RRAFTTTPFTQIDRIIRTSIQGLSGNEVYIDRIEFPVVEVTEAYEYDPEKAQEV 655

Qy 664 FTSTNPRGLTKTDVKYHIDQVSNLVESLSDEFYLDKRELFETVVKAKQLHIERNM 719
Db 656 FTNTNPRGLTKTDVKYHIDQVSNLVESLSDEFYLDKRELFETVVKAKQLHIERNM 711

RESULT 5
US-09-988-462-7
; Sequence 7, Application US/09988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Desai, Nalini M.
```

Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Launis, Karen L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Syngenta Biotechnology, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 09/988,462  
FILING DATE: 20-NO. US20030046726A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/547,422  
FILING DATE: 11-APR-2000  
APPLICATION NUMBER: US 08/459,504  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-188051  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Query Match 60.3%; Score 2265.5; DB 10; Length 1207;  
Best Local Similarity 64.3%; Pred. No. 1.2e-182;  
Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;

QY 40 EDCLMSYENVEPVSASTIQTGIGIAGKILGTLPVFPAGQVSLXSLFGLWPKGKN 99  
DB 10 EDSLCIAEGNIDFVSASTVQTGINIAGRLGVLPVFPAGQVSLXSLFGLWPKGRD 69  
QY 100 QWEIFMEHVEEIIINQKISTYARNKALTDKGLGDALAVYHDSLSWGNRNNTRARSVVK 159  
DB 70 QWEIFMEHVEEIIINQKISTYARNKALTDKGLGDALAVYHDSLSWGNRNNTRARSVVK 129  
QY 160 SQYALELMMFVKLPSPAVSGEEVPLPIYAQAANHLILLRDSIFKKEWGLSSSEIST 219  
DB 130 TQYTALEDLDFNAMFLFAIRNQEVPLLMVYAQAANHLILLRDSIFKKEWGLSSSEIST 189  
QY 220 FYNROVERAGDYSCHVCWKYSTGLNLRGTNAESWVRYNQFRDRLTMLVLDLVALFPSYD 279  
DB 190 YEROVERTRIDYSDYCVENYNTGLNLRGTNAESWVRYNQFRDRLTMLVLDLVALFPSYD 249  
QY 280 TQMPYIKTAQLTREYVTDAGTGVHPHPSFTSTTWNNNAPSFSAIEAAVVRNPHLLDFL 339

DB 250 TRTYPINTSAQLTREYVTDAGT--GVNWSMWNVNNNAPSFSAIEAAVVRNPHLLDFL 307  
QY 340 EQVTIYSLLSRWSTQYMNMMGKLEFRITGIGTLNISTOGSTNTSINPVTLPTSDVY 399  
DB 308 EQVTIYSLLSRWSTQYMNMMGKLEFRITGIGTLNISTOGSTNTSINPVTLPTSDVY 367  
QY 400 RTESLAGLNF--LTQPVNGVPRVDFHVKFVTHP-----IASDNFFYPGYAGIGTQDQS 452  
DB 368 RTESYAGVLLWGIYLEPIHGVPTVRNF---TNPQNISDRGTANYSP-YESPLQLKDS 423  
QY 453 ENELPPEATQPNVSYSHSLSHIGLISASHVVALVYSWTHRSADRNTTTPSITQPL 512  
DB 424 ETELPPETTERPNVSYSHSLSHIGLISASHVVALVYSWTHRSADRNTTTPSITQPL 483  
QY 513 VKAFNLSSGAUVRGPGCTGDIILRRNTGTFGDIRVINPNNPPAQRVVRIRVASTTDLQ 572  
DB 484 VKASELPQGTTVVRGPGCTGDIILRRNTGTFGDIRVINPNNPPAQRVVRIRVASTTDLQ 543  
QY 573 FHTSINGKAINQGNFSAFMNREGDLDYKTFRTVGTFTTFFSFLDQVQSTFTTCAMNFFSGNE 632  
DB 544 FFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRAFTTFTTQIQDIIRTSIQLSNGE 603  
QY 633 VYIDRIEFPVPEVYEAQYFKAQKVTALFTSTNPRGLKTDVKDHIQVSNLVESLS 692  
DB 604 VYIDKIEIIPVTATFEAYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACL 663  
QY 693 DEFVLDEKRELFELVKYAKOLHIERNM 719  
DB 664 DEFCLDEKRELEKVKYAKRLSDERNL 690

## RESULT 6

US-10-428-961-63  
; Sequence 63, Application US/10428961  
; Publication No. US2003023711A1  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Ruper, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
; FILE REFERENCE: MECO201--1  
; CURRENT APPLICATION NUMBER: US/10/428,961  
; CURRENT FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: 09/661,322  
; PRIOR FILING DATE: 2000-09-13  
; PRIOR APPLICATION NUMBER: 60/153,995  
; PRIOR FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 63  
; LENGTH: 1227  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-428-961-63

Query Match 58.2%; Score 2186.5; DB 15; Length 1227;  
Best Local Similarity 59.2%; Pred. No. 6.3e-176;  
Matches 423; Conservative 105; Mismatches 173; Indels 13; Gaps 3;

QY 13 SSNAKVDKISTDSIKN-----ETDELQINNHEDCLKMSYENVEPVFSASTIQTGIG 65  
DB 7 NENIINALSIPAVNSHSAQMNJSTDARI-----EDSLCAEGNIDFVSASTIQTGIG 61  
QY 66 IAGKILGTLPVFPAGQVSLXSLFGLWPKGKNQWEIFMEHVEEIIINQKISTYARNKAL 125  
DB 62 IAGRLGVLPVFPAGQVSLXSLFGLWPKGKNQWEIFMEHVEEIIINQKISTYARNKAL 121  
QY 126 TDLKGLGDALAVYHDSLSWGNRNNTRARSVVKSVIALELMMFVKLPSPAVSGEEVPL 185







<p> ; FILE REFERENCE: Q68821  ; CURRENT APPLICATION NUMBER: US/10/089,678  ; CURRENT FILING DATE: 2002-05-02  ; PRIOR APPLICATION NUMBER: JP 2000-236140  ; PRIOR FILING DATE: 2000-08-03  ; PRIOR APPLICATION NUMBER: PCT/JP01/06660  ; PRIOR FILING DATE: 2001-08-02  ; NUMBER OF SEQ ID NOS: 3  ; SOFTWARE: Patent in version 3.1  ; SEQ ID NO 1  ; LENGTH: 1167  ; TYPE: PRT  ; ORGANISM: Bacillus thuringiensis  ; US-10-089-678-1 </p>	<p> Query Match 45.8%; Score 1722.5; DB 14; Length 1167;  Best Local Similarity 47.9%; Pred. No. 1.4e-136;  Matches 361; Conservative 126; Mismatches 218; Indels 49; Gaps 12; </p>	
<p> ; QY 1 MKLKNDQKHQ---SFSSNAKVDKISTDSLKNETDIELONINHEHDCLEKMSYEVE-----NV 51  ; DB 1 MSPNNQNEIYLDASSSTVSVDNSVRYPLANDQTTLLQNNYKDYLRMSGEPNLPFGNP 60  ; QY 52 EPPVSASTIOTGIGIAGKILGTVGPAGQVASYLSYFELGELAPKKG-NOWEIFMEHVEE 110  ; DB 61 ETFISSSTVQTGIGIVGQVGLGALGVPFAGQIASYSPFVIGQLPSSVSVWEMIMKQVED 120  ; QY 111 INQKISTYARKKALTDLKGLGDALAVVYHDSLEWGNRNNTARSVVKQYIALELMFV 170  ; DB 121 LIDQKITVSVKYTAGLAGLQGLDGLDYQKSLKNWLENRNDTRARSVVVYQYIALELDV 180  ; QY 171 QKLPFAVSGBEVPLLPYIAQAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGD 230  ; DB 181 AKIPSAISGQEVPLLSVYAAQANLHLLLRDASIFGAENGFTPGCEISTFYDRQVTRTAQ 240  ; QY 231 YSDHCVKYKSTGLNNLRCTNAESVVRVNOFRDMTLMVLVDLVALFPYSYDTQMPYIKTTAQ 290  ; DB 241 YSDYCVKYNLTGDKLKGNTAASWLKYHQFERREMTLLVLDLVALFPNYDRTYPIETTAQ 300  ; QY 291 LTRREVYDAIGTVHPHPSTSTTWNNNAPSFAIEAAVVRNPHLLDLEQVITYSLLS- 349  ; DB 301 LTRREVYTDPIVFNRETSGGFCRWSLNSDISFSVESAVIRSPHLPDILSEIFYTTTRAG 360  ; QY 350 -RWSNTQTMNMGWGHKLEFRTIGTGLNISTQSTNTSINPVTLPFTSRDVRVYTESL-AGL 407  ; DB 361 LPLANNTEYLEYVWGHISIKYKTNASSALLERNYGITTSNKIKYDLANCKDIFQVRSGLADL 420  ; QY 408 NLFLTPQVNGVPRVDVFWKFTVTHPIASDNFYYPYAGIG-----TQLQDSE 453  ; DB 421 ANYYAAQ-VYGVYASVF-----TLDDKN---TGSGSVGGFTYSKPHTTMQVCTQNTNTI 469  ; QY 454 NELPPEATGQNYESYSHRLSHIGLIS-----ASHVKALVYSWTHRSADRTNTEPN 505  ; DB 470 DRIPPE--NEPLSGYSHRLSHITTSYFSKNAASSPARYGNLPVPAWTHRGADVTNTYS 527  ; QY 506 SITQIPLVKAFNLNSGAAVVRGPGFTGGDILRLRTNTGTGDIRVNIINPPFAQRVRI 565  ; DB 528 KITQIPVKAHTLVSGTTVIKPGPGFTGGNLLKRTSSGPLAYTSVSVKSPLSQRYRARI 587  ; QY 566 ASTTDLQHTTSINGKAINQGNFSAITMARGEDLDYKTRTPTVGTFTPPSFDFVQSTFTIGAW 625  ; DB 588 ASTTNLRLFVITISGTRIYSINVNKTMKGGDGLTENTFDLATIGTAFPTFSYSDSLTVGAD 647  ; QY 626 NPSSGNEVYIDRIEIPVPEVVEYEAEDPEKAQKVTAFTSTNPRGLKTDVKDVIDQVS 685  ; DB 648 SPASGGEVYDKFELIPVNATFEABEBDLVDVAKKAVNGLFTSKKD-ALQTSVTDTYQVNNAA 706  ; QY 686 NLVESLSDSEFVDEKRELFEIVKYAKQLHIERNM 719  ; DB 707 NLVECLSDLEYPNEKXLMWDVAKKRLVQARNL 740 </p>	<p> ; QY 13 SSNAKVDKISTDSLK-----ETDIELONINHEHDCLEKMSYENVPFVSASTIQTGIG 65  ; DB 7 NENEIINALSIPAVNSHAQMLNSTDARI-----EDSLCIAEGNIDPFVSASTVQTGIN 61  ; QY 66 IAGKILGTVGPAGQVASYLSYFELGELWPKGQKQWEIFMEHVEEIIINQKISTYARKAL 125  ; DB 62 IAGRILGVLGVPFAGQIASFYSLFVGLWPRGRDPWEIFLEHVQRLIRQQVTTENDRTAL 121  ; QY 126 TDLKGLGDALAVVYHDSLEWGNRNNTARSVVKQYIALELMFVQKLPFAVSGBEVPL 185  ; DB 122 ARLOGLGNSFRAYQOSLEWLENRNDATRSVLYTQYIALELDLFLNAMPFAIRNQEVPL 181  ; QY 186 LPIYAAQANLHLLLRDASIFGKEMGLSSSISTFYNRQVERAGDYSDHCVKWYSTGLNN 245  ; DB 182 LMVYAAQANLHLLLRDASLFSFSEGLTSQBIQRYERQVEKREYSYCARWYNTGLNN 241  ; QY 246 LGRTNAESVVRVNOFRDMTLMVLVDLVALFPYSYDTQMPYIKTTAQLTRREVYTDAGTVHP 305  ; DB 242 LGRTNAESVLRVNOFRDMLTGLVDLVALFPYSYDTRVYPNMNTSAQLTREIYTDPIGRNTA 301  ; QY 306 HPSFTSTTWNNNAPSFAIEAAVVRNPHLLDLEQVITYSLRWSNTQTMNMGWGHKL 365  ; DB 302 PGCFASTNWNFNNAAPSFAIEAAVVRNPHLLDLEQVITYSLRWSNTQTMNMGWGHKL 361  ; QY 366 EPRITGGLTNISTQSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTPQVNGVPRVDVFW 425  ; DB 362 ESRTIRGSLSTSTHGNNTSINPVTLPFTSRDVRVYTESLAGLNLFLTPQVNGVPRVDVFW 421  ; QY 426 KFVTHPIASDNFYYPYAGIGTQLQDSENLPEATGQNYESYSHRLSHIGLISASHVK 485  ; DB 422 RNPLNSLRGSLLYTIGYGVGTQFDSSETLPPTTERPNYESSYSHRLSNIRLISGNTLR 481  ; QY 486 ALVYSWTHRSADRTNTEPNSTIQTPLVKAFNLNSGAAVVRGPGFTGGDILRLRTNTCTFG 545  ; DB 482 APVYSWTHRSADRTNTEPNSTIQTPLVKAFNLNSGAAVVRGPGFTGGDILRLRTNTCTFG 541  ; QY 546 DIRVNIINPPFAQRVRIYASTTDLQHTTSINGKAINQGNFSAITMARGEDLDYKTRT 605  ; DB 542 SMLGNFNNTSLQRYVRVRYAASQTMVLRTVVGSTTFDQGFPTSMANESLTSQSFRFA 601  ; QY 606 GFTTTPSFDFVQSTFTIGAWNFSSGNEVYIDRIEIPVPEVVEY 648  ; DB 602 EPPVGISASGSGQ-TAGISISNAGRQTFHDKIEFIPITATLE 643 </p>	<p> ; QY 686 NLVESLSDSEFVDEKRELFEIVKYAKQLHIERNM 719  ; DB 707 NLVECLSDLEYPNEKXLMWDVAKKRLVQARNL 740 </p>
<p> ; PRIOR APPLICATION NUMBER: 09/178,252  ; PRIOR FILING DATE: 1998-10-23  ; PRIOR APPLICATION NUMBER: 60/065,215  ; PRIOR FILING DATE: 1997-11-12  ; PRIOR APPLICATION NUMBER: 60/076,445  ; PRIOR FILING DATE: 1998-03-02  ; NUMBER OF SEQ ID NOS: 27  ; SOFTWARE: Patent in Ver. 2.0  ; SEQ ID NO 25  ; LENGTH: 643  ; TYPE: PRT  ; ORGANISM: Artificial Sequence  ; FEATURE:  ; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene  ; US-09-826-660-25 </p>	<p> Query Match 51.4%; Score 1932.5; DB 9; Length 643;  Best Local Similarity 57.7%; Pred. No. 8.3e-155;  Matches 371; Conservative 100; Mismatches 159; Indels 13; Gaps 3; </p>	
<p> ; QY 13 SSNAKVDKISTDSLK-----ETDIELONINHEHDCLEKMSYENVPFVSASTIQTGIG 65  ; DB 7 NENEIINALSIPAVNSHAQMLNSTDARI-----EDSLCIAEGNIDPFVSASTVQTGIN 61  ; QY 66 IAGKILGTVGPAGQVASYLSYFELGELWPKGQKQWEIFMEHVEEIIINQKISTYARKAL 125  ; DB 62 IAGRILGVLGVPFAGQIASFYSLFVGLWPRGRDPWEIFLEHVQRLIRQQVTTENDRTAL 121  ; QY 126 TDLKGLGDALAVVYHDSLEWGNRNNTARSVVKQYIALELMFVQKLPFAVSGBEVPL 185  ; DB 122 ARLOGLGNSFRAYQOSLEWLENRNDATRSVLYTQYIALELDLFLNAMPFAIRNQEVPL 181  ; QY 186 LPIYAAQANLHLLLRDASIFGKEMGLSSSISTFYNRQVERAGDYSDHCVKWYSTGLNN 245  ; DB 182 LMVYAAQANLHLLLRDASLFSFSEGLTSQBIQRYERQVEKREYSYCARWYNTGLNN 241  ; QY 246 LGRTNAESVVRVNOFRDMTLMVLVDLVALFPYSYDTQMPYIKTTAQLTRREVYTDAGTVHP 305  ; DB 242 LGRTNAESVLRVNOFRDMLTGLVDLVALFPYSYDTRVYPNMNTSAQLTREIYTDPIGRNTA 301  ; QY 306 HPSFTSTTWNNNAPSFAIEAAVVRNPHLLDLEQVITYSLRWSNTQTMNMGWGHKL 365  ; DB 302 PGCFASTNWNFNNAAPSFAIEAAVVRNPHLLDLEQVITYSLRWSNTQTMNMGWGHKL 361  ; QY 366 EPRITGGLTNISTQSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTPQVNGVPRVDVFW 425  ; DB 362 ESRTIRGSLSTSTHGNNTSINPVTLPFTSRDVRVYTESLAGLNLFLTPQVNGVPRVDVFW 421  ; QY 426 KFVTHPIASDNFYYPYAGIGTQLQDSENLPEATGQNYESYSHRLSHIGLISASHVK 485  ; DB 422 RNPLNSLRGSLLYTIGYGVGTQFDSSETLPPTTERPNYESSYSHRLSNIRLISGNTLR 481  ; QY 486 ALVYSWTHRSADRTNTEPNSTIQTPLVKAFNLNSGAAVVRGPGFTGGDILRLRTNTCTFG 545  ; DB 482 APVYSWTHRSADRTNTEPNSTIQTPLVKAFNLNSGAAVVRGPGFTGGDILRLRTNTCTFG 541  ; QY 546 DIRVNIINPPFAQRVRIYASTTDLQHTTSINGKAINQGNFSAITMARGEDLDYKTRT 605  ; DB 542 SMLGNFNNTSLQRYVRVRYAASQTMVLRTVVGSTTFDQGFPTSMANESLTSQSFRFA 601  ; QY 606 GFTTTPSFDFVQSTFTIGAWNFSSGNEVYIDRIEIPVPEVVEY 648  ; DB 602 EPPVGISASGSGQ-TAGISISNAGRQTFHDKIEFIPITATLE 643 </p>	<p> ; QY 686 NLVESLSDSEFVDEKRELFEIVKYAKQLHIERNM 719  ; DB 707 NLVECLSDLEYPNEKXLMWDVAKKRLVQARNL 740 </p>	

## RESULT 12

Qy	647 YEAEYFEKAOE 658 :      ::  :
Dd	641 FEVEYDLERAOK 652
RESULT 13	
US-10-782-141-16	
; Sequence 16, Application US/10782141	
; Publication No. US20040197917A1	
; GENERAL INFORMATION:	
; APPLICANT: Carozzi, Nadine	
; APPLICANT: Hargiss, Tracy	
; APPLICANT: Kozziel, Michael G.	
; APPLICANT: Duck, Nicholas B.	
; APPLICANT: Carr, Brian	
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and	
; FILE REFERENCE: 045600/274143	
; CURRENT APPLICATION NUMBER: US/10/782,141	
; PRIOR FILING DATE: 2004-02-20	
; PRIOR APPLICATION NUMBER: 60/448,632	
; PRIORITY FILING DATE: 2003-02-20	
; NUMBER OF SEQ ID NOS: 23	
; SOFTWARE: FastSeq for Windows Version 4.0	
; SEQ ID NO 16	
; LENGTH: 1157	
; TYPE: PRT	
; ORGANISM: Bacillus thuringiensis	
US-10-782-141-16	
Query Match            44.4%;    Score 1670.5; DB 16; Length 1157;	
Best Local Similarity 49.1%; Pred. No. 3.6e-132;	
Matches 371; Conservative 98; Mismatches 230; Indels 57; Gaps 18;	
Qy	1 MLKNODKHOFSSNAKVDKISTDS---LXNETDIELOINHEDCCLKMSEYE-----N 50
Dd	1 MSPNNQNEVEIIDATPST-SVSDSNRYFPANEPDTALQNMVKYDKLKSGGENPELFGN 59
Qy	51 VEPFVSASTIQTGIGIAGKILGTLPVPFAQQVASLYSFILGELWP-KGRNQWEIFMEHVE 109
Dd	60 PETFISSTIQTGIGIVGRIGALGVPPAFASQIASFSFVIGQLWPSKSVDMGEIMERVE 119
Qy	110 EIINOKISTYARKALTDLKGLGDALAVYHDSLESWVGRENNTFRASVYKSVIALELMF 169
Dd	120 ELVDQKLEIKYVKDKALAEKLGKGNALDVQQSLEDWLENRNDARTSRVSNQFIADLNF 179
Qy	170 VQKLPSFVSGEBEVLPIYAQAANLHLILLRDASIFGKEWGLSSSEISTSFYNQRVERAG 229
Dd	180 VSSIPFVSGHEVLLAVYAQAUNLHLILLRDASIFGEWGTFPEISFYNQRVOLTA 239
Qy	230 DYSDDCKVYSTGLNNLRGNAESWVRYNQFRDMTAMVLDLVALFPSYDTQMYPKTITA 289
Dd	240 EYSDYCKWKYKIGLDKLGKTTSKSLNWYHQFREMTLLVLIDLVALFPNYDTHMPYIETTA 299
Qy	290 QLTREVTYDAIGTVHPHPFTST----TWNNNAPSFAEAARVNPHLLDFLEQVTIY 345
Dd	300 QLTRDYVTDPDIA----FNIVTSTGFCONPWSTHSIGLFVEVENNVIRPPHLDLTLSSVEIN 355
Qy	346 SLLSR----WSNTQYMNWMGGHKLEER----TIGETLNISTOGSNTNTSINPTLPTSTR 396
Dd	356 T--SRGGITLNDAYINYWSGHTLKYRPRTADSVITYANYGRITSEKNS-----FALEDR 408
Qy	397 DVYRTESLAGNLFLTPQVNGVPRVDHFHWKVTHTPIASNFY-----YPCYAGIGTOLQD 451
Dd	409 DIPEINSTVANLANYYQKAYGVPGSWFH--MVKRGTSTTAVLYSKYTKHTALQGC-TQVVE 465
Qy	452 SENELPPEATGONYESYSHRLSHI-----GLLSASHVAALVYSWTHRSADRNTTIE 503
Dd	466 SSDEIPDLRT-VPVASSYSHRLSHITSHGSFKNG--SAYGSPFVFVWTHTSADLNTTIY 522
Qy	504 PNSITQIPLVKAFNLSSGAAVVRGPQGTGGDILLRRNTTGTFGDIRVINPINPPAQRYRVRI 563

Db 523 SDKITQIPAVKGMVLYGSSVQPGFTGGDIKRTNPISILGTFATVNGSLSORVRRI 582  
Qy 564 RYASTDQLQFHTSINGKAINQGNFSATMNRGEDLDYKTRTGVTFPPFSLDQSTFTIG 623  
Db 583 RYASTDDEF-TLYGLDTIEKRNFKTMDNGASLTVETPKFASFIITDFQFRETQKILLS 641  
Qy 624 ANPSSGNEVYIDRIEFPVVEVYEAEDFEKAQEKVLTALFTSTNPRGLKTDVKYDHIQ 683  
Db 642 MGDFSSGQVEYIDRIEFPVDETYEAQDLAAKAVNALFTNTKD-GLRPGVTDYVNO 700  
Qy 684 VSNLVSLSDBEFLDEKRELFEIVKAKOLHIERNM 719  
Db 701 AANLVECLSDDLYPNEKELLFDVAREAKRLSGARNL 736

RESULT 14  
US-10-032-717-2  
; Sequence 2, Application US/10032717  
; Publication No. US20020151709A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With  
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/032,717  
; CURRENT FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 2001-10-23  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1206  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-032-717-2

Query Match 40.2%; Score 1511; DB 13; Length 1206;  
Best Local Similarity 44.3%; Pred. No. 1.3e-118;  
Matches 337; Conservative 130; Mismatches 229; Indels 64; Gaps 22;

Qy 1 MKLNQDKHQSFSNAKVVKISTDS----LKNETDIELQNHEDCLKM-----SEYE-N 50  
Db 1 MSPNNQNEYIIDATPST-SVNSDSNRYPPFANEPTNALQNDYKYLKMSAGNASYPGS 59

Qy 51 VEPFVSA-STIQIGIAGKILGTLPVFPAGQVASYLSFILGELWPKG-KNQEWFMEHV 108  
Db 60 PEVLVSQDAAKAAIDIVGKLSGLGVPFVGPVIVSLYTQILIDILWPSGKSWEIFMEQV 119

Qy 109 EELINQKISTYARNKALTDLKGLDALAVYHDSLESWGNRNTRARSVVKSYIALELM 168  
Db 120 EELINQKIAEYARNKALSELEGNNYQLYLTALAEENPNPNSGSRALDRVNRFEILDLSL 179

Qy 169 FVOKLPSPFVSGBEVPLPIYAQANLHLLLRDASIFGKEWGLSSSEISTFYNNROVERA 228  
Db 180 FTQYMFSPRVNTEVPPLTVYMAANLHLLLRDASIFGKEWGSWTITINYYDROKMLT 239

Qy 229 GDYSDHCVKWYSTGLANLRGTNAESWYRNQFRDMLVLDLVALFPSPDYDTQYPIKT 288  
Db 240 AYSDDHCVKWYETGLAKIKGTSAKQWVDYVQFRREMTLAVLDVVALFPFNYDTRTYMETK 299

Qy 289 AQLTREYVTDAGTVHPHPSFTSTTWNNAAPSAIEAAVNRNPHLLDPLEQVITYSL 348  
Db 300 AQLTREYVTDPLGAVNVS-----SIGSWY-DKAPSGFVIESSVIRPPHVFYDITGLTYTQS 355

Qy 349 SRWSNTQYMNMGWGHKLEFRITIGTLNISTQGSTNTSINPV-TLPPTSRDVRVETESLAGL 407  
Db 356 RSISSARYIRHWAGHQISYHVRSGSLNQMYGTQNQLHSTSTFDFTNTYDIYKTLSDAV 415

Qy 408 NLFLTOP-----VNGVPRVDLFWKFWTHFIASDN---FYYPGAGIGTQLODSENELPPE 459  
Db 416 LLDIVVPGYTYIFGMEVEF---FMVNQNLNTRKTKYNPVSQDLIASTRDSELELPEE 472  
Qy 460 ATGQPNYESYSHRLSHIGLISAS-HVKAL--VYSWTHRSADRTNTIEPNSITQIPLVKAP 516  
Db 473 TSDQPNYESYSHRLCHITSIPATGTTGLVPFVSWTHRSADLNNITYSKITQIPAVKCM 532  
Qy 517 NLSSGAAVVRGPGFTGGDILR-RTWGTGFDI---RVNINPPFAQRYRIRYASTTDLQ 572  
Db 533 DNLPPFVVPVKGPGHTGGDLLQYNRSTGSGVTFLARYGLALEKAGKYRVLRYATDADIV 592  
Qy 573 FHTSINGKAINQGNFSATMNRGEDLDYKTR-----TVGFTTPPSFL-----DVQST 619  
Db 593 LH--VNDAAQI---QMPKTMNPGEDLTSKTFKVADAITTLNLTATDSSLAKHNLGDPNST 647  
Qy 620 FTIGAWNPFSSGNEVYIDRIEFPVVEVYEAEDFEKAQEKVLTALFTSTNPRGLKTDVKDY 679  
Db 648 LS-----GIVVVDRIEFPVDETYEAQDLAAKAVNALFTNTKD-GLRPGVTDY 697

Qy 680 HIDQVSNLVSLSDBEFLDEKRELFEIVKAKOLHIERNM 719  
Db 698 EVNQAANLVECLSDDLYPNEKELLFDVAREAKRLSEARNL 737

RESULT 15  
US-10-414-637-2  
; Sequence 2, Application US/10414637  
; Publication No. US20030177528A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With  
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/414,637  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: US/10/032,717  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/242,838  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1206  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-414-637-2

Query Match 40.2%; Score 1511; DB 14; Length 1206;  
Best Local Similarity 44.3%; Pred. No. 1.3e-118;  
Matches 337; Conservative 130; Mismatches 229; Indels 64; Gaps 22;

Qy 1 MKLNQDKHQSFSNAKVVKISTDS----LKNETDIELQNHEDCLKM-----SEYE-N 50  
Db 1 MSPNNQNEYIIDATPST-SVNSDSNRYPPFANEPTNALQNDYKYLKMSAGNASYPGS 59

Qy 51 VEPFVSA-STIQIGIAGKILGTLPVFPAGQVASYLSFILGELWPKG-KNQEWFMEHV 108  
Db 60 PEVLVSQDAAKAAIDIVGKLSGLGVPFVGPVIVSLYTQILIDILWPSGKSWEIFMEQV 119

Qy 109 EELINQKISTYARNKALTDLKGLDALAVYHDSLESWGNRNTRARSVVKSYIALELM 168  
Db 120 EELINQKIAEYARNKALSELEGNNYQLYLTALAEENPNPNSGSRALDRVNRFEILDLSL 179

Qy 169 FVOKLPSPFVSGBEVPLPIYAQANLHLLLRDASIFGKEWGLSSSEISTFYNNROVERA 228  
Db 180 FTQYMFSPRVNTEVPPLTVYMAANLHLLLRDASIFGKEWGSWTITINYYDROKMLT 239



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:24:54 ; Search time 22.3302 Seconds  
(without alignments)  
2403.590 Million cell updates/sec

Title: US-10-019-823B-55  
Perfect score: 3760  
Sequence: 1 MKLKNQKHQSPSSNAKVDK.....KELFEIVKYAKQLHIERM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2.6/prodata/1/iaa/5A COMB.pep.\*  
2: /cgn2.6/prodata/1/iaa/5B COMB.pep.\*  
3: /cgn2.6/prodata/1/iaa/6A COMB.pep.\*  
4: /cgn2.6/prodata/1/iaa/6B COMB.pep.\*  
5: /cgn2.6/prodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2.6/prodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3756	99.9	719	3	US-08-286-870A-8
2	3476.5	92.5	710	4	US-09-661-322A-42
3	3398	90.4	648	3	US-08-286-870A-4
4	3377	89.8	719	2	US-09-003-217-2
5	3372	89.7	719	3	US-09-218-942-2
6	2804	74.6	535	3	US-08-286-870A-6
7	2446.5	65.1	1229	1	US-08-100-709-4
8	2446.5	65.1	1229	1	US-08-176-865-4
9	2446.5	65.1	1229	1	US-08-474-038-4
10	2446.5	65.1	1229	2	US-08-779-046-4
11	2446.5	65.1	1229	1	US-08-881-340-4
12	2344.5	62.4	488	1	US-08-448-170-10
13	2344.5	62.4	488	3	US-08-961-803-10
14	2265.5	60.3	1207	1	US-07-951-715A-7
15	2265.5	60.3	1207	2	US-08-459-448A-7
16	2265.5	60.3	1207	3	US-08-459-595A-7
17	2265.5	60.3	1207	3	US-08-459-504B-7
18	2265.5	60.3	1207	3	US-08-459-444-7
19	2265.5	60.3	1207	3	US-09-053-549-8
20	2265.5	60.3	1207	3	US-09-547-422-7
21	2265.5	60.3	1207	4	US-09-988-462-7
22	2264.5	60.2	1227	3	US-09-053-549-2
23	2195.5	58.4	1227	1	US-08-448-170-8
24	2195.5	58.4	1227	1	US-08-961-803-9
25	2186.5	58.2	1227	4	US-09-661-322A-63
26	2171.5	57.8	1186	3	US-09-178-252-23
27	2171.5	57.8	1186	4	US-09-826-660-23

28	2116	56.3	1228	4	US-09-661-322A-38	Sequence 38, Appl
29	1932.5	51.4	643	3	US-09-178-252-25	Sequence 25, Appl
30	1932.5	51.4	643	4	US-09-826-660-25	Sequence 25, Appl
31	1900	50.5	380	5	PCT-US91-02560-4	Sequence 4, Appl
32	1681.5	44.7	653	4	US-09-661-322A-6	Sequence 6, Appl
33	1670.5	44.4	1157	1	US-07-876-280-30	Sequence 30, Appl
34	1670.5	44.4	1157	1	US-07-812-180A-2	Sequence 2, Appl
35	1670.5	44.4	1157	3	US-07-941-650A-2	Sequence 2, Appl
36	1670.5	44.4	1157	3	US-08-315-468-2	Sequence 2, Appl
37	1507.5	40.1	1176	1	US-08-257-999-2	Sequence 5, Appl
38	1492	39.7	1157	2	US-08-532-547-5	Sequence 5, Appl
39	1492	39.7	1157	2	US-08-379-656B-5	Sequence 5, Appl
40	1492	39.7	1157	3	US-08-455-838-5	Sequence 5, Appl
41	1492	39.7	1157	3	US-09-019-809-5	Sequence 5, Appl
42	1492	39.7	1157	4	US-09-471-177-5	Sequence 5, Appl
43	1492	39.7	1157	4	US-09-220-806-5	Sequence 5, Appl
44	1486.5	39.5	1169	1	US-08-315-468-4	Sequence 4, Appl
45	1485.5	39.5	1156	3	US-09-002-285-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1  
US-08-286-870A-8  
; Sequence 8, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PAUL N. KOKULIS  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 70608/220720  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-286-870A-8

Query Match 99.9%; Score 3756; DB 3; Length 719;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 718; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60  
D b 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60

QY 61 Q T G I G A G K I L G T L G V P F A G O V A S L Y S F I L G E L W P K G K N O W E I F M E H V E I I N Q K I S T Y A 120  
D b 61 Q T G I G A G K I L G T L G V P F A G O V A S L Y S F I L G E L W P K G K N O W E I F M E H V E I I N Q K I S T Y A 120

QY 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
D b 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180

QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q R V E R A G D Y S D H C V K W Y S 240  
D b 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q R V E R A G D Y S D H C V K W Y S 240

QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P P S Y D T Q M Y P I K T T A O L T R E V Y T D A I 300  
D b 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P P S Y D T Q M Y P I K T T A O L T R E V Y T D A I 300

QY 301 G T V H P H P S F T S T T W Y N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y N M W 360  
D b 301 G T V H P H P S F T S T T W Y N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y N M W 360

QY 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420  
D b 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420

QY 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
D b 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480

QY 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R T N 540  
D b 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R T N 540

QY 541 T G T F G D I R V N I N P P P A Q R Y R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
D b 541 T G T F G D I R V N I N P P P A Q R Y R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600

QY 601 T F R T V G F T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E V 660  
D b 601 T F R T V G F T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E V 660

QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719  
D b 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719

RESULT 2  
US-09-661-322A-42  
; Sequence 42, Application US/09661322A  
; Patent No. 6593293  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Ruper, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo  
; FILE REFERENCE: MECO201  
; CURRENT APPLICATION NUMBER: US/09/661,322A  
; CURRENT FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 42  
; LENGTH: 710  
; TYPE: PRT

ORGANISM: Bacillus thuringiensis  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (200)-(200)  
OTHER INFORMATION: No. 6593293-Coding  
US-09-661-322A-42

Query Match 92.5%; Score 3476.5; DB 4; Length 710;  
Best Local Similarity 92.5%; Pred. No. 5.5e-303;  
Matches 665; Conservative 15; Mismatches 30; Indels 9; Gaps 1;

QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60  
D b 1 M K S K N Q M H Q S L S N N A T V D K N F T G S L E N N T N T E L Q N F N H -----E G I E F F V S V S T I 51

QY 61 Q T G I G A G K I L G T L G V P F A G O V A S L Y S F I L G E L W P K G K N O W E I F M E H V E I I N Q K I S T Y A 120  
D b 52 Q T G I G A G K I L G T L G V P F A G O V A S L Y S F I L G E L W P K G K N O W E I F M E H V E I I N Q K I S T Y A 111

QY 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
D b 112 R N K A L A D L K G L G D A L A V Y H E S L E S W I E N R N N T R T R S V K S Q Y I T L E L M F V Q S L P S F A V S G 171

QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q R V E R A G D Y S D H C V K W Y S 240  
D b 172 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q R S G K S E Y S D H C V K W Y N 231

QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P P S Y D T Q M Y P I K T T A O L T R E V Y T D A I 300  
D b 232 T G L N R L M G N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A O L T R E V Y T D A I 291

QY 301 G T V H P H P S F T S T T W Y N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y N M W 360  
D b 292 G T V H P H P S F T S T T W Y N N A P S F S T I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y N M W 351

QY 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420  
D b 352 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 411

QY 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
D b 412 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 471

QY 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R T N 540  
D b 472 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R K N 531

QY 541 T G T F G D I R V N I N P P P A Q R Y R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
D b 532 T G T F G D I R V N I N P P P A Q R Y R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 591

QY 601 T F R T V G F T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E V 660  
D b 592 T F R T V G F T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E V 651

QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719  
D b 652 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D F Y L D E K R E L F E I V K Y A K Q L H I E R N M 710

RESULT 3  
US-08-286-870A-4  
; Sequence 4, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENN, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DAREY & CUSHMAN

ADDRESSEE: Intellectual Property Group of  
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/286,870A  
FILING DATE: 05-AUG-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520228  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8910624.9  
FILING DATE: 09-MAY-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: PAUL N. KOKULIS  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 70608/220720  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 648 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-286-870A-4

Query Match 90.4%; Score 3398; DB 3; Length 648;  
Best Local Similarity 100.0%; Pred. No. 5.3e-296;  
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 M L K N Q D K H Q S F S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60  
1 M L K N Q D K H Q S F S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60  
61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G N Q W E I F M E H V E I I N K I S T Y A 120  
61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G N Q W E I F M E H V E I I N K I S T Y A 120  
121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
181 E E V P L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q R V E R A G D Y S D H C V K W Y S 240  
181 E E V P L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q R V E R A G D Y S D H C V K W Y S 240  
241 T G L N N L R G T W A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A O L T R E V Y T D A I 300  
241 T G L N N L R G T W A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A O L T R E V Y T D A I 300  
301 G T V H P H S F S T T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
301 G T V H P H S F S T T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
361 G G H K L E P R T T G G T L N I S T Q S T N T S I N P V T L P T S R D V Y T E S L A G L N L F L T O P V N G V P R 420  
361 G G H K L E P R T T G G T L N I S T Q S T N T S I N P V T L P T S R D V Y T E S L A G L N L F L T O P V N G V P R 420  
421 V D F H W K V P T H I A S D N F Y P C Y A G I G T Q L O D S N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 480  
421 V D F H W K V P T H I A S D N F Y P C Y A G I G T Q L O D S N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 480

481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L W A F N L S S G A A V V R G P G T G D I L R R T N 540  
481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L W A F N L S S G A A V V R G P G T G D I L R R T N 540  
541 T G T F G D I R V N I N P P F A Q R V R V R I A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
541 T G T F G D I R V N I N P P F A Q R V R V R I A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
601 T P R T V G T T P F S F L D V Q S T T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E 648  
601 T P R T V G T T P F S F L D V Q S T T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E 648

RESULT 4  
US-09-003-217-2  
Sequence 2, Application US/09003217  
Patent No. 5986177  
GENERAL INFORMATION:  
APPLICANT: Osman, Yehia A.  
APPLICANT: Madkour, Magdy A.  
APPLICANT: Bulla, Lee A.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH  
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)  
STREET: 3605 Glenwood Ave. Suite 310  
CITY: Raleigh  
STATE: NC  
COUNTRY: US  
ZIP: 27622  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/003,217  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: 5718-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919 420 2202  
TELEFAX: 919 881 3175  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 719 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-003-217-2

Query Match 89.8%; Score 3377; DB 2; Length 719;  
Best Local Similarity 89.8%; Pred. No. 4.8e-294;  
Matches 646; Conservative 33; Mismatches 40; Indels 0; Gaps 0;

1 M L K N Q D K H Q S F S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60  
1 M L K N Q D K H Q S F S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60  
61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G N Q W E I F M E H V E I I N K I S T Y A 120  
61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G N Q W E I F M E H V E I I N K I S T Y A 120  
121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
181 E E V P L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q R V E R A G D Y S D H C V K W Y S 240  
181 E E V P L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q R V E R A G D Y S D H C V K W Y S 240

181 EVELLPPIAQAANLHLLLRDASIFKNGGLSASEISTFYNRQVTRDYSHVCVKWN 240  
 241 TGLNLRGTNAESWVRNQRRDMLVLDLVALFSDYDQMYPIKTTAQLTREVYTDI 300  
 241 TGLNLRATNGQSWVRNQFRKDIEMVLDLVRFFSYDVLVPIKTTSQLTREVYTDI 300  
 301 GTVHPHPSFTSTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVTTIYSLGRWSNTQYNNMW 360  
 301 GTVDPNQALRSTTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVTTIYSLGRWSNTQYNNMW 360  
 361 GGHKLEFRTIGTINISSTQGSTNTSINPVTLPFTSRDVTETESLAGNLFLTOPVNGVPR 420  
 361 GGHRLSPRIGALNTSTQGSTNTSINPVTLPFTSRDVTETESLAGNLFLTOPVNGVPR 420  
 421 VDFHWKFTPLIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 421 VDFHWKFTPLIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGTGGDILRTN 540  
 481 GSHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGTGGDILRTK 540  
 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLKY 600  
 541 SGTFGHIRVNIINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLKY 600  
 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSNGNEVIIDRIEFVPEVTEAEYDFEKAQEKV 660  
 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSNGNEVIIDRIEFVPEVTEAEYDFEKAQEKV 660  
 661 TALFTSTNPRGLTKDVKYHIDQVSNLVSLSDELYLDEKRELFEIVYAKQIHERNM 719  
 661 TALFTSTNPRGLTKDVKYHIDQVSNLVSLSDELYLDEKRELFEIVYAKQIHERNM 719

RESULT 5  
 US-09-218-942-2  
 ; Sequence 2, Application US/09218942  
 ; Patent No. 6232439  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Osman, Yehia  
 ; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum  
 ; TITLE OF INVENTION: Activity  
 ; FILE REFERENCE: C7V11  
 ; CURRENT APPLICATION NUMBER: US/09/218,942  
 ; CURRENT FILING DATE: 1998-12-22  
 ; EARLIER APPLICATION NUMBER: 60/035,361  
 ; EARLIER FILING DATE: 1997-01-10  
 ; EARLIER APPLICATION NUMBER: 09/003,217  
 ; EARLIER FILING DATE: 1998-01-06  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-09-218-942-2

Query Match 89.7%; Score 3372; DB 3; Length 719;  
 Best Local Similarity 89.8%; Pred. No. 1.3e-293;  
 Matches 646; Conservative 33; Mismatches 40; Indels 0; Gaps 0;

QY 1 MKLKNQDQKHQSFSSNAKVDKISTDLSKNETDIELONINHEDECLMSEYENVEPVGSASTI 60  
 DB 1 MKLKNPDKHQTLSSNAKVDKIATDLSKNETDIELKNMNNEDYLRMSHESIDPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELPKGNOWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELPKGNOWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGDLALVYHDSLESVWGNRNTRARSVKSQYIALELMFVQKLPSPAVSG 180  
 DB 121 RNKALTDLKGDLALVYHDSLESVWGNRNTRARSVKSQYIALELMFVQKLPSPAVSG 180

RESULT 6  
 US-08-286-870A-6  
 ; Sequence 6, Application US/08286870A  
 ; Patent No. 6063605  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ELY, S  
 ; APPLICANT: TAILOR, RH  
 ; APPLICANT: TIPPETT, JM  
 ; APPLICANT: BLENK, RG  
 ; TITLE OF INVENTION: BACTERIAL GENES  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
 ; ADDRESSEE: Intellectual Property Group of  
 ; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
 ; STREET: 1100 New York Avenue, N.W.  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005-3918  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/286,870A  
 ; FILING DATE: 05-AUG-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/520228  
 ; FILING DATE: 09-MAY-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 8910624.9  
 ; FILING DATE: 09-MAY-1989

181 EVELLPPIAQAANLHLLLRDASIFKNGGLSASEISTFYNRQVTRDYSHVCVKWN 240  
 181 EVELLPPIAQAANLHLLLRDASIFKNGGLSASEISTFYNRQVTRDYSHVCVKWN 240  
 241 TGLNLRGTNAESWVRNQRRDMLVLDLVALFSDYDQMYPIKTTAQLTREVYTDI 300  
 241 TGLNLRATNGQSWVRNQFRKDIEMVLDLVRFFSYDVLVPIKTTSQLTREVYTDI 300  
 301 GTVHPHPSFTSTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVTTIYSLGRWSNTQYNNMW 360  
 301 GTVDPNQALRSTTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVTTIYSLGRWSNTQYNNMW 360  
 361 GGHKLEFRTIGTINISSTQGSTNTSINPVTLPFTSRDVTETESLAGNLFLTOPVNGVPR 420  
 361 GGHRLSPRIGALNTSTQGSTNTSINPVTLPFTSRDVTETESLAGNLFLTOPVNGVPR 420  
 421 VDFHWKFTPLIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 421 VDFHWKFTPLIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGTGGDILRTN 540  
 481 GSHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGTGGDILRTK 540  
 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLKY 600  
 541 SGTFGHIRVNIINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLKY 600  
 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSNGNEVIIDRIEFVPEVTEAEYDFEKAQEKV 660  
 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSNGNEVIIDRIEFVPEVTEAEYDFEKAQEKV 660  
 661 TALFTSTNPRGLTKDVKYHIDQVSNLVSLSDELYLDEKRELFEIVYAKQIHERNM 719  
 661 TALFTSTNPRGLTKDVKYHIDQVSNLVSLSDELYLDEKRELFEIVYAKQIHERNM 719



```
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-870A-6

Query Match 74.6%; Score 2804; DB 3; Length 535;
Best Local Similarity 100.0%; Pred. No. 8.1e-243; Indels 0; Gaps 0;
Matches 535; Conservative 0; Mismatches 0;

QY 1 MKLNQDKHQSPSSNAKVDKISTDSLKNETDIBLQININHEDECLKMSYENVEPVSASTI 60
DB 1 MKLNQDKHQSPSSNAKVDKISTDSLKNETDIBLQININHEDECLKMSYENVEPVSASTI 60
QY 61 QTGIGTAGKILGTVPPFAGQVSLYSFILGELWPKGKQWEIFMEHVEEIIINOKISTYA 120
DB 61 QTGIGTAGKILGTVPPFAGQVSLYSFILGELWPKGKQWEIFMEHVEEIIINOKISTYA 120
QY 121 RNKALTDLKGDLGALAVYHDSLSWGNRNTRARSVVKSOYIALELMFVKLPSPFAVSG 180
DB 121 RNKALTDLKGDLGALAVYHDSLSWGNRNTRARSVVKSOYIALELMFVKLPSPFAVSG 180
QY 181 EYVPLPIYAAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWYS 240
DB 181 EYVPLPIYAAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWYS 240
QY 241 TGLNLRGTVNAESWRYNQPRDMLVLDLVALPFSYDTQMPYIKTTAQLTREVTDAI 300
DB 241 TGLNLRGTVNAESWRYNQPRDMLVLDLVALPFSYDTQMPYIKTTAQLTREVTDAI 300
QY 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVTIYSLLSWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVTIYSLLSWSNTQYNNMW 360
QY 361 GGHKLEFRITGGTINISTQGSTNTSINPVLPTFSRDVYRTESLAGLNFLTPQVNGVPR 420
DB 361 GGHKLEFRITGGTINISTQGSTNTSINPVLPTFSRDVYRTESLAGLNFLTPQVNGVPR 420
QY 421 VDFHWKFTVPIASDNFYYPGYAGIGTQLODSNELPPEATQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFTVPIASDNFYYPGYAGIGTQLODSNELPPEATQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDI 535
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDI 535

RESULT 7
US-08-100-709-4
; Sequence 4, Application US/08100709
; Patent No. 532687
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryE4 AND cryE5
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
```

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; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,709
; FILING DATE: 19930729
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-100-709-4

Query Match 65.1%; Score 2446.5; DB 1; Length 1229;
Best Local Similarity 65.6%; Pred. No. 3.9e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIBLQ-NINHEDECLKMSYENVEPVSASTIQTGIGTAGKI 70
DB 7 NENEIINALSIPTVSNPSTQMNLSDPARIEDSLCAEVNNDIPFVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPFAGQVSLYSFILGELWPKGKQWEIFMEHVEEIIINOKISTYARNKALTDLKG 130
DB 67 LGVLGVPPFAGQVSLYSFILGELWPKGKQWEIFMEHVEEIIINOKISTYARNKALTDLKG 136
QY 131 LGDALAVYHDSLSWGNRNTRARSVVKSOYIALELMFVKLPSPFAVSGEYVPLPIYA 190
DB 127 LGRGYSYQOALETMDLNDNRDARSIIILERYVALELDITAIPLFRIRNEEYVPLMWYA 186
QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWYSTGLNLRGTVN 250
DB 187 QAANLHLLLRDASIFGSEWGMASDVNOYQOIRYTBESYHNCVQWYNTGLNLRGTVN 246
QY 251 AESSWRYNQPRDMLVLDLVALPFSYDTQMPYIKTTAQLTREVTDAIGTVHPHPSFT 310
DB 247 AESSWRYNQPRDMLVLDLVALPFSYDTQMPYIKTTAQLTREVTDAIGTVHPHPSFT 306
QY 311 STTWYNNAPSAIEAAVVRNPHLLDLEQVTIYSLLSWSNTQYNNMWGGHKLFRITI 370
DB 307 STTWYNNAPSAIEAAVVRNPHLLDLEQVTIYSLLSWSNTQYNNMWGGHKLFRITI 366
QY 371 GGTLANISTQGST-NTSINPVLPTFSRDVYRTESLAGLNFLTPQVNGVPRVDFHMKFTV 429
DB 367 GGTLANISTQGST-NTSINPVLPTFSRDVYRTESLAGLNFLTPQVNGVPRVDFHMKFTV 422
QY 430 HPIASDNFYYPG-----YAGIGTQLODSNELPPEATQPNYESYSHRLSHIGLISAS 482
DB 423 --INPQNIYERGATTVSYQYQVIGIQLFDSSETLPETTERPNYESYSHRLSHIGLIS 480
QY 483 HVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRTNTG 542
DB 481 TRAPVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRTNTG 540
QY 543 TFGDIRVNIINPPAQRYRIRYASTTDIQHTSINGKAINQGNFSAITWNRGBDLKYKTF 602
DB 541 TFGDIRVNIINPPAQRYRIRYASTTDIQHTSINGKAINQGNFSAITWNRGBDLKYKTF 600
QY 603 RTVGFTTTPSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEAKQEKVTA 662
DB 601 RTAGFTTTPFNFLNAQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEAKQEKVTA 659
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; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1229 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-474-038-4

Query Match 65.1%; Score 2446.5; DB 1; Length 1229;  
Best Local Similarity 65.6%; Pred. No. 3.9e-210;  
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;  
  
QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMKSEYENVEPVASSTIQTGIGIAGKI 70  
DB 7 NENEIINALSIPVSNPSTOMNLSDPARIEDSLCVAEVNIDPFVSASTVQTGINIAGRI 66  
  
QY 71 LGTLGVPPFAQVASLYSFLIGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALDCLKG 130  
DB 67 LGVLGVPPFAQVASFYSFLVGLWPSGRDPWEIFLHVQELIRQQVTENTRTAIARLEG 126  
  
QY 131 LGDALAVYHDSLSWGNRNNTARSVVKSOYIALELMFVQKLPSPAVSGEEVPLPIYA 190  
DB 127 LGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLRIRNEEVPLLMVYA 186  
  
QY 191 QAAHLHLLLRDASIFGKESGLSSSEISTFYNNRQVERAGDYSCHVKWYSTGLNNLRGTN 250  
DB 187 QAAHLHLLLRDASLFGSEWGMASDVNQYQEIYRTEYSNHCYQWYNTGLNNLRGTN 246  
  
QY 251 AESWRYNQPRDRTMLVLDLVALFPSYDTOMYPIKTTAQLTREVTDAIGTVHPHPSFT 310  
DB 247 AESWRYNQPRDLTLGLVDLVALFPSYDTRTPINTSAQLTREIYTDPIGRNAPSFGA 306  
  
QY 311 STTWYNNNAPSFAIEAAVVRNPHLLDPLEQVITYSLLRSWNTQYNNMMWGHKLEFRTI 370  
DB 307 STWYNNNAPSFAIEAIPRPHLLDPLEQVITYSASSRSWSTQHMWYVGHRLNRPRI 366  
  
QY 371 GGTLLNTSTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVPRVDFHMKFVT 429  
DB 367 GGTLLNTSTQGLTNTSINPVTLPFTSRDVRVYTESNAGTNILFTTPVNGVPMWAFNPF 422  
  
QY 430 HPIASDNFYYPG-----YAGIGTQLQDSNELPPEATQPNVESYSHRSLHIGLISAS 482  
DB 423 --INPQNIYERGATTSYQPGVGIQLFDSSETLPPTETTERPNYESYSHRSLHIGLI 480  
  
QY 483 HVKALVYSWTHRSADRTNTIENSIITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTG 542  
DB 481 TLRAPIVSWTHRSADRTNTIGPNRIQIPLVKALNLSHGVTVVGGPGFTGGDILRRNTG 540  
  
QY 543 TFGDIRVNPAPQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMWRGSDLDYKTF 602  
DB 541 TFGDIRLNVPLSQRYRVRIRYASTTDLQFTRINGTNNIGNFSRTMWRGNLBYRSF 600  
  
QY 603 RTVGFTTPPSFLDVQSTFTIGANNFSSGNEVYIDRIEFVPEVITYAEYDFEKAQEKVTA 662  
DB 601 RTAGFTSTPFLNQAQSTFTLGAQSPN-QEYVIDRVEFVPAEVTFEAYDLERAQKAVNA 659  
  
QY 663 LFTSTNPRGLKTDVQYHIDQVNLVESLSDEFYLDKRELFBIYKAKOLHIERNM 719  
DB 660 LFTSTNPRRLKTDVTHIDQVSNMVAQLSDEFCLDEKRELFKVKYAKELSDERNL 716

## RESULT 10

US-08-779-046-4  
; Sequence 4, Application US/08779046  
; Patent No. 5854053  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yuting  
; APPLICANT: Jan, Christine S.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: RACILLUS THURINGIENSIS CYTET4 AND CYTETS  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
; ADDRESSEE: Nadel  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/779,046  
; FILING DATE: 06-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/100,709  
; FILING DATE: 29-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Egolf, Christopher  
; REGISTRATION NUMBER: 27633  
; REFERENCE/DOCKET NUMBER: 7205-49  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-757-1590  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1229 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-779-046-4

Query Match 65.1%; Score 2446.5; DB 2; Length 1229;  
Best Local Similarity 65.6%; Pred. No. 3.9e-210;  
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;  
  
QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMKSEYENVEPVASSTIQTGIGIAGKI 70  
DB 7 NENEIINALSIPVSNPSTOMNLSDPARIEDSLCVAEVNIDPFVSASTVQTGINIAGRI 66  
  
QY 71 LGTLGVPPFAQVASLYSFLIGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALDCLKG 130  
DB 67 LGVLGVPPFAQVASFYSFLVGLWPSGRDPWEIFLHVQELIRQQVTENTRTAIARLEG 126  
  
QY 131 LGDALAVYHDSLSWGNRNNTARSVVKSOYIALELMFVQKLPSPAVSGEEVPLPIYA 190  
DB 127 LGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLRIRNEEVPLLMVYA 186  
  
QY 191 QAAHLHLLLRDASIFGKESGLSSSEISTFYNNRQVERAGDYSCHVKWYSTGLNNLRGTN 250  
DB 187 QAAHLHLLLRDASLFGSEWGMASDVNQYQEIYRTEYSNHCYQWYNTGLNNLRGTN 246  
  
QY 251 AESWRYNQPRDRTMLVLDLVALFPSYDTOMYPIKTTAQLTREVTDAIGTVHPHPSFT 310  
DB 247 AESWRYNQPRDLTLGLVDLVALFPSYDTRTPINTSAQLTREIYTDPIGRNAPSFGA 306  
  
QY 311 STTWYNNNAPSFAIEAAVVRNPHLLDPLEQVITYSLLRSWNTQYNNMMWGHKLEFRTI 370  
DB 307 STWYNNNAPSFAIEAIPRPHLLDPLEQVITYSASSRSWSTQHMWYVGHRLNRPRI 366  
  
QY 371 GGTLLNTSTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVPRVDFHMKFVT 429  
DB 367 GGTLLNTSTQGLTNTSINPVTLPFTSRDVRVYTESNAGTNILFTTPVNGVPMWAFNPF 422  
  
QY 430 HPIASDNFYYPG-----YAGIGTQLQDSNELPPEATQPNYESYSHRSLHIGLISAS 482  
DB 423 --INPQNIYERGATTSYQPGVGIQLFDSSETLPPTETTERPNYESYSHRSLHIGLI 480  
  
QY 483 HVKALVYSWTHRSADRTNTIENSIITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTG 542  
DB 481 TLRAPIVSWTHRSADRTNTIGPNRIQIPLVKALNLSHGVTVVGGPGFTGGDILRRNTG 540

QY 543 TFGDIRVNINPPFAQRVVRIRVASTTDLQFHTSINGKAINOGNFATMNRGEDIYKTF 602  
 Db 541 TFGDIRVNINPVSQRVVRIRVASTTDLQFTRINGTNNIGNFSRTNWRGDNLEYSF 600  
 QY 603 RTVGFTTFFSFLDVQSTFTICAMNFSNGNEVYIDRIEFVPEVVEVYAEYDFEKAQKVTA 662  
 Db 601 RTAGSIPFNLNAQSTFTLGAQFSN-QEYVIDRVEFVPAEVTFEAYDLERAQKAVNA 659  
 QY 663 LFTSTNPRGLKTDVVDHIDVSNVLSDEFLVDEKRELFEVYAKOLHTERNM 719  
 Db 660 LFTSTNPRRLKTDVTDYHIDQVSNVACLSEFLVDEKRELFEVYAKOLHTERNM 716

RESULT 11  
 US-08-881-340-4  
 ; Sequence 4, Application US/08881340  
 ; Patent No. 5942658  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yiping  
 ; APPLICANT: Jany, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESSEE: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/881,340  
 ; FILING DATE: 24-JUN-1997  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/100,709  
 ; FILING DATE: 29-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egolf, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1229 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-881-340-4

Query Match 65.1%; Score 2446.5; DB 2; Length 1229;  
 Best Local Similarity 65.6%; Pred. No. 3.9e-210;  
 Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECKWSEYENVEPVASITQTGTGIAGKI 70  
 Db 7 NENETINALSTPTVSNPSTONWLSFDARIEDSLCAEVNNDIDPVASITVQTGINIAGRI 66  
 QY 71 LGTLGVFPAGVASLYSPILGELMPKGNOWEIFMVEHVEILINQKISTYARNKALTDLKG 130  
 Db 67 LGVLGVFPAGLASFYSLVGLMPSGRDPWEIFLEHVEQLIROQVNTENTNTAARLEG 126  
 QY 131 LGDALAVYHDSLESVWGNRNTARSVVKSVYALALEMFMVQKLPSPFAVSGEVPLLPIYA 190

Db 127 LGRGYRSVQQALETWLDNRDARSRSIILERYVALELDITTAIPLFRIRNEEVEPLLMVYA 186  
 QY 191 QAAHLHLLLRDASIFKKEWGLSSEISTFYNQVERAGDYSCHVKWYSTGLNNLRGTN 250  
 Db 187 QAAHLHLLLRDASLFGSEWGMASSDVNYQYQSOIRYETEEYSHCHVQWYNTGLNNLRGTN 246  
 QY 251 AESWVRYNQPRDMDLWLDLVALFPSPYDQMPYKTKTAQLTRREYVYDAITGVVHPHSFT 310  
 Db 247 AESWLRYNQFRDITLGVLDLVALFPSPYDQMPYKTKTAQLTRREYVYDAITGVVHPHSFT 306  
 QY 311 STTWYNNAPSAEIAEAVVRNPHLLDPLFEOVTIYLSRWSNTQYNNMGHGLKLEPRTI 370  
 Db 307 STTWYNNAPSAEIAEAVVRNPHLLDPLFEOVTIYLSRWSNTQYNNMGHGLKLEPRTI 366  
 QY 371 GGTINISTQGST-NTSINPVTLPFTSRDVRVYTESLAGINLFLTPQVANGVPRVDFPHWKEVT 429  
 Db 367 GGTINISTQGST-NTSINPVTLPFTSRDVRVYTESLAGINLFLTPQVANGVPRVDFPHWKEVT 422  
 QY 430 HPIASDNFYFG-----YAGIGTQLODSENEIPPEATGQPNYVESYSHRSLHSHIGLISAS 482  
 Db 423 --INPQNIYERGATTYSQPYQGVIGLFDSETLPPETTERPNERNYESYSHRSLHSHIGLIGN 480  
 QY 483 HVKALVYSWTHRSADRTWTIEPNSITQIPLKAFNLSGAAVVRGPGFTGGDILRRRTWG 542  
 Db 481 TLRAPIYVSWTHRSADRTWTIEPNSITQIPLKAFNLSGAAVVRGPGFTGGDILRRRTWG 540  
 QY 543 TFGDIRVNINPPFAQRVVRIRVASTTDLQFHTSINGKAINOGNFATMNRGEDIYKTF 602  
 Db 541 TFGDIRVNINPVSQRVVRIRVASTTDLQFTRINGTNNIGNFSRTNWRGDNLEYSF 600  
 QY 603 RTVGFTTFFSFLDVQSTFTICAMNFSNGNEVYIDRIEFVPEVVEVYAEYDFEKAQKVTA 662  
 Db 601 RTAGSIPFNLNAQSTFTLGAQFSN-QEYVIDRVEFVPAEVTFEAYDLERAQKAVNA 659  
 QY 663 LFTSTNPRGLKTDVVDHIDVSNVLSDEFLVDEKRELFEVYAKOLHTERNM 719  
 Db 660 LFTSTNPRRLKTDVTDYHIDQVSNVACLSEFLVDEKRELFEVYAKOLHTERNM 716

RESULT 12  
 US-08-448-170-10  
 ; Sequence 10, Application US/08448170  
 ; Patent No. 5723758  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Payne, Jewel  
 ; APPLICANT: Cummings, David A.  
 ; APPLICANT: Cannon, Raymond J.C.  
 ; APPLICANT: Narva, Kenneth E.  
 ; APPLICANT: Stelman, Steve  
 ; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted  
 ; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes  
 ; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: David R. Saliwanchik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/448,170  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/069,902  
 ; FILING DATE: 01-JUNE-1993  
 ; CLASSIFICATION: 424

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/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/759,247
/ FILING DATE: 13-SEPT-1991
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Salivanchik, David R.
/ REGISTRATION NUMBER: 31,794
/ REFERENCE/DOCKET NUMBER: M/S 102D.C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (904) 375-8100
/ TELEFAX: (904) 372-5800
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 488 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-448-170-10

Query Match      62.4%; Score 2344.5; DB 1; Length 488;
Best Local Similarity 89.7%; Pred. No. 1.2e-201;
Matches 446; Conservative 13; Mismatches 29; Indels 9; Gaps 1;

QY 1 MKLNQDQKQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFSASTI 60
DB 1 MRSKNQNMHQSLSNATVDKNFTGSLNNTNTELQNFH-----EGIEPFSVSTI 51

QY 61 QTGIGTAGKILGTLPVFPAGQVASYSLFGELMPPKQKQWEIFMEHVBEIINOKISTYA 120
DB 52 QTGIGTAGKILGTLPVFPAGQVASYSLFGELMPPKQKQWEIFMEHVBEIINOKISTYA 111

QY 121 RNKALTDLKGDLGDAVYHDSLESVGNRNTRARSVVKSOYIALELMFVKLPSPAVSG 180
DB 112 RNKALADLKGDLGDAVYHDSLESVGNRNTRARSVVKSOYIALELMFVKLPSPAVSG 171

QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSCHCKWYS 240
DB 172 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSCHCKWYN 231

QY 241 TGLNLRGTNAESVWRYNQFRDMLTMDLVALPFSYDTQMPYIKTTAQLTREVYTDI 300
DB 232 TGLNLRGMNAESVWRYNQFRDMLTMDLVALPFSYDTQMPYIKTTAQLTREVYTDI 291

QY 301 GTVHPHPSFTSTTWNNAAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW 360
DB 292 GTVHPHPSFTSTTWNNAAPSFSTIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW 351

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/ RESULT 13
/ US-08-961-803-10
/ Sequence 10, Application US/08961803
/ Patent No. 6150589
/ GENERAL INFORMATION:
/ APPLICANT: Payne, Jewel
/ APPLICANT: Cummings, David A.
/ APPLICANT: Cannon, Raymond J.C.
/ APPLICANT: Narva, Kenneth E.
/ APPLICANT: Stelman, Steve
/ TITLE OF INVENTION: No. 6150589e1 Bacillus thuringiensis Isolate Denoted
/ TITLE OF INVENTION: B.t. PSI58C2, Active Against Lepidopteran Pests, and Genes
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/
/ TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Jay M. Sanders
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: Florida
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/961,803
/ FILING DATE: 31-OCT-1997
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/069,902
/ FILING DATE: 01-JUNE-1993
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/759,247
/ FILING DATE: 13-SEPT-1991
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/448,170
/ FILING DATE: 23-MAY-1995
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sanders, Jay M.
/ REGISTRATION NUMBER: 39,355
/ REFERENCE/DOCKET NUMBER: M/S 102DCD1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (352) 375-8100
/ TELEFAX: (352) 372-5800
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 488 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-961-803-10

Query Match      62.4%; Score 2344.5; DB 3; Length 488;
Best Local Similarity 89.7%; Pred. No. 1.2e-201;
Matches 446; Conservative 13; Mismatches 29; Indels 9; Gaps 1;

QY 1 MKLNQDQKQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFSASTI 60
DB 1 MRSKNQNMHQSLSNATVDKNFTGSLNNTNTELQNFH-----EGIEPFSVSTI 51

QY 61 QTGIGTAGKILGTLPVFPAGQVASYSLFGELMPPKQKQWEIFMEHVBEIINOKISTYA 120
DB 52 QTGIGTAGKILGTLPVFPAGQVASYSLFGELMPPKQKQWEIFMEHVBEIINOKISTYA 111

QY 121 RNKALTDLKGDLGDAVYHDSLESVGNRNTRARSVVKSOYIALELMFVKLPSPAVSG 180
DB 112 RNKALADLKGDLGDAVYHDSLESVGNRNTRARSVVKSOYIALELMFVKLPSPAVSG 171

QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSCHCKWYS 240
DB 172 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSCHCKWYN 231

QY 241 TGLNLRGTNAESVWRYNQFRDMLTMDLVALPFSYDTQMPYIKTTAQLTREVYTDI 300
DB 232 TGLNLRGMNAESVWRYNQFRDMLTMDLVALPFSYDTQMPYIKTTAQLTREVYTDI 291

QY 301 GTVHPHPSFTSTTWNNAAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW 360
DB 292 GTVHPHPSFTSTTWNNAAPSFSTIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW 351
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Best Local Similarity 64.3%; Pred. No. 6.7e-194;  
Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;  
QY 40 EDCKMSEYENPFVPSASTIQTGIGIAGKILCTGLVPPAGQVASYLSFILGELMPKGN 99  
Db 10 EDSICIAEGNNIDPFVSASIVQIGINAGILGLVGPFPAGQLASFYSFLVGLMPPGRD 69  
QY 100 QWEIFMHEVBEIINOKISTYARNKALTDLKGLGDALAVHDSLESWVGNRNNTAASVVK 159  
Db 70 QWEIFLHEVQLINQITENARTALARLOGLGDSFRAYQQSLEDWLENDDARTSVLY 129  
QY 160 SQYTALELMFVKLPSPAVSGEVEPLPIVAQAANLHLLLRDASIFGKEWGLSSSEIST 219  
Db 130 TQYTALELDFLNAEPLFAIRNQEVPLMVAQAANLHLLLRDASLFGSEGLTSQEIQR 189  
QY 220 FYNQVERAGDYSCHCVKWTSTGLNNLRGTNAESWVRYNOFRDMTLMVLDAVALPSPYD 279  
Db 190 YEROVERTRDYSYCVWEYNTGLNSLRGTNAASWVRYNQFRDLTLGLVLDLVALPSPYD 249  
QY 280 TOMYPIKTAQLTREVTYDAIGTVHPHPSFTSTTWNNAAPSFSAIEAAVVRNPHLLDFL 339  
Db 250 TRTYPINTSAQLTREVTYDAIGAT - GVNMAWNNNNNAPSFSAIEAAAIRSHLLDFL 307  
QY 340 EQVTIYSLLSRWNTQVNMWGHKLEPRITIGTINISTOGSTNTSINPVTLPSTSDVY 399  
Db 308 EQLTIFSASSRWSNRHTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPSTSDVY 367  
QY 400 RTESLAGLNLFP - LTQPVNGVRVDVFWKFWTHP - - - - - IASDNFYVGYAGIGTQLODS 452  
Db 368 RTESYAGVLLGMYLEPIHGVPTVRFNF - - - - - TNPONISDRGTANYSQP - YESPGLQLXDS 423  
QY 453 ENELPPEATQPNYESYSHLSHIGLISASHVKALVYSWTHRSADRTNTIPNSITQIPL 512  
Db 424 ETELPPEPPERPNYESYSHLSHIGLILQSRVNVVYVSWTHRSADRTNTIPNRTQIPM 483  
QY 513 VKAFNLSSGAAVVRGPGFTGGDILARTNTGTGDIRVNVINPPFAORVRYRYASTTDLQ 572  
Db 484 VKASELPQGTTVVRGPGFTGGDILARTNTGTGDIRVNVINPPFAORVRYRYASTTDLQ 543  
QY 573 FHTSINGKAINQGNFSATWNRGDLDTKFTVGTTPFSDVDQVSTFTIGAMNFSNGNE 632  
Db 544 FFVSRGTTVNNPFRFLRTWNSGDELKYNFVRAFTTPTFTQIDIRTSIQLSGNGE 603  
QY 633 VYIDRIEFVPEVTEAEYDFFKAEKQVATLFTSTNPRGLKTDVKDYHIDVSNLVESLS 692  
Db 604 VYIDKIEIIPVATFPAEYDLERAQAVNALEFNTNPNRLKTDVTDYHIDVSNLVACLS 663  
QY 693 DEFYLDKRELFEIVKAKOLHIERNM 719  
Db 664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 15  
US-08-459-448A-7  
; Sequence 7, Application US/08459448A  
; Patent No. 5859336  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.

QY 361 GGKLEPRTTGGTNTSTOGSTNTSINPVTLPFTSDVYRTESLAGLNLFLTPQVNGVR 420  
Db 352 GGKLEPRTTGGTNTSTOGSTNTSINPVTLPFTSDVYRTESLAGLNLFLTPQVNGVR 411  
QY 421 VDFHKKFVTHPIASDNFYFGYAGIGTQLODSNELPPPEATQPNYESYSHLSHIGLIS 480  
Db 412 VDFHKKFVTHPIASDNFYFGYAGIGTQLODSNELPPPEATQPNYESYSHLSHIGLIS 471  
QY 481 ASHKALVYSWTHRSAD 497  
Db 472 ASHKALVYSWTHRSAD 488

RESULT 14  
US-07-951-715A-7  
; Sequence 7, Application US/07951715A  
; Patent No. 5625136  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/951,715A  
; FILING DATE: 25-SEP-1992  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sprull, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: S-18805/A/COC 1577/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8615  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1207 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-951-715A-7  
Query Match 60.3%; Score 2265.5; DB 1; Length 1207;

;; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
;; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
;; NUMBER OF SEQUENCES: 94  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: No. 5859136artis Corporation  
;; STREET: Patent & Trademark Dept., 520 White Plains  
;; STREET: Rd., POB 2005  
;; CITY: Tarrytown  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10591-9005  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/459,448A  
;; FILING DATE: 02-JUN-1995  
;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/951,715  
;; FILING DATE: 25-SEP-1992  
;; PRIOR APPLICATION DATA: US 07/772,027  
;; APPLICATION NUMBER: 04-OCT-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Pace, Gary M.  
;; REGISTRATION NUMBER: 40403  
;; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (919)541-8582  
;; TELEFAX: (919)541-8689  
;; INFORMATION FOR SEQ ID NO: 7:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1207 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-459-448A-7

Query Match 60.3%; Score 2265.5; DB 2; Length 1207;  
Best Local Similarity 64.3%; Pred. No. 6.7e-194;  
Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;  
Qy 40 EDCLKMSEYENVPFVSASTIQTGIGIAGKILGTGVPPFAGQVASYSLFGLBWPCKGN 99  
Db 10 EDSLCIAEGNNIDPFVSASTVQGINAGILGVLPFAGQVASYSLFGLBWPCKGN 69  
Qy 100 QWEIFMEHVEEIIINQKISTYARNKALTDKGLDALAVYHDSLSWVGNRNNTARSVVK 159  
Db 70 QWEIFLEHVEQLINQITENARNALTALRLQGLGDSFRAYQQSLEDWLENRDDARTSVLY 129  
Qy 160 SQVIALELMFVKLPSPAVSGEEVPLPIYQAANLHLLLRDASFGKWLSSSEIST 219  
Db 130 TQVIALELDFLNAMPLFAIRNQEVPLLMVYQAANLHLLLRDASLFGSEFGLTSQEIQR 189  
Qy 220 FYNROVERAGDYSDHCVKWTSTGLNLRGNNAESWRYNQFRDMLTMDLVALPSSYD 279  
Db 190 YYERQVERTDYSDYCVENWTNGLNSLRGNNAESWRYNQFRDMLTMDLVALPSSYD 249  
Qy 280 TOMYPKTKTAQLTREVTDAIGTVHPPSPSTSTTWNNNAPSFSAIEAAVVRNPHLLDFL 339  
Db 250 TRTYPINTSAQLTREVTDAIGAT--GVNMAWMNNYNNAPSFSAIEAAVVRNPHLLDFL 307  
Qy 340 EQWTIYSLLSRWSTQYNNWGGHLEPRIGGTINISTOGSTNTSINPVTLPTSRDVI 399  
Db 308 EQLTIFASRWSTNTRHTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLFASRDVI 367  
Qy 400 RTESLAGLNLFF--LTQPVNGVPRVDHKKFWTHP-----IASDNFYYPGAGIGTOLQDS 452  
Db 368 RTESYAGVLLWGIYLEPIHGVTFRVNF---TNPQNISDRGTANYSQP--YESFGLQLKDS 423

Qy 453 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSTQIPL 512  
Db 424 ETELPPETTEREPNYESYSHRLSHIGLILQSRVNVVPYVSWTHRSADRTNTIGPNRITQIPM 483  
Qy 513 VKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNIWPPPAQRYRVRIYASTTDLQ 572  
Db 484 VRASELPQSTTVVRGPGFTGGDILRRNTGGFGPIRVTVNGPLTQRYRIGFRVASTVDFD 543  
Qy 573 PHTSINGKAINQGNFSATMNRGDELDDYKTFRTVGTTPFPESFLDVQSTFTTIGAMNFSGNE 632  
Db 544 FVVSRGTTVNNFRFLRTWNSGDELKYGNFVRRATFTTPTFTQIQDIIRTSIQGLSGNGE 603  
Qy 633 VYIDRIEFVPEVTEYAEYDFEKAQEKVTALTSTNPRGLKTDVVDYHIDQVSNLVESLS 692  
Db 604 VYIDKIEIIPVTATFEAEYDLERAQEAVALFTNTNPRELKTVDVTDYHIDQVSNLVACLS 663  
Qy 693 DRFYLDKRELFEIVKYAKOLHIERNM 719  
Db 664 DEFCLDEKRELLEKVKYAKRLSDERNL 690  
Search completed: February 14, 2005, 20:59:01  
Job time : 25.3302 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2005, 20:20:21 ; Search time 98.3514 Seconds  
(without alignments)  
2827.419 Million cell updates/sec

Title: US-10-019-823B-55

Perfect score: 3760

Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KRELFEIVKAKQLHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3760	100.0	719	4	AAB66908	Insectici
2	3760	100.0	719	6	AAE36272	B. thurin
3	3760	100.0	719	8	ADR89421	Adr89421 cryIIa. 1
4	3756	99.9	719	4	AAB66910	Insectici
5	3755	99.9	719	6	AAE36274	B. thurin
6	3751	99.8	719	4	AAU02095	Bacillus
7	3749	99.7	719	4	AAB66911	Insectici
8	3749	99.7	719	6	AAE36275	B. thurin
9	3743	99.5	719	4	AAB66909	Insectici
10	3743	99.5	719	6	AAE36273	B. thurin
11	3739	99.4	719	2	AAE36271	B. thurin
12	3728.5	99.2	718	6	AAE36271	B. thurin
13	3722.5	99.0	718	4	AAB66907	Insectici
14	3551	94.6	719	7	ADM74717	B. thurin
15	3520	93.6	719	4	AAB66912	Insectici
16	3520	93.6	719	6	AAE36276	B. thurin
17	3476.5	92.5	710	4	AAU02041	B. thurin
18	3397	90.3	719	3	ABB07073	Bacillus
19	3377	89.8	719	2	AAW49089	Bacillus
20	3291	87.5	1217	4	AAU02092	Bacillus
21	2734	72.7	1208	8	ADK98484	B. thuring
22	2448	65.1	1230	8	ADK98489	B. thuring
23	2448	65.1	1230	8	ADK98481	B. thuring
24	2448	65.1	1230	8	ADK98491	B. thuring
25	2448	65.1	1230	8	ADK98491	B. thuring

26	2448	65.1	1230	8	ADK98487	B. thuring
27	2446.5	65.1	1229	2	AAK54074	CryET5. 2
28	2446.5	65.1	1229	2	AAW35259	Bacillus
29	2446.5	65.1	1229	2	AAW17699	CryET5. 3
30	2446.5	65.1	1229	2	AAW87633	CryET5 pr
31	2446.5	65.1	1229	2	AAV30923	B. thurin
32	2446.5	65.1	1229	8	ADK98479	B. thuring
33	2444.5	62.4	488	2	AAW44322	Bacillus
34	2344.5	62.4	488	4	AAH19947	Bacillus
35	2278.5	60.6	1228	2	AAH50955	Bacillus
36	2273.5	60.5	1209	4	AAU02094	Bacillus
37	2264.5	60.2	1227	2	AAV31990	Chimeric
38	2195.5	58.4	1227	2	AAW44321	Bacillus
39	2195.5	58.4	1227	4	AAH19950	Bacillus
40	2186.5	58.2	1227	4	AAU02046	B. thurin
41	2171.5	57.8	1186	2	AAV16796	Amino aci
42	2156.5	57.4	1221	4	AAU00421	B. thurin
43	2142.5	57.0	1221	4	AAU00420	B. thurin
44	2116	56.3	1228	4	AAH84628	Amino aci
45	2116	56.3	1228	4	AAU02039	B. thurin

ALIGNMENTS

RESULT 1  
AAB66908  
ID AAB66908 standard; protein; 719 AA.  
XX  
AC AAB66908;  
XX  
DT 12-APR-2001 (first entry)  
XX  
DE Insecticidal protein cryIIa2.  
XX  
KW Insecticide; transgenic plant; insect-resistance.  
XX  
OS Paecilomyces sp.  
XX  
PN WO200100841-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-GB002457.  
XX  
PR 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX  
DR WPI; 2001-123015/13.  
XX  
PT Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
production.  
XX  
PS Claim 14; Page 55-57; 72pp; English.  
XX  
CC The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX  
SQ Sequence 719 AA;

Query Match 100.0%; Score 3760; DB 4; Length 719;  
Best Local Similarity 100.0%; Pred. No. 1.1e-293;  
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Tue Feb 15 10:07:50 2005

QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P P F V S A S T I 60  
 D b 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P P F V S A S T I 60  
 QY 61 Q T G I G I A G K I L G T L G V P P A G V A S L Y S F I L G E L W P K G K Q W E I F M E H V E E I I N O K I S T Y A 120  
 D b 61 Q T G I G I A G K I L G T L G V P P A G V A S L Y S F I L G E L W P K G K Q W E I F M E H V E E I I N O K I S T Y A 120  
 QY 121 R N K A L T D L K G L D A L A V H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
 D b 121 R N K A L T D L K G L D A L A V H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
 QY 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V R A G D Y S H C V K W Y S 240  
 D b 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V R A G D Y S H C V K W Y S 240  
 QY 241 T G L N N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 D b 241 T G L N N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 QY 301 G T V H P H S F T S T T W Y N N A P S A I E A A V V R N P H L L D F L E Q V T T Y S L L S R W S N T Q Y M N W 360  
 D b 301 G T V H P H S F T S T T W Y N N A P S A I E A A V V R N P H L L D F L E Q V T T Y S L L S R W S N T Q Y M N W 360  
 QY 361 G G H K L E F R T I G T L N I S T Q S T N T S I N P V T L P T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 D b 361 G G H K L E F R T I G T L N I S T Q S T N T S I N P V T L P T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 QY 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T O L Q D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
 D b 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T O L Q D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
 QY 481 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R T N 540  
 D b 481 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R T N 540  
 QY 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
 D b 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
 QY 601 T F R T V G T T P F S F L D V Q S T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E A Y D F E K A Q E K V 660  
 D b 601 T F R T V G T T P F S F L D V Q S T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E A Y D F E K A Q E K V 660  
 QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719  
 D b 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719

RESULT 2  
 ID AAE36272 standard; protein; 719 AA.  
 XX AC AAE36272;  
 XX DT 26-JUN-2003 (first entry)  
 XX DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.  
 XX KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX OS Bacillus thuringiensis.  
 XX PN WO200298911-A2.  
 XX PD 12-DEC-2002.  
 XX PF 30-MAY-2002; 2002WO-GB002666.  
 XX PR 07-JUN-2001; 2001GB-00013900.  
 XX PA (SYGN ) SYNGENTA LTD.  
 XX

PI Vincent JL, Viner R;  
 DR WPI; 2003-175137/17.  
 XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PT Claim 12; Page 44-47; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 CC Sequence 719 AA;  
 QY Query Match 100.0%; Score 3760; DB 6; Length 719;  
 D b Best Local Similarity 100.0%; Pred. No. 1.1e-293;  
 Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P P F V S A S T I 60  
 D b 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P P F V S A S T I 60  
 QY 61 Q T G I G I A G K I L G T L G V P P A G V A S L Y S F I L G E L W P K G K Q W E I F M E H V E E I I N O K I S T Y A 120  
 D b 61 Q T G I G I A G K I L G T L G V P P A G V A S L Y S F I L G E L W P K G K Q W E I F M E H V E E I I N O K I S T Y A 120  
 QY 121 R N K A L T D L K G L D A L A V H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
 D b 121 R N K A L T D L K G L D A L A V H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
 QY 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V R A G D Y S H C V K W Y S 240  
 D b 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V R A G D Y S H C V K W Y S 240  
 QY 241 T G L N N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 D b 241 T G L N N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 QY 301 G T V H P H S F T S T T W Y N N A P S A I E A A V V R N P H L L D F L E Q V T T Y S L L S R W S N T Q Y M N W 360  
 D b 301 G T V H P H S F T S T T W Y N N A P S A I E A A V V R N P H L L D F L E Q V T T Y S L L S R W S N T Q Y M N W 360  
 QY 361 G G H K L E F R T I G T L N I S T Q S T N T S I N P V T L P T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 D b 361 G G H K L E F R T I G T L N I S T Q S T N T S I N P V T L P T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 QY 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T O L Q D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
 D b 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T O L Q D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
 QY 481 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R T N 540  
 D b 481 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R T N 540  
 QY 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
 D b 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
 QY 601 T F R T V G T T P F S F L D V Q S T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E A Y D F E K A Q E K V 660  
 D b 601 T F R T V G T T P F S F L D V Q S T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E A Y D F E K A Q E K V 660  
 QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719  
 D b 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719

RESULT 3  
ADR89421  
ID ADR89421 standard; protein; 719 AA.  
XX AC ADR89421;  
XX AC ADR89421;  
XX DT 18-NOV-2004 (first entry)  
XX XX cryIIa.  
XX XX delta-endotoxin; delta-endotoxin associate polypeptide;  
XX KW expression cassette; transformation; transgenic; plant; bacteria;  
XX KW lepidoptera; coleoptera; pest; pesticide; resistance;  
XX KW pesticidal activity.  
XX OS Bacillus thuringiensis.  
XX OS  
XX PN WO2004074462-A2.  
XX XX  
XX PD 02-SEP-2004.  
XX PF  
XX PF 20-FEB-2004; 2004WO-US005829.  
XX XX  
XX PR 20-FEB-2003; 2003US-0448632P.  
XX PR 20-FEB-2003; 2003US-0448633P.  
XX PR 20-FEB-2003; 2003US-0448737P.  
XX PR 20-FEB-2003; 2003US-0448806P.  
XX PR 20-FEB-2003; 2003US-0448810P.  
XX PR 20-FEB-2003; 2003US-0448812P.  
XX PR 19-FEB-2004; 2004US-00781979.  
XX PR 19-FEB-2004; 2004US-00782020.  
XX PR 19-FEB-2004; 2004US-00782096.  
XX PR 19-FEB-2004; 2004US-00782141.  
XX PR 19-FEB-2004; 2004US-00782570.  
XX PR 19-FEB-2004; 2004US-00783417.  
XX XX  
XX PA (ATHE-) ATHENIX CORP.  
XX PI  
XX PI Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;  
XX XX WPI; 2004-635574/61.  
XX XX  
XX PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
XX PT and polypeptides, useful for killing lepidopteran or coleopteran pests or  
XX PT for producing organisms with pesticide resistance.  
XX XX  
XX XX Example 6; SEQ ID NO 33; 178pp; English.  
XX XX  
XX CC This sequence represents a delta-endotoxin crystal protein. This protein  
XX CC was included in the scope of the invention as a comparison to the delta-  
XX CC endotoxins of the invention. Some of the delta-endotoxin coding sequences  
XX CC of the invention have alternative start codons, producing more than one  
XX CC protein from a single open reading frame. The nucleic acid sequences of  
XX CC the invention are useful in DNA constructs or expression cassettes for  
XX CC transformation and expression in plants and bacteria. The nucleic acids  
XX CC and corresponding polypeptides are useful for killing lepidopteran or  
XX CC coleopteran pests. Compositions containing the delta-endotoxins of the  
XX CC invention, and methods for their production, are useful for the  
XX CC production of organisms with pesticide resistance, specifically bacteria  
XX CC and plants. These organisms are useful for generating altered or improved  
XX CC delta-endotoxin or delta-endotoxin-associated proteins that have  
XX CC pesticidal activity, or for detecting the presence of delta-endotoxin or  
XX CC delta-endotoxin-associated proteins or nucleic acids in products or  
XX CC organisms.  
XX XX  
XX SQ Sequence 719 AA;  
XX XX  
XX XX Query Match 100.0%; Score 3760; DB 8; Length 719;  
XX XX Best Local Similarity 100.0%; Pred. No. 1.1e-293; Indels 0; Gaps 0;  
XX XX Matches 719; Conservative 0; Mismatches 0;  
QV 1 MLLKNQKHQSFSSNAKVDKISTLSKNETDIELQNIHEDCLKMSYEVENPEFVSASTI 60

PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX WPI; 2001-123015/13.  
DR Novel insecticidal protein obtained from species of Paecilomyces for  
XX controlling insects, and for insect-resistant transgenic plant  
PT production.  
PT  
XX Claim 14; Page 60-62; 72pp; English.  
PS  
XX The present invention relates to novel insecticidal proteins obtained  
XX from Paecilomyces sp. (see AAB6699 to AAB6901 and AAB6913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX  
XX Sequence 719 AA;  
SQ  
Query Match 99.9%; Score 3756; DB 4; Length 719;  
Best Local Similarity 99.9%; Pred. No. 2.4e-293;  
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60  
DB 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASLYSFTLGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
DB 61 QTGIGIAGKILGTGVPFAGQVASLYSFTLGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
QY 121 RNKALTDLKGLDALAVYHDSLESVGNRNTRARSVVKSVQYIALELMFVKLPSPFVSG 180  
DB 121 RNKALTDLKGLDALAVYHDSLESVGNRNTRARSVVKSVQYIALELMFVKLPSPFVSG 180  
QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240  
DB 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240  
QY 241 TGLNNLRGTNAESWRYNQFRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREYVTDAI 300  
DB 241 TGLNNLRGTNAESWRYNQFRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREYVTDAI 300  
QY 301 GTVHPHPSFTTWTYNNAPSPAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360  
DB 301 GTVHPHPSFTTWTYNNAPSPAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360  
QY 361 GGHKLEFRTTIGTTLNISTQGSTNTSINPVTLPFTSRDVRTSLAGLNLFLTQPVNGVPR 420  
DB 361 GGHKLEFRTTIGTTLNISTQGSTNTSINPVTLPFTSRDVRTSLAGLNLFLTQPVNGVPR 420  
QY 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSNELPPPEATQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSNELPPPEATQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHESADRTNTEBNSITQIPLKAFNLSGAAVVRGPGFTGDIILRRN 540  
DB 481 ASHVKALVYSWTHESADRTNTEBNSITQIPLKAFNLSGAAVVRGPGFTGDIILRRN 540  
QY 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLQHTSINGKAINQGNFSAATNAGEDLDYK 600  
DB 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLQHTSINGKAINQGNFSAATNAGEDLDYK 600  
QY 601 TFRVGTFTTPTPSFLDVOSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
DB 601 TFRVGTFTTPTPSFLDVOSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVQYHIDQVNLVESLSDFYLDKRELFVIVKAKQHLIERNM 719  
DB 661 TALFTSTNPRGLKTDVQYHIDQVNLVESLSDFYLDKRELFVIVKAKQHLIERNM 719

AAE36274  
ID AAE36274 standard; protein; 719 AA.  
XX  
AC AAE36274;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.  
XX  
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
XX  
OS Bacillus thuringiensis.  
XX  
PN WO200298911-A2.  
XX  
PD 12-DEC-2002.  
XX  
PF 30-MAY-2002; 2002WO-GB002666.  
XX  
PR 07-JUN-2001; 2001GB-00013900.  
XX  
PA (SYGN ) SYNGENTA LTD.  
XX  
PI Vincent JL, Viner R;  
XX  
DR WPI; 2003-175137/17.  
XX  
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
XX  
PS Claim 12; Page 50-53; 67pp; English.  
XX  
CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
XX  
SQ Sequence 719 AA;  
Query Match 99.9%; Score 3756; DB 6; Length 719;  
Best Local Similarity 99.9%; Pred. No. 2.4e-293;  
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60  
DB 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASLYSFTLGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
DB 61 QTGIGIAGKILGTGVPFAGQVASLYSFTLGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
QY 121 RNKALTDLKGLDALAVYHDSLESVGNRNTRARSVVKSVQYIALELMFVKLPSPFVSG 180  
DB 121 RNKALTDLKGLDALAVYHDSLESVGNRNTRARSVVKSVQYIALELMFVKLPSPFVSG 180  
QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240  
DB 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240  
QY 241 TGLNNLRGTNAESWRYNQFRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREYVTDAI 300  
DB 241 TGLNNLRGTNAESWRYNQFRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREYVTDAI 300  
QY 301 GTVHPHPSFTTWTYNNAPSPAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360  
DB 301 GTVHPHPSFTTWTYNNAPSPAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360  
QY 361 GGHKLEFRTTIGTTLNISTQGSTNTSINPVTLPFTSRDVRTSLAGLNLFLTQPVNGVPR 420

Db 361 GGHKLEFRITGGTINISQSGTNTSINPVTLPTSDRVYRTESLAGLNFLTPQVNGVPR 420  
Qy 421 VDFHWKFVTHPIASDNFYYPGVAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 480  
Db 421 VDFHWKFVTHPIASDNFYYPGVAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 480  
Qy 481 ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGCDILRRTN 540  
Db 481 ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGCDILRRTN 540  
Qy 541 TGFPGDIRVNIINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSAATMRGDLGYK 600  
Db 541 TGFPGDIRVNIINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSAATMRGDLGYK 600  
Qy 601 TFRVTGFTTFFSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
Db 601 TFRVTGFTTFFSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
Qy 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

## RESULT 6

AAU02095  
ID AAU02095 standard; protein; 719 AA.

AC AAU02095;

XX 07-SEP-2001 (first entry)

DE Bacillus thuringiensis partial mutant CryIIa.

XX Crystal protein; CryIIa; CryIIa; moth; butterfly; Colorado potato beetle;  
mutant; mutein.

OS Bacillus thuringiensis.

FT Key Location/Qualifiers

FT Peptide 1-19 /label= Signal\_peptide

FT Protein 20..719 /label= Mature\_CryIIa

FT EP1099760-A1.

PN 16-MAY-2001.

XX 09-NOV-1999; 99EP-00203723.

XX 09-NOV-1999; 99EP-00203723.

PA (CPRO-) CPRO-DIO CENT PLANTENVERDEBLINGS REPROD.

XX De Maagd RA, Bosch HJ;

XX WPI; 2001-337141/36.

XX N-PSDB; AAS04855.

XX New hybrid Bacillus thuringiensis hybrid toxins comprising structural  
PT domains derived from at least 2 different crystal proteins, such as  
PT CryIIa and CryIIa, and having insecticidal activity, useful for combating  
PT insects.

PS Example; Page 30-32; 43pp; English.

XX The sequence is B. thuringiensis (Bt) crystal protein CryIIa, the DNA  
CC encoding which was mutated to allow cloning of domain III or domains I  
CC and II, to make the hybrid protoxins of the invention. The hybrid toxins  
CC of the invention, having structural domains I, II and III in this order  
CC starting from the N-terminal derived from at least 2 different crystal  
CC proteins, are useful for protecting plants against pest insects, e.g.

CC moths, butterflies and Colorado potato beetle or for combating insects  
XX Sequence 719 AA;

Query Match 99.8%; Score 3751; DB 4; Length 719;  
Best Local Similarity 99.9%; Pred. No. 6.1e-293;  
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKNQDQHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVPFVSASTI 60

Db 1 MKLKNQDQHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVPFVSASTI 60

Qy 61 QTGIGIAGKILGTLPFAGQVASYLSFILGELWPKGNQWEIFMEHVSEIINQKISTYA 120

Db 61 QTGIGIAGKILGTLPFAGQVASYLSFILGELWPKGNQWEIFMEHVSEIINQKISTYA 120

Qy 121 RNKALTDLKGLGDALAVYHDSLESVWGNRNTRARSVVKVQYIALELMFVQKLPFAVSG 180

Db 121 RNKALTDLKGLGDALAVYHDSLESVWGNRNTRARSVVKVQYIALELMFVQKLPFAVSG 180

Qy 181 BEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSVHCWKYS 240

Db 181 BEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSVHCWKYS 240

Qy 241 TGLNNLRGTNAESWRYNQFRDMLAVLDLVALPSPYDTQMPYIKTTAQLTREVYTDAT 300

Db 241 TGLNNLRGTNAESWRYNQFRDMLAVLDLVALPSPYDTQMPYIKTTAQLTREVYTDAT 300

Qy 301 GTVHPHPSFTSTTWNNNAPSFAJEAADVVRNPHLLDLEQVTIYSLSRNWTQMMNMW 360

Db 301 GTVHPHPSFTSTTWNNNAPSFAJEAADVVRNPHLLDLEQVTIYSLSRNWTQMMNMW 360

Qy 361 GGHKLEFRITGGTINISQSGTNTSINPVTLPTSDRVYRTESLAGLNFLTPQVNGVPR 420

Db 361 GGHKLEFRITGGTINISQSGTNTSINPVTLPTSDRVYRTESLAGLNFLTPQVNGVPR 420

Qy 421 VDFHWKFVTHPIASDNFYYPGVAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 480

Db 421 VDFHWKFVTHPIASDNFYYPGVAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 480

Qy 481 ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGCDILRRTN 540

Db 481 ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGCDILRRTN 540

Qy 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSAATMRGDLGYK 600

Db 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSAATMRGDLGYK 600

Qy 601 TFRVTGFTTFFSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660

Db 601 TFRVTGFTTFFSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660

Qy 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

Db 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

## RESULT 7

AA666911  
ID AAB66911 standard; protein; 719 AA.

XX AAB66911;

XX 12-APR-2001 (first entry)

XX Insecticidal protein cryIIa5.

XX Insecticide; transgenic plant; insect-resistance.

XX Paecilomyces sp.

XX WO200100841-A1.

XX



QY 241 TGLNLRGTAESWVRNQRRDWTLMVLVLPFSYDTQMPYPIKTTAQLTREVYTDAL 300  
 Db 241 TGLNLRGTAESWVRNQRRDWTLMVLVLPFSYDTQMPYPIKTTAQLTREVYTDAL 300  
 QY 301 GTVHPHPSFTSTWYNNAPSFAIAA VVRNPHLLDFLEQVTIYSLLSWSNTQYMNW 360  
 Db 301 GTVHPHPSFTSTWYNNAPSFAIAA VVRNPHLLDFLEQVTIYSLLSWSNTQYMNW 360  
 QY 361 GGHKLEPRTTGGTINISTQSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPR 420  
 Db 361 GGHKLEPRTTGGTINISTQSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPR 420  
 QY 421 VDFHMKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHMKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGA VVRGPGTGGDILRRTN 540  
 Db 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGA VVRGPGTGGDILRRTN 540  
 QY 541 TGTFGDIRVINPFPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 Db 541 TGTFGDIRVINPFPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 QY 601 TFRVTGFTTFFSFLDVQSTTIGAMNPFSSGNEVYIDRIEFVVPVEVYEAEDPEKAQEKV 660  
 Db 601 TFRVTGFTTFFSFLDVQSTTIGAMNPFSSGNEVYIDRIEFVVPVEVYEAEDPEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKOLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKOLHIERNM 719

RESULT 9  
 AAB66909  
 ID AAB66909 standard; protein; 719 AA.  
 XX AC AAB66909;  
 XX AC AAB66909;  
 DT 12-APR-2001 (first entry)  
 XX Insecticidal protein cryIIa3.  
 DE Insecticide; transgenic plant; insect-resistance.  
 KW Insecticide; transgenic plant; insect-resistance.  
 OS Paecilomyces sp.  
 XX Paecilomyces sp.  
 XX WO200100841-A1.  
 XX 04-JAN-2001.  
 XX 23-JUN-2000; 2000WO-GB002457.  
 XX 29-JUN-1999; 99GB-00015215.  
 PR 23-DEC-1999; 99GB-00030536.  
 XX (ZENE ) ZENECA LTD.  
 XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent J-L, Lee MD;  
 XX WPI; 2001-123015/13.  
 XX Novel insecticidal protein obtained from species of Paecilomyces for  
 PT controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 XX Claim 14; Page 57-59; 72pp; English.  
 XX The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB6699 to AAB6901 and AAB6913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for

CC controlling insects by providing them at a locus where insects feed  
 XX Sequence 719 AA;  
 SQ Query Match 99.5%; Score 3743; DB 4; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 2.7e-292;  
 Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDLELQNHEDCLKMEYENVEFPVASTI 60  
 Db 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDLELQNHEDCLKMEYENVEFPVASTI 60  
 QY 61 QTGIGIAGKILGTLPVPFAGQVASYLSPILGELMPKQKQWEIFMHHVEEINQKISTYA 120  
 Db 61 QTGIGIAGKILGTLPVPFAGQVASYLSPILGELMPKQKQWEIFMHHVEEINQKISTYA 120  
 QY 121 RNKALTDLAGLDALAVHDSLESVGNRNNTARSVVKSOYIALELMPVKLPSPAVSG 180  
 Db 121 RNKALTDLAGLDALAVHDSLESVGNRNNTARSVVKSOYIALELMPVKLPSPAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSHCVKWYS 240  
 Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSHCVKWYS 240  
 QY 241 TGLNLRGTAESWVRNQRRDWTLMVLVLPFSYDTQMPYPIKTTAQLTREVYTDAL 300  
 Db 241 TGLNLRGTAESWVRNQRRDWTLMVLVLPFSYDTQMPYPIKTTAQLTREVYTDAL 300  
 QY 301 GTVHPHPSFTSTWYNNAPSFAIAA VVRNPHLLDFLEQVTIYSLLSWSNTQYMNW 360  
 Db 301 GTVHPHPSFTSTWYNNAPSFAIAA VVRNPHLLDFLEQVTIYSLLSWSNTQYMNW 360  
 QY 361 GGHKLEPRTTGGTINISTQSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPR 420  
 Db 361 GGHKLEPRTTGGTINISTQSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPR 420  
 QY 421 VDFHMKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHMKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGA VVRGPGTGGDILRRTN 540  
 Db 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGA VVRGPGTGGDILRRTN 540  
 QY 541 TGTFGDIRVINPFPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 Db 541 TGTFGDIRVINPFPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 QY 601 TFRVTGFTTFFSFLDVQSTTIGAMNPFSSGNEVYIDRIEFVVPVEVYEAEDPEKAQEKV 660  
 Db 601 TFRVTGFTTFFSFLDVQSTTIGAMNPFSSGNEVYIDRIEFVVPVEVYEAEDPEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKOLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKOLHIERNM 719

RESULT 10  
 AAE36273  
 ID AAE36273 standard; protein; 719 AA.  
 XX AC AAE36273;  
 XX AC AAE36273;  
 DT 26-JUN-2003 (first entry)  
 XX B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.  
 DE Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 KW Bacillus thuringiensis.  
 XX Bacillus thuringiensis.  
 XX WO200298911-A2.  
 PN WO200298911-A2.  
 XX

PD	12-DEC-2002.	QY	601	TFRTVGTTPPSFLDVOSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYAEYDFEKAQEKV	660
XX		DB	601	TFRTVGTTPPSFLDVOSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYAEYDFEKAQEKV	660
PF	30-MAY-2002; 2002WO-GB002666.	QY	661	TALFTSTNPRGLKTDVXDYHIDQVSNLVSLSDEFLYDKRELFEIVKYAKOLHIERNM	719
XX		DB	661	TALFTSTNPRGLKTDVXDYHIDQVSNLVSLSDEFLYDKRELFEIVKYAKOLHIERNM	719
PR	07-JUN-2001; 2001GB-00013900.				
XX	(SYGN ) SYNGENTA LTD.				
PA					
XX	Vincent JL, Viner R;				
PI	WPI; 2003-175137/17.				
XX					
DR	New insecticidal protein comprising an X-glycine motif at the amino-				
XX	terminus, useful as an active ingredient of a pesticide.				
PT					
PT					
XX	Claim 12; Page 47-50; 67pp; English.				
XX					
XX	The invention relates to insecticidal protein comprising an X-glycine				
CC	motif at the amino-terminus. Polynucleotide or DNA constructs of the				
CC	invention are useful for producing plants or plant constructs that are				
CC	resistant to insects. The protein or synergistic combination is useful as				
CC	an active ingredient of a pesticide or for controlling insects.				
CC	Antibodies raised to the insecticidal proteins can be used to identify				
CC	other proteins with insecticidal activity. The present sequence is				
CC	Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This				
CC	sequence is used in the invention				
XX					
SQ	Sequence 719 AA;				
	Query Match 99.5%; Score 3743; DB 6; Length 719;				
	Best Local Similarity 99.6%; Pred. No. 2.7e-292;				
	Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;				
QY	1	1	MLKNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKSEYENVEPFVSASTI	60	
DB	1	1	MLKNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKSEYENVEPFVSASTI	60	
QY	61	61	QTGIGTAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA	120	
DB	61	61	QTGIGTAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA	120	
QY	121	121	RNKALTDKLGDALAVYHDSLSWGNRNTRARSVKSQYIALELMPVKLPFAVSG	180	
DB	121	121	RNKALTDKLGDALAVYHDSLSWGNRNTRARSVKSQYIALELMPVKLPFAVSG	180	
QY	181	181	EEVPLLPITYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDSDHCKWYS	240	
DB	181	181	EEVPLLPITYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDSDHCKWYS	240	
QY	241	241	TGLNLRGTNAESWVRYNQFRDNTLMLVDLVALFPSYDTQMPYIKTTAQLTREVYTDAL	300	
DB	241	241	TGLNLRGTNAESWVRYNQFRDNTLMLVDLVALFPSYDTQMPYIKTTAQLTREVYTDAL	300	
QY	301	301	GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLSLRSWNTQYMNW	360	
DB	301	301	GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLSLRSWNTQYMNW	360	
QY	361	361	GGHKLFEFTIGTGLNISTQSGTNTSINPVTLPFTSRDVRITESIAGLNLFELTQPVNGVPR	420	
DB	361	361	GGHKLFEFTIGTGLNISTQSGTNTSINPVTLPFTSRDVRITESIAGLNLFELTQPVNGVPR	420	
QY	421	421	VDHFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATQPNYESYSHRISHIGLIS	480	
DB	421	421	VDHFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATQPNYESYSHRISHIGLIS	480	
QY	481	481	ASHVKALYVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540	
DB	481	481	ASHVKALYVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540	
QY	541	541	TGTFGDIRVINPFPFAQRVVRIRYASTTDLQFHTSINGKAINQCNFSATNWRGEDLDYK	600	
DB	541	541	TGTFGDIRVINPFPFAQRVVRIRYASTTDLQFHTSINGKAINQCNFSATNWRGEDLDYK	600	



Db 181 BEVPLPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
Qy 241 TGLNLRGTNAESWVRVYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAL 300  
Db 241 TGLNLRGTNAESWVRVYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAL 300  
Qy 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
Db 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
Qy 361 GGHKLEFRITGGTLNISTQSTNTSINPVTLPFTSRDVRVYTESLAGLNLFTQPVNGVPR 420  
Db 361 GGHKLEFRITGGTLNISTQSTNTSINPVTLPFTSRDVRVYTESLAGLNLFTQPVNGVPR 420  
Qy 421 VDFHWKFTVHPPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
Db 421 VDFHWKFTVHPPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
Qy 481 ASHVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
Db 481 ASHVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
Qy 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYK 600  
Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYK 600  
Qy 601 TFRVTGFTTFFSLDDVOSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
Db 601 TFRVTGFTTFFSLDDVOSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
Qy 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 12  
AAE36271  
ID AAE36271 standard; protein; 718 AA.  
AC AAE36271;  
XX  
XX 26-JUN-2003 (first entry)  
XX  
XX B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa1.  
XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
XX  
XX Bacillus thuringiensis.  
XX  
XX WO200298911-A2.  
XX  
XX 12-DEC-2002.  
XX  
XX 30-MAY-2002; 2002WO-GB002666.  
XX  
XX 07-JUN-2001; 2001GB-00013900.  
XX  
XX (SYGN ) SYNGENTA LTD.  
XX  
XX Vincent JL, Viner R;  
XX WPI; 2003-175137/17.  
XX  
XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
XX  
XX Claim 12; Page 42-44; 67pp; English.  
XX  
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as

CC an active ingredient of a pesticide or for controlling insects.  
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This CC sequence is used in the invention  
XX  
SQ Sequence 718 AA;  
Query Match 99.2%; Score 3728.5; DB 6; Length 718;  
Best Local Similarity 99.6%; Pred. No. 3.9e-291;  
Matches 716; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
Qy 1 MKLNQDKHQSPSSNAKVDKISTDSLKNETDIELQINHEDCLKMEYENVEFPVSASTI 60  
Db 1 MKLNQDKHQSPSSNAKVDKISTDSLKNETDIELQINHEDCLKMEYENVEFPVSASTI 60  
Qy 61 QTGIGTAGKTLGTLGVPPAGQVASYLSFIIIGELWPKGKQWEIFMEHVEEIIINOKISTYA 120  
Db 61 QTGIGTAGKTLGTLGVPPAGQVASYLSFIIIGELWPKGKQWEIFMEHVEEIIINOKISTYA 120  
Qy 121 RNKALTDLKGDLGDLAVYHDSLESWGNRNNTREARSVVKSQYIALBELMFVQKLPFAVSG 180  
Db 121 RNKALTDLKGDLGDLAVYHDSLESWGNRNNTREARSVVKSQYIALBELMFVQKLPFAVSG 180  
Qy 181 BEVPLPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
Db 181 BEVPLPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
Qy 241 TGLNLRGTNAESWVRVYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAL 300  
Db 241 TGLNLRGTNAESWVRVYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAL 300  
Qy 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
Db 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
Qy 361 GGHKLEFRITGGTLNISTQSTNTSINPVTLPFTSRDVRVYTESLAGLNLFTQPVNGVPR 420  
Db 361 GGHKLEFRITGGTLNISTQSTNTSINPVTLPFTSRDVRVYTESLAGLNLFTQPVNGVPR 420  
Qy 421 VDFHWKFTVHPPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
Db 421 VDFHWKFTVHPPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
Qy 481 ASHVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
Db 481 ASHVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
Qy 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYK 600  
Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYK 600  
Qy 601 TFRVTGFTTFFSLDDVOSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
Db 601 TFRVTGFTTFFSLDDVOSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
Qy 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
RESULT 13  
AAB66907  
ID AAB66907 standard; protein; 718 AA.  
XX  
XX AAB66907;  
XX  
XX 12-APR-2001 (first entry)  
XX  
XX Insecticidal protein cryIIa1.  
XX  
XX Insecticide; transgenic plant; insect-resistance.  
XX

OS	Paecilomyces sp.	Db	540	TGTFGDIRVNNPPFAQRYVRIRYASTTDLQHTSINGKAINQGNFSATMNRGEDLDYK	599
XX	WO200100841-A1.	Qy	601	TFTVGTTPFPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV	660
XX	04-JAN-2001.	Db	600	TFXTVGTTPFPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV	659
XX	23-JUN-2000; 2000WO-GB002457.	Qy	661	TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDBFYLDKRELFVVKYAKQLHIERNM	719
XX	29-JUN-1999; 99GB-00015215.	Db	660	TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDBFYLDKRELFVVKYAKQLHIERNM	718
PR	23-DEC-1999; 99GB-00030536.				
XX	(ZENE ) ZENECA LTD.				
PA	Griffin J, Carlile AJ, Cayley RJ, Mackay EA, Warner SAJ;				
XX	Vincent JL, Lee MD;				
PI	WPI; 2001-123015/13.				
XX	Novel insecticidal protein obtained from species of Paecilomyces for				
XX	controlling insects, and for insect-resistant transgenic plant				
PT	production.				
PT	Claim 14; Page 53-55; 72pp; English.				
XX	The present invention relates to novel insecticidal proteins obtained				
XX	from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The				
CC	insecticidal proteins can be used to produce transgenic plants, which are				
CC	insect-resistant. Also, the insecticidal proteins are useful for				
CC	controlling insects by providing them at a locus where insects feed				
XX	Sequence 718 AA;				
SQ	Query Match 99.0%; Score 3722.5; DB 4; Length 718;				
	Best Local Similarity 99.4%; Pred. No. 1.2e-290;				
	Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;				
Qy	1 MCLKNQDKHQSFSSNAKVDKISTDSLNKNETDIELQINNHEDCLKSEYENVEPFSASTI	60			
Db	1 MCLKNQDKHQSFSSNAKVDKISTDSLNKNETDIELQINNHEDCLKSEYENVEPFSASTI	60			
Qy	61 QTGIGIAGKILGTGVFPAGQVSLYSFILGELWPKGKQWEIFMEHVEEIIINOKISTYA	120			
Db	61 QTGIGIAGKILGTGVFPAGQVSLYSFILGELWPKGKQWEIFMEHVEEIIINOKISTYA	120			
Qy	121 RNKALTDLKGIGDALAVYHDSLSWVGNRNNTARSVKSOYIALMLFVQKLPSPAVSG	180			
Db	121 RNKALTDLKGIGDALAVYHDSLSWVGNRNNTARSVKSOYIALMLFVQKLPSPAVSG	180			
Qy	181 BEVPLLPYIAQAANLHLLLRDASIFGKWLGSSEISTFYNQVERAGDYSYHCVKWS	240			
Db	181 BEVPLLPYIAQAANLHLLLRDASIFGKWLGSSEISTFYNQVERAGDYSYHCVKWS	240			
Qy	241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVYDAI	300			
Db	241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVYDAI	300			
Qy	301 GTVHPHPSFTSTWYNNAPSFSALEAVVRNPHLLDFLEQVTIYLSLRSWNTQYNNW	360			
Db	301 GTVHPHPSFTSTWYNNAPSFSALEAVVRNPHLLDFLEQVTIYLSLRSWNTQYNNW	360			
Qy	361 GGHKLEFRITGTLNISTQGSTINTSINPVTLPFTSRDYRTESLAGNLFLTPQVNGVPR	420			
Db	361 GGHKLEFRITGTLNISTQGSTINTSINPVTLPFTSRDYRTESLAGNLFLTPQVNGVPR	419			
Qy	421 VDFHMKFVTHPIASDNFYYPGAGIGTQLODSENELPEATQPNYSYSHRSLHIGLIS	480			
Db	420 VDFHMKFVTHPIASDNFYYPGAGIGTQLODSENELPEATQPNYSYSHRSLHIGLIS	479			
Qy	481 ASHVKALVSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540			
Db	480 ASHVKALVSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	539			
Qy	541 TGTFGDIRVNNPPFAQRYVRIRYASTTDLQHTSINGKAINQGNFSATMNRGEDLDYK	600			

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Db 121 RNIALADLKGDLAVYHESLWIKRNNAATSVVKSQYIALELLFVKQLPSPFAVSG 180
Qy 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNROVERAGDYSRHCVKWYS 240
Db 181 EEVPLPIYAQAANLHLLLRDASVFGKEWGLSSQISTFYNROVERTSDYSDHCVKWYS 240
Qy 241 TGLNLRGTNAESVWRVYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYDAI 300
Db 241 TGLNLRGTNAESVWRVYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYDAI 300
Qy 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW 360
Db 301 GTVHPNASFASTWYNNAPSPSAIESAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW 360
Qy 361 GGHKLEFRTTGGTINISQSTNTSINPVTLPFTSRDVTYTESLAGLNLELFTQPVNGVPR 420
Db 361 GGHKLEFRTTGGVLTSTQSTNTSINPVTLPFTSRDVTYTESLAGLNLELFTQPVNGVPR 420
Qy 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480
Db 421 VDFHWKFTATLPPIASDNFYLYGAGVGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVINPFPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 541 TGTFGDIRVINPFPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Qy 601 TFRVTGTTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEVYEAEDFEKAQEKV 660
Db 601 TFRVTGTTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEVYEAEDFEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

```

## RESULT 15

AAB66912 standard; protein; 719 AA.

XX AAB66912;

DT 12-APR-2001 (first entry)

DE Insecticidal protein cry11b1.

XX Insecticide; transgenic plant; insect-resistance.

XX Paecilomyces sp.

XX WO200100841-A1.

XX 04-JAN-2001.

XX 23-JUN-2000; 2000WO-GB002457.

XX 29-JUN-1999; 99GB-00015215.

XX 23-DEC-1999; 99GB-00030536.

XX (ZENE ) ZENECA LTD.

XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;

XX Vincent JL, Lee MD;

XX WPI; 2001-123015/13.

XX Novel insecticidal protein obtained from species of Paecilomyces for  
 PT controlling insects, and for insect-resistant transgenic plant  
 PT production.

XX Claim 14; Page 64-66; 72pp; English.

XX The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB66912 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed

XX Sequence 719 AA;

Query Match 93.6%; Score 3520; DB 4; Length 719;  
 Best Local Similarity 92.9%; Pred. NO. 2.5e-274;  
 Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDIELQNIHEDCLKMEYENVEPFVSASTI 60

Db 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDIELQNIHEDCLKMEYENVEPFVSASTI 60

Qy 61 QTGIGIAGKILGTLGVPPFAGQVAVSLYSPILGELWPKGKQWEIFMEHVBEIINQKISTYA 120

Db 61 QTGIGIAGKILGTLGVPPFAGQVAVSLYSPILGELWPKGKQWEIFMEHVBEIINQKISTYA 120

Qy 121 RNKALTDLKGDLAVYHDSLESWYGNNTTARSVVKSOYIALELMFVKQLPSPFAVSG 180

Db 121 RNKALSDRLGDLAVYHDSLESWYGNNTTARSVVKSOYIALELMFVKQLPSPFAVSG 180

Qy 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNROVERAGDYSRHCVKWYS 240

Db 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNROVERAGDYSRHCVKWYS 240

Qy 241 TGLNLRGTNAESVWRVYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYDAI 300

Db 241 TGLNLRGTNAESVWRVYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYDAI 300

Qy 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW 360

Db 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW 360

Qy 361 GGHKLEFRTTGGTINISQSTNTSINPVTLPFTSRDVTYTESLAGLNLELFTQPVNGVPR 420

Db 361 GGHKLEFRTTGGTINISQSTNTSINPVTLPFTSRDVTYTESLAGLNLELFTQPVNGVPR 420

Qy 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480

Db 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480

Qy 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540

Db 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540

Qy 541 TGTFGDIRVINPFPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600

Db 541 TGTFGDIRVINPFPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600

Qy 601 TFRVTGTTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEVYEAEDFEKAQEKV 660

Db 601 TFRVTGTTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEVYEAEDFEKAQEKV 660

Qy 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

Search completed: February 14, 2005, 20:50:27  
 Job time : 101.351 secs

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1	3760	100.0	719	16	US-10-782-020-10	Sequence 10, Appl
2	3460	100.0	719	16	US-10-782-141-8	Sequence 8, Appl
3	3476.5	92.5	710	15	US-10-782-961-42	Sequence 42, Appl
4	2278.5	60.6	1228	16	US-10-809-953-10	Sequence 10, Appl
5	2265.5	60.3	1207	10	US-09-388-462-7	Sequence 7, Appl
6	2186.5	58.2	1227	15	US-10-428-961-63	Sequence 63, Appl
7	2171.5	57.8	1186	9	US-09-826-660-23	Sequence 23, Appl
8	2116	56.3	1228	15	US-10-428-961-38	Sequence 38, Appl
9	2116	56.3	1228	15	US-10-614-524-2	Sequence 2, Appl
10	1932.5	51.4	643	9	US-09-826-660-25	Sequence 25, Appl
11	1722.5	45.8	1167	14	US-10-089-678-1	Sequence 1, Appl
12	1681.5	44.7	653	15	US-10-428-961-6	Sequence 6, Appl
13	1670.5	44.4	1157	16	US-10-782-141-16	Sequence 16, Appl

Query Match	100.0%;	Score 3760;	DB 16;	Length 719;
Best Local Similarity	100.0%;	Pred. No. 5.9e-310;		
Matches 719;	Conservative	0; Mismatches	0; Indels	0; Gaps
Oy	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDI	ELQNINHEDCCLKMSEYENVEPFSASTI	60
Dd	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDI	ELQNINHEDCCLKMSEYENVEPFSASTI	60
Oy	61	QTGIGTAGKI LGTGLVFPFAGQVASLYSFFILGE	LWPKGKNQWEIFMEHVBESI INOKISTYA	120
Dd	61	OTSIGTAGKI LGTGLVFPFAGQVASLYSFFILGE	LWPKGKNQWEIFMEHVBESI INOKISTYA	120

QY	121	RNKALTDLKGGLDALAVYHDSLSWGNRNNTARSVVKSOYIALELMFVQKLPSEAVSG	180
DB	121	RNKALTDLKGGLDALAVYHDSLSWGNRNNTARSVVKSOYIALELMFVQKLPSEAVSG	180
QY	181	BEVPLLPYIAQAANLHLLLRDASIFGKENGWGLSSSEISTFYNQVRAGDYSCHCVKWS	240
DB	181	BEVPLLPYIAQAANLHLLLRDASIFGKENGWGLSSSEISTFYNQVRAGDYSCHCVKWS	240
QY	241	TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTOMPIKTTAQLTREVTYDAI	300
DB	241	TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTOMPIKTTAQLTREVTYDAI	300
QY	301	GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW	360
DB	301	GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW	360
QY	361	GGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLOTQVNGVPR	420
DB	361	GGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLOTQVNGVPR	420
QY	421	VDHFWKFTVHTPIASDNFYYPGAGIGTQDSENELPEATGQPNYESYSHRSHIGLIS	480
DB	421	VDHFWKFTVHTPIASDNFYYPGAGIGTQDSENELPEATGQPNYESYSHRSHIGLIS	480
QY	481	ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
DB	481	ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
QY	541	TGTFGDIRVNIINPPFAQRYRVRIRVASTTDLQFHTSINGKAINQGNFATWNRGDDLYK	600
DB	541	TGTFGDIRVNIINPPFAQRYRVRIRVASTTDLQFHTSINGKAINQGNFATWNRGDDLYK	600
QY	601	TFTVGTFTPFSLDQSTFTTIGAMNFFSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV	660
DB	601	TFTVGTFTPFSLDQSTFTTIGAMNFFSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV	660
QY	661	TALFTSTNPRGLKTDVKDHYDIDQVSNLVSLSDEFLDEKRELFEIVKAKOLHIERNM	719
DB	661	TALFTSTNPRGLKTDVKDHYDIDQVSNLVSLSDEFLDEKRELFEIVKAKOLHIERNM	719
RESULT 2			
US-10-782-141-8			
; Sequence 8, Application US/10782141			
; Publication No. US20040197917A1			
; GENERAL INFORMATION:			
; APPLICANT: Carozzi, Nadine			
; APPLICANT: Hargies, Tracy			
; APPLICANT: Koziel, Michael G.			
; APPLICANT: Duck, Nicholas B.			
; APPLICANT: Carr, Brian			
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and			
; TITLE OF INVENTION: Methods for Its Use			
; FILE REFERENCE: 045600/274143			
; CURRENT APPLICATION NUMBER: US/10782.141			
; CURRENT FILING DATE: 2004-02-20			
; PRIOR APPLICATION NUMBER: 60/448,632			
; PRIOR FILING DATE: 2003-02-20			
; NUMBER OF SEQ ID NOS: 23			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 8			
; LENGTH: 719			
; TYPE: PRT			
; ORGANISM: Bacillus thuringiensis			
US-10-782-141-8			
Query Match 100.0%; Score 3760; DB 16; Length 719;			
Best Local Similarity 100.0%; Pred. No. 5.9e-310; Indels 0; Gaps 0;			
Matches 719; Conservative 0; Mismatches 0;			
QY	1	MKLKNQKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLMKSEYENVEPFSASTI	60

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; NAME/KEY: misc_feature
; LOCATION: (200)..(200)
; OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid
US-10-428-961-42

Query Match      92.5%; Score 3476.5; DB 15; Length 710;
Best Local Similarity 92.5%; Pred. No. 6.8e-286;
Matches 665; Conservative 15; Mismatches 30; Indels 9; Gaps 1;

Qy 1 MGLNQDKHQSFSSNAKVDKISTDLKNETDIELQNIHEDCLKMSSEVENVEPVSASTI 60
Db 1 MGLNQDKHQSFSSNAKVDKISTDLKNETDIELQNIHEDCLKMSSEVENVEPVSASTI 60

Qy 61 QTGIGIAGKILGTLGVPAGQVASYLSPILGELWPKGNQKQWEIFMEHVEEIIINOKISTYA 120
Db 52 QTGIGIAGKILGTLGVPAGQVASYLSPILGELWPKGNQKQWEIFMEHVEEIIINOKISTYA 111

Qy 121 RNKALTDLKGIGDALAVVHDSLESVGNRNNTTRRSVVKSYQIYALELDFVQKLSFAVSG 180
Db 112 RNKALADLKGIGDALAVVHDSLESVGNRNNTTRRSVVKSYQIYALELDFVQKLSFAVSG 171

Qy 181 EEPVLLPIYAAQANLHLLLDASIFGKXWGLSDSEISTFFNRQSGKSEYSDHCWKYNS 240
Db 172 EEPVLLPIYAAQANLHLLLDASIFGKXWGLSDSEISTFFNRQSGKSEYSDHCWKYNS 231

Qy 241 TGLNLLRGKTNAESWVRYNQFRDMLVLDLVALFPSPYDTQMPYIKTTAQLTREYVYTDAL 300
Db 232 TGLNRLGNNAESWVRYNQFRDMLVLDLVALFPSPYDTQMPYIKTTAQLTREYVYTDAL 291

Qy 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVITYSLLSRWSNTQYNNMW 360
Db 292 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVITYSLLSRWSNTQYNNMW 351

Qy 361 GGHKLEPRTIGTLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPR 420
Db 352 GGHKLEPRTIGTLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPR 411

Qy 421 VDFHKKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 412 VDFHKKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 471

Qy 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
Db 472 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRKN 531

Qy 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLPFTSINGKAINQGNFSATWNRGEDLDYK 600
Db 532 TGTGDIRVNIINPPFAQRYRIRYASTTDLPFTSINGKAINQGNFSATWNRGEDLDYK 591

Qy 601 TFRTVGFTTPPSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYBAEYDFEKAQEV 660
Db 592 TFRTVGFTTPPSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYBAEYDFEKAQEV 651

Qy 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVSLSDFYLDKEKRELFEIVKYAKQLHIERNM 719
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RESULT 4
US-10-809-953-10
; Sequence 10, Application US/10809953
; Publication No. US20040181825A1
; GENERAL INFORMATION:
; APPLICANT: Van Mellaert, Herman
; APPLICANT: Botterman, Johan
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Joos, Henk
; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTICIDAL PROTEINS
; FILE REFERENCE: 021565-078
; CURRENT APPLICATION NUMBER: US/10/809,953
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/09/661,016
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; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: PCT/EP90/00905
; PRIOR FILING DATE: 1990-05-30
; PRIOR APPLICATION NUMBER: GB 89401499.2
; PRIOR FILING DATE: 1989-05-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-809-953-10

Query Match      60.6%; Score 2278.5; DB 16; Length 1228;
Best Local Similarity 62.7%; Pred. No. 8.6e-184;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

Qy 23 TDSLKNETDIELQNIH-----ECLKMSSEVENVEPVSASTIOTGIGIAGKI 70
Db 2 TSNRKNENEIINAVNSHSAQMDLLPDARIEDSLCIAEGNNDPPFVSASTVQTGINIAGRI 61

Qy 71 LGTLGVFPAGQVASYLSPILGELWPKGNQKQWEIFMEHVEEIIINOKISTYARNKALTDLKG 130
Db 62 LGVLGVFPAGQVASYLSPILGELWPKGNQKQWEIFMEHVEEIIINOKISTYARNKALTDLKG 121

Qy 131 LGDALAVVHDSLESVGNRNNTTRRSVVKSYQIYALELDFVQKLSFAVSGEVPLPIYA 190
Db 122 LGDSFRAYQQSLEDWLENRRDARTSVLHTQYIALELDFLNAAMPLFAIRNOEVPVLLMVA 181

Qy 191 QAAANLHLLLDASIFGKXWGLSDSEISTFFNRQVERAGDYSDHCWKYNSGLNLRCTN 250
Db 182 QAAANLHLLLDASIFGKXWGLSDSEISTFFNRQVERAGDYSDHCWKYNSGLNLRCTN 241

Qy 251 AESWVRYNQFRDMLVLDLVALFPSPYDTQMPYIKTTAQLTREYVYTDALGTVHPHPSFT 310
Db 242 AASWVRYNQFRDMLVLDLVALFPSPYDTQMPYIKTTAQLTREYVYTDALGT--GVNMA 299

Qy 311 STTWYNNNAPSFAIEAAVVRNPHLLDLEQVITYSLLSRWSNTQYNNMWGKHLEFRTI 370
Db 300 SMWYNNNAPSFAIEAAVVRNPHLLDLEQVITYSLLSRWSNTQYNNMWGKHLEFRTI 359

Qy 371 GGTNLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPRVDFHKKFV 428
Db 360 GGGLNTSTHGTATNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPRVDFHKKFV 416

Qy 429 THP-----IASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISASH 483
Db 417 TNPNQISDRGTANTYQSP-YESFGLQKLDSETELPEPETERPNYESYSHRLSHIGLISQR 475

Qy 484 VKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTNRTGT 543
Db 476 VNVVYVSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTNRTGT 535

Qy 544 FGDTRVNIINPPFAQRYRIRYASTTDLPFTSINGKAINQGNFSATWNRGEDLDYKTFR 603
Db 536 FGPTRVTVNGELTQRYRIRYASTTDLPFTSINGKAINQGNFSATWNRGEDLDYKTFR 595

Qy 604 TVGFTTPPSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYBAEYDFEKAQEV 663
Db 596 RRAFTTTPFTQIQDIIRTSIQGLSGNGEVYIDRIEFVPEVVEYBAEYDFEKAQEV 655

Qy 664 FTSTNPRGLKTDVVDYHIDQVSNLVSLSDFYLDKEKRELFEIVKYAKQLHIERNM 719
Db 656 FTNTNPRRLKTDVVDYHIDQVSNLVSLSDFYLDKEKRELFEIVKYAKQLHIERNM 711

RESULT 5
US-09-988-462-7
; Sequence 7, Application US/09988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
```

Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Lauais, Karen L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Syngenta Biotechnology, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/988,462  
FILING DATE: 20-No. US20030046726A1-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/547,422  
FILING DATE: 11-APR-2000  
APPLICATION NUMBER: US 08/459,504  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-188051  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7  
Query Match 60.3%; Score 2265.5; DB 10; Length 1207;  
Best Local Similarity 64.3%; Pred. No. 1.1e-182;  
Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;  
QY 40 EDCLKMSEYENVEPVSAITQTGTGAGKILGTLPVFPAGQVNASLYSIFLGLWPKGN 99  
DB 10 EDSLCAAGNIDPPVSASTVQTGINAGRLVGLVFPAGQLASFYSFLVGLWPRGRD 69  
QY 100 QWEIFMEHVEEITNOKISTYARNKALTDLKGGLDALAVYHDSLESWVGNRNTFARSVVK 159  
DB 70 QWEIFLEHVEQLNQITENARTALRQLGLGDSFRAYQOQSLDLENRDDAKTRSVLY 129  
QY 160 SQYIALELMFVKQLPSFAVSGEVPFLPYQAANLHLLLRDASIFGKWLSSRIST 219  
DB 130 TQYIALELDPLNAPLFAIRNVEVFLMVAQAANLHLLLRDASLFGSEPLTSQBIOR 189  
QY 220 FYNQROVERAGDSYDHCVKWYSTGLNLRGTNAESWVRYNQPRRDMTLMVLDLVALFPSYD 279  
DB 190 YERQOVERTRDYSDYCVENYNTGLNSLRGTNAESWVRYNQPRRDLTLGLVLDLVALFPSYD 249  
QY 280 TOMYPKTKTAQLTREYVTDATGTVHPHPSFTSTTWNNNAPSFSAIEAAVVRNPHLLDFL 339

DB 250 TRTYPINTSAQLTREYVTDATGAT--GVNMAWMWNNNAPSFSAIEAAAIRSPHLLDFL 307  
QY 340 EQVTIYLLSRWNTQYMMNMGHLEFRITGTLNISTOGSTNTSINPVTLPTFRDYY 399  
DB 308 EQLTIFSSASRWSNTRMTYWRGHTIOSRPIGGLNTSIHGATNTSINPVTLRFASRDY 367  
QY 400 RTESLAGLNLF--LTQPVNGVPRVDFHFKFVTHP-----IASNFYYPGAGTGTOLDS 452  
DB 368 RTESVAGVLLWGIYLEPIHGVTVRNF--TNPQNISDRGTANYSOP--YESPGLQKDS 423  
QY 453 ENELPPEATQPNYESYSHRSLSHIGLSASHKALVYSWTHRSADRNTTNPNSITQIPL 512  
DB 424 ETELPPETTERPNYESYSHRSLSHIGILOSQVNVVYSWTHRSADRNTTGNRITQIPM 483  
QY 513 VKAFNLSSGAAVVRGPGTGGDILRRNTTGTGDIRVNINPPPPAQRVVRIRIYASTTDLQ 572  
DB 484 VKASELPQGTTVVRGPGTGGDILRRNTTGGGPIRVTVANGPLTQRYRIGFRYASTVDFD 543  
QY 573 FHTSINGKAINQGNFSATMNRGEDIYKTFRTVGTFTTPESELDYQSTFTICAMNFSGNE 632  
DB 544 FVSRGGTTVANNFRFLRTMNSGDELKYGNFVRRAPFTTPTFTQDIIRTSIOGLSGNGE 603  
QY 633 VVIDRIEFVPEVTEYAEYDEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLS 692  
DB 604 VYIDKIEIIPVTATFEAYDLERAQEAVALFTNINPRRLKTDVTDYHIDQVSNLVACLS 663  
QY 693 DEFYLDKRELFELVKYAKQLHIRMN 719  
DB 664 DEFCLDEKELLEKVKYAKRLSDERNL 690

RESULT 6  
US-10-428-961-63  
Sequence 63, Application US/10428961  
Publication No. US20030237111A1  
GENERAL INFORMATION:  
APPLICANT: Baum, James A.  
APPLICANT: Chu, Chih-Rei  
APPLICANT: Donovan, William P.  
APPLICANT: Gilmer, Amy J.  
APPLICANT: Rupar, Mark J.  
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)  
FILE REFERENCE: MECO201-1  
CURRENT APPLICATION NUMBER: US/10/428,961  
CURRENT FILING DATE: 2003-05-02  
PRIOR APPLICATION NUMBER: 09/661,322  
PRIOR FILING DATE: 2000-09-13  
PRIOR APPLICATION NUMBER: 60/153,995  
PRIOR FILING DATE: 1999-09-15  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 63  
LENGTH: 1227  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis  
US-10-428-961-63

Query Match 58.2%; Score 2186.5; DB 15; Length 1227;  
Best Local Similarity 59.2%; Pred. No. 5.6e-176;  
Matches 423; Conservative 105; Mismatches 173; Indels 13; Gaps 3;  
QY 13 SSNAKVDKISTDSLKN-----ETDIELQNIHEDCLKMSEYENVEPVSAITQTGTG 65  
DB 7 NENEIINALSIPAVNSHSAQNMNSTDARI-----EDSLCAAGNIDPPVSASTVQTGIN 61  
QY 66 IAGKILGTLPVFPAGQVNASLYSIFLGLWPKGNQWEIFMEHVEEITNOKISTYARNKAL 125  
DB 62 IAGRILGVLGVFPAGQIASFYFLVGLWPRGRDPWEIFLEHVEHLIRQVTEINTRDAL 121  
QY 126 TDLKGLGDALAVYHDSLESWVGNRNTFARSVVKSOYIALELMFVKQLPSFAVSGEVP 185





Thu Mar 10 14:26:04 2005

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; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; US-10-614-524-2

Query Match      56.3%; Score 2116; DB 15; Length 1228;
Best Local Similarity 59.5%; Pred. No. 5,4e-170;
Matches 424; Conservative 98; Mismatches 181; Indels 10; Gaps 7;

QY 13 SSNAKVDKISDLSKN-ETDIELQ-NINHEDCMKSEYENVEPVFVASTIQTGIGIAGKI 70
Db 7 NENEIINALSPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPAGQVASYLSFILGELMPKGNQWEIEMHEVEEIIINOKISITYARNKALTDLKG 130
Db 67 LGVLGVPPAGQIASFYSFLVGLMWRGRDQWEIIEHVEQLINQOITENARNATALARLQ 126
QY 131 LGDALAVYHDSLESVWGNRNTRARSVVKSOYIALELMFVOKLPSPFAVSGEEVPLPIYA 190
Db 127 LGDSFRAYQOQSLDLEWENRDDRARSVLTYQYIALELDLFLNAMPFLAIRNQEVPLLMVYA 186
QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSDHCVKWYSTGLNNLRGTN 250
Db 247 AASWRYNQFRDLTLGVLDLVALPSPYDTRTYPINTSAQLTREVVYDAIGAT--GVNMA 304
QY 311 STTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLSRWNTQYMMNGHKLFRIT 370
Db 305 SMWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSRWSATRHMTYWRGHTIQSRPI 364
QY 371 GGTINTSTQGSTNTSINPVTLPFTSRDVTYRTESLAGLNF--LTOPVNGVPRVDFHMKFV 428
Db 365 GGGINTSTHGSTNTSINPVLRSFFSRDVTYRTESLAGLNF--LTOPVNGVPRVDFHMKFV 424
QY 429 --THPIASDNFYPGVAGIGTLODSENELPPEATGQPNYESYSHRLSHIGLISASHVKA 486
Db 425 QNTFERGTANYSQP--YESPGLQKLDSELPETTERPNYESYSHRLSHIGLISASHVKA 483
QY 487 LVYSWTHRSADRTNTIENPNSITQIPVKAFNLSGAAVRGPGTGGDILRRNTGTGFGD 546
Db 484 PVYSWTHRSADRTNTISSDITQIPVKFNLNSGTSVSGPGTGGDILRRNVNGSVLS 543
QY 547 IRVNIINPPFAORYVRIRYASTTDLQPHTSINGKAINQGNFSAATMNRGEBDLYKTRTVG 606
Db 544 MGLNFNTSLQRYVRVRYAASQTMVLRTVVGSTTDFDQGFPTMSANESLTSQSFRAE 603
QY 607 FTTPFSLDVQSTFTICAMNPFSSGNEVYIDRIEFVPEVYEAEDYFEKAQEKVTAFTS 666
Db 604 FPVGISASGSQ--TAGISISNNAQRQTDFDKIEFIPITATFEAEYDLERAQEAVALFTN 662
QY 667 TNPRLKTDVVDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 663 TNPRLKTDVTDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 715

RESULT 10
US-09-826-660-25
; Sequence 25, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05

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; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in ver. 2.0
; SEQ ID NO 25
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-25

Query Match      51.4%; Score 1932.5; DB 9; Length 643;
Best Local Similarity 57.7%; Pred. No. 7.5e-155;
Matches 371; Conservative 100; Mismatches 159; Indels 13; Gaps 3;

Qy 13 SSNAKVDKISTDSLN-----ETDIELQNHEDCLKMSSEYENVEPVFVASTIQTGIG 65
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
7 NENEIINALSPAVNSHSAQMNLSIDARI-----EDSLCIAEGNIDPFVSASTVQTGIN 61

Qy 66 IAGKILGTGVFPAGQVASLYSFLGELWPKGKQWEIFMEHVEEIIINOKISTYARKAL 125
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 IAGRILGVLGVPFAGQIASFSYFLVGLWPRGRDFEFLSHVEQLIRQQVTENTRDAL 121

Qy 126 TDLKGLGDALAVYHDSLSWGNRNTRARSVKSQYIALELMFVKQLPSFAVSGEEVPL 185
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
122 ARLOGLGNSFRAYQOSLEDWLENRDDATRSVLTYQYIALELDFLNAFPLFAIRNQEVPL 181

Qy 186 LPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKVKTSTGLNN 245
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
182 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEKREYSDYCARWYNTGLNN 241

Qy 246 LRGTAESWRYNPOFRDMTLMVLDLVALFPSYDTQMTPIKTTAQLTREVTDAIGTVHP 305
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
242 LRGTAESWLYNPOFRDLTLGLVDLVALFPSYDTRVYPMNTSAQLTREIYTDPIGRNA 301

Qy 306 HPSFTSTWYNNAPSAIEAAVVRNPHLDLEOVITYSLRWSNTQYMMWMMGGHKL 365
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
302 PSGFASTWFWNNAPSAIEAAVVRNPHLDLDFPEQLTIFSVLRWSNTQYMMWMMGGHKL 361

Qy 366 EFRTIGTGLNISTOGSTNTSINPVLTPTRSDVYRTESLAGINLFLTPVNGVPRVDPHW 425
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
362 ESRTIGSLSTHGTNTSINPVLTPTRSDVYRTESFAGINILLITPVNGVPPWARENW 421

Qy 426 KFTVHTPIASDNFYPGYAGITQLODSNELPPATGQPNYESYSHRLSHGLISASHVK 485
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
422 RNPLNSLRGSLTYTIGYGVGTQQLFDSSETLPPETTERPNYESYSHRLSNRLISGNTLR 481

Qy 486 ALVYSWTHRSADRTNTEPNSTIQTPLKAFNLGSAVVRGPGFTGGDILRRNTGTFG 545
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
482 APVYSWTHRSADRTNTEPNSTIQTPLKAFNLGSAVVRGPGFTGGDILRRNTGTFG 541

Qy 546 DIRVNINPPFAQRVRYRYASTTDLPQHTSINGKAINQGNFSAFMNKGEDLDYKTFRTV 605
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
542 SMGLNFNNTSLQRVRYRYAASQTMVLRTVVGSGTTDFQGFPTMSANESLTSQSFEFA 601

Qy 606 GFTTFPSFLDVQSTFTIGAMFPSSGNEVYIDRIEFPVVEVTEYE 648
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
602 EFPVGISASGSQ-TAGISISNNAAGRTQPFHFKIEFIPITATLE 643

RESULT 11
US-10-089-678-1
; Sequence 1, Application US/10089678
; Publication No. US20030017967A1
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shinichiro
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A
; TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
```

```
; FILE REFERENCE: Q68821
; CURRENT APPLICATION NUMBER: US/10/089,678
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: JP 2000-236140
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/JP01/06660
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-089-678-1

Query Match      45.8%; Score 1722.5; DB 14; Length 1167;
Best Local Similarity 47.9%; Pred. No. 1.3e-136;
Matches 361; Conservative 126; Mismatches 218; Indels 49; Gaps 12;

Qy 1 MKLNQKQKHQ---SFSSNAKVDKISTDSLNKNETDIELQNHEDCLKQSEYE-----NV 51
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MSPNNQNEYELDDASSSTVSNSVRYPLANDQTTTLQNNMYKDYLRMSEGENPELFGNP 60

Qy 52 EPPVSASTIOTGIGIAGKILGTGVFPAGQVASLYSFLGELWPKGK-NQWEIFMEHVEE 110
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 ETFISSSTVQTGIGVGOVLGALGVFPAGQIASFSYFIVGQWPSSTVSVMEMMKQVED 120

Qy 111 IINOKISTYARKALTDLKGGLDALAVYHDSLSWGNRNTRARSVKSQYIALELMFV 170
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121 LIDOKITDSVRKTALAGLOGLDGVDYQKSLKNWLENENDTRARSVVVTVYIALELDFV 180

Qy 171 QKLPFSAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGD 230
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
181 AKIPSAISGQEVPLLSVYAQAANLHLLLRDASIFGAEWGFTGCEISTFYDRQVTRTAQ 240

Qy 231 YSDHCVKWYSGLNLLRGTAESWRYNPOFRDMTLMVLDLVALFPSYDTQMTPIKTTAQ 290
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
241 YSDYCVKWYNTGLDKLGTNAASWLKHYQHFREMTLLVLDLVALFPNDYTRTPYLETAAQ 300

Qy 291 LTRVYVYDAIGTVHPSPFTSTWYNNAPSAIEAAVVRNPHLDLDFLEOVITYSLS- 349
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
301 LTRVYVYDPIVFNRETSGGFCRRMSLNSDISFSEVESAVIRSPHLFDLSIEFFYTRAG 360

Qy 350 -RWSNTQYMMWMMGGHKLFFRTIGTGLNISTOGSTNTSINPVLTPTRSDVYRTESL-AGL 407
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
361 LPLNTEYLEYVWGHGSIKYKNTNASSALERNYGTITSNKIKYYDLANKDIFQVRSLGADL 420

Qy 408 NLFLTQPVNGVPRVDVPHWKVTHPIASDNFYPGYAGIG-----TQLQDSE 453
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
421 ANYTAQ-VYGVYASFP-----TLDDKN---TSGSGVGGFTYSKPHPTTMQVCTQNYNTI 469

Qy 454 NELPPEATGQPNYESYSHRLSHGLIS-----ASHVKALVYSWTHRSADRTNTEPN 505
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
470 DEIPEE--NEPLSGYSHRLSHITSYSFKNASSPARYGNLPVFAWTHRSADRTNTEPN 527

Qy 506 SITQIPLVKAFNLGSAVVRGPGFTGGDILRRNTGTFGDIRVNINPPFAQRVRYRY 565
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
528 KITQIPVKAHTLVSGTTVIKPGPGTGCNLLKRTSSGGLAVTSVSKVSPLSQRYRARIY 587

Qy 566 ASTTDLQHTSINGKAINQGNFSAFMNKGEDLDYKTFRTVGTFTFPFSLDVQSTFTIGAW 625
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
588 ASTTNLRLFTVISGTRIYSINVNKTMKGGDLTFTNTFDLATIGTAFTEFNSYSDSLTVGAD 647

Qy 626 NFSGNEVYIDRIEFPVVEVTEYAEYDEKAEQKVLTALFTSTNPRGLKTDVKDHYHDQVS 685
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
648 SFASGGEVYVDKFEIIPVNATFEABEDLDVAKKAVNGLFTSKKD-ALQTSVTDVQVNOAA 706

Qy 686 NLVESLSDDEFYLDREKRELFEIVKYAKQLHIERNM 719
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
707 NLVECLSDLEYPNKRMWDAVKEAKRLVQARNL 740
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RESULT 12

647	YEAAYDFEYKAE	658
:	: ::   :	:
641	FEVEYDLERAQK	652
RESULT 13		
US-10-782-141-16		
; Sequence 16, Application US/10782141		
; Publication No. US2004019791A1		
; GENERAL INFORMATION:		
; APPLICANT: Carozzi, Nadine		
; APPLICANT: Harziss, Tracy		
; APPLICANT: Koziel, Michael G.		
; APPLICANT: Duck, Nicholas B.		
; APPLICANT: Carr, Brian		
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and		
; TITLE OF INVENTION: Methods for Its Use		
; FILE REFERENCE: 045600/274143		
; CURRENT APPLICATION NUMBER: US/10782,141		
; CURRENT FILING DATE: 2004-02-20		
; PRIOR APPLICATION NUMBER: 60/448,632		
; PRIOR FILING DATE: 2003-02-20		
; NUMBER OF SEQ ID NOS: 23		
; SOFTWARE: FastSeq for Windows Version 4.0		
; SEQ ID NO 16		
; LENGTH: 1157		
; TYPE: PRT		
; ORGANISM: Bacillus thuringiensis		
US-10-782-141-16		
Query Match      44.4%; Score 1670.5; DB 16; Length 1157;		
Best Local Similarity 49.1%; Pred. No. 3.3e-132; Indels 57; Gaps 18;		
Matches 371; Conservative 98; Mismatches 230;		
QY	1 MKLNQDQHQSFSNAKYDKISTDS----	
DB	1 MSPNNQNEYIILIDATPST-SVSSDSNRYPFANEPTDALONMNYDYLKMSGGENPELFGN 59 ;	
QY	51 VEPFVSASTIQTGIGIAKIIGTGVPPAGVASLYSIFLGELWP-KGKNOWEIFMEHVE 109 ;	
DB	60 PETFISSTIQTGIVGRILLGALGVPPASQAFYSFVIGQLWPSKSVDIWGIMEERVE 119 ;	
QY	110 EIINKIKISTYARNKALTDLKGLGDALAVYHDSLSWSVGNNRNTARSVVKSQYIALELMFP 169 ;	
DB	120 ELVDQKIEKYKKALKALBELKGLNALDVYQQSLDWLENRDARTSRVVSNQFIALDLNF 179 ;	
QY	170 VKQLSPFAVSGBEVFLPIYAQAAMHLHLRLDASIFGKEWGLSSSEISTFNVRVERAG 229 ;	
DB	180 VSSIPSFVAVSGHEVLLAVYAQVNHLHLRLDASIFGEEWGFTEGEISRFRNVQRQLTA 239 ;	
QY	230 DYSDHCWKYVYGLNNLRGTNAESVRYNPNRPDRMTLWLVLVALFPSYDTQMYPKTTA 289 ;	
DB	240 EYSDYCVRWYKTLGDKLKGTTSKMLNHQFREMTLLVLDLVALFPNYDTHMYPIETTA 299 ;	
QY	290 QLTREYVTDAIGTVHPHPSFTST----TWYNNNAPSFSAIEAAVRNPHELLFLFQVITY 345 ;	
DB	300 QLTRDYVTDPIA----FNIVTSGFCNPNWSTHSGLIFYEVENNVRPRPHLPFILSSVEIN 355 ;	
QY	346 SLLSR-----WSNQTYANMGGHLEPR-----TIGGTLANISQTGSTNTSINPVTLPPFTR 396 ;	
DB	356 T--SRGGITLNDDAYINYWSGHTLKYRRADSTVTVTANYGRITSEKNS-----PALED 408 ;	
QY	397 DVYRTESLAGNLFLTQPNGVGRVDFHWKFVTHPIASDNFY-----YPGYAGIGTOLOD 451 ;	
DB	409 DIFEINSTVANLAYQYKAYGVPGSWFH--MVKRGTSSTTAVLYSKTHATALOGC-TQVYE 465 ;	
QY	452 SENELPPEATGPQNYGSYSHRLSHI-----GLISASHVKALVYSWTHRSADRNTTIE 503 ;	
DB	466 SSDEIPLDRT-VPVABSYSHRLSHITSHPFSKNG--SAYYGSFPVFVWHTSADLANNTY 522 ;	
QY	504 PNSITOTPLVKAFNLSSGAADVPGPFGTDGILRRNTGTGFDIRVINNPFFAQRVRI 563 ;	

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Db 523 SDKITQIPAVKGMILYLGSSVVGPGFTGGDILKRTNPISILGTFAVTNGSLSQRYRVI 582
Qy 564 RYASTDLOFHTSINGKAINQGNFSATMNRGDLDTYKTRFVGTTPPSFLDVGSTFTIG 623
Db 583 RYASTDDEF-TLYLGDITIEKNRKNKMDNGASLTETFEASFITDQFRETQDKILLS 641
Qy 624 AWFSSGNEVYIDRIEFVPEVVEAEYDFEKAQEKVTALETSTNPRGLKTDVXDYHDO 683
Db 642 MGFSSGVEVYIDRIEFIPVDETVEAEODLEAAKAVNALFTNTKD-GLRPGVTDYEVNQ 700
Qy 684 VSNLVESLSDFYLDEKRELFIEVKYAKQLHIERNM 719
Db 701 AANLVECLSDLLYPNEKRLLFDAVREAKRLSGARNL 736

RESULT 14
US-10-032-717-2
; Sequence 2, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-032-717-2

Query Match 40.2%; Score 1511; DB 13; Length 1206;
Best Local Similarity 44.3%; Pred. No. 1.2e-118;
Matches 337; Conservative 130; Mismatches 229; Indels 64; Gaps 22;

Qy 1 MCLKNQDKHQSFSNAKVDKISTDS---LKNETDIELQINIHEDCLKM-----SEYE-N 50
Db 1 MSPNNQNEYEIIDATPST-SVNSDSNRYPPFANEPTNALQNDYKDYLKMSAGNASEYPGS 59
Qy 51 VEPFVSA-STIQTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKG-KNQWEIFMEHV 108
Db 60 PEVLVSGQDAAKAIDIVGKLSGLGVFPVGVPIVSLYTQLIDILWPSGEKSQWEIFMEQV 119
Qy 109 EEINQKISTYARNKALTDLKGDLALAVYHDSLESWVGNRNNTFARSVVKSOYALELM 168
Db 120 EEINQKIAEYARNKALSELEGLNYYQLYLTALSEENPNNGSRALDRVRNREILDSL 179
Qy 169 FVQKLPSFAVSGEEVPLPIYAOANLHLLLRDASIFGKEWGLSSSSEISTFYNROVERA 228
Db 180 FTQWPSFRVTNFEVPLTVYAMAANLHLLLRDASIFGEEWGSTTITNNYDQMKLT 239
Qy 229 GDYSDHCWKYSTGLNNLRGTNAESWRYNQFRDRMTLMVLDLVALFPSTQYMPYIKTT 288
Db 240 AEYSDHCWKYETGLAKLKGTSKQWVDYQFRREMTLAVLDVVALFNYDTRTPMETK 299
Qy 289 AOLTRVYTDIAITVHPHSTSTTWYNNNAPSFAIEAAVVRPHLLDFLEQVITYSL 348
Db 300 AOLTRVYTDPLGAVNVS---SIGSWY-DKAPSGFVIESSVIRPBPVDPYITGLTVYTQS 355
Qy 349 SRWNTQTMNMWGHKLEFRITGTLNISTQGSTNTSINPV-TLPFTSRDVRVRESLAGL 407
Db 356 RSISARYIRHWAGHQISYHRVSRGSLQQMYGTNQNLHSTSTDFDTNYDIKTLSDKAV 415
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Qy 408 NLFLTQP-----VNGVPRVDFHWKVTHTPIASDN---FYYPGYAGIGTQLQDSENELPPE 459
Db 416 LLDIVYPGYTYIFFGMEPEF---FMVQLANNTRKTLKYNPVSOKDIIIASTRDSLELPPE 472
Qy 460 ATGPDPNYESYSHRLSHIGLISAS-HVKAL--VYSWTHRSADRTNTIEPNSITQIPLVKAF 516
Db 473 TSDQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNIYSDKITQIIPAVKCM 532
Qy 517 NLSGAAVVRGPGFTGGDILR-RTNWTGTFGDI---RVNINPPFAQRYRVRIRYASTTDIQ 572
Db 533 DNLFPVPVVGPGFTGGDILQVNRSTGSGVTLFLARYGLALEKAGKYRVLRYATDADIV 592
Qy 573 PHTSINGKAINQGNFSATMNRGDLDTYKTR-----TVGFTTPPSFL-----DVQST 619
Db 593 LH--VNDAAQI---QMPKTMNPGEDLTSKTFKVADAITTLNLATDSSSLAKHNLGSDPNST 647
Qy 620 FTIGAWNPFSSGNEVYIDRIEFVPEVVEAEYDFEKAQEKVTALETSTNPRGLKTDVXDY 679
Db 648 LS-----GIVYVDRIEFIPVDETVEAEODLEAAKAVNALFTNTKD-GLRPGVTDY 697
Qy 680 HIDQVSNLVESLSDFYLDEKRELFIEVKYAKQLHIERNM 719
Db 698 EVNQAAANLVECLSDLLYPNEKRLLFDAVREAKRLSEARNL 737

RESULT 15
US-10-414-637-2
; Sequence 2, Application US/10414637
; Publication No. US20030177528A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With
; FILE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/414,637
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-414-637-2

Query Match 40.2%; Score 1511; DB 14; Length 1206;
Best Local Similarity 44.3%; Pred. No. 1.2e-118;
Matches 337; Conservative 130; Mismatches 229; Indels 64; Gaps 22;

Qy 1 MCLKNQDKHQSFSNAKVDKISTDS---LKNETDIELQINIHEDCLKM-----SEYE-N 50
Db 1 MSPNNQNEYEIIDATPST-SVNSDSNRYPPFANEPTNALQNDYKDYLKMSAGNASEYPGS 59
Qy 51 VEPFVSA-STIQTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKG-KNQWEIFMEHV 108
Db 60 PEVLVSGQDAAKAIDIVGKLSGLGVFPVGVPIVSLYTQLIDILWPSGEKSQWEIFMEQV 119
Qy 109 EEINQKISTYARNKALTDLKGDLALAVYHDSLESWVGNRNNTFARSVVKSOYALELM 168
Db 120 EEINQKIAEYARNKALSELEGLNYYQLYLTALSEENPNNGSRALDRVRNREILDSL 179
Qy 169 FVQKLPSFAVSGEEVPLPIYAOANLHLLLRDASIFGKEWGLSSSSEISTFYNROVERA 228
Db 180 FTQWPSFRVTNFEVPLTVYAMAANLHLLLRDASIFGEEWGSTTITNNYDQMKLT 239
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2005, 17:18:14 ; Search time 23.1512 Seconds  
(without alignments)  
2318.356 Million cell updates/sec

Title: US-10-019-823B-55  
Perfect score: 3760  
Sequence: 1 MLLKNQKHQSFSNAKVDK.....KRELFEIVKYAKQLHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3756	99.9	719	3	US-08-286-870A-8
2	3476.5	92.5	710	4	Sequence 8, Appli
3	3398	90.4	648	3	Sequence 42, Appl
4	3377	89.8	719	2	Sequence 4, Appli
5	3372	89.7	719	3	Sequence 2, Appli
6	2804	74.6	535	3	Sequence 6, Appli
7	2446.5	65.1	1229	1	Sequence 4, Appli
8	2446.5	65.1	1229	1	Sequence 4, Appli
9	2446.5	65.1	1229	1	Sequence 4, Appli
10	2446.5	65.1	1229	2	Sequence 4, Appli
11	2446.5	65.1	1229	2	Sequence 4, Appli
12	2344.5	62.4	488	1	Sequence 10, Appl
13	2344.5	62.4	488	3	Sequence 10, Appl
14	2265.5	60.3	1207	1	Sequence 7, Appli
15	2265.5	60.3	1207	2	Sequence 7, Appli
16	2265.5	60.3	1207	3	Sequence 7, Appli
17	2265.5	60.3	1207	3	Sequence 7, Appli
18	2265.5	60.3	1207	3	Sequence 7, Appli
19	2265.5	60.3	1207	3	Sequence 7, Appli
20	2265.5	60.3	1207	3	Sequence 7, Appli
21	2265.5	60.3	1207	3	Sequence 7, Appli
22	2264.5	60.2	1227	3	Sequence 2, Appli
23	2195.5	58.4	1227	1	Sequence 8, Appli
24	2195.5	58.4	1227	3	Sequence 9, Appli
25	2186.5	58.2	1227	4	Sequence 63, Appl
26	2171.5	57.8	1186	3	Sequence 23, Appl
27	2171.5	57.8	1186	4	Sequence 23, Appl

28 2116 56.3 1228 4 US-09-661-322A-38  
29 1932.5 51.4 643 3 US-09-178-252-25  
30 1932.5 51.4 643 4 US-09-826-660-25  
31 1900 50.5 380 5 PCT-US91-02560-4  
32 1681.5 44.7 653 4 US-09-661-322A-6  
33 1670.5 44.4 1157 1 US-07-876-380-30  
34 1670.5 44.4 1157 1 US-07-812-180A-2  
35 1670.5 44.4 1157 1 US-08-315-468-2  
36 1670.5 44.4 1157 3 US-07-941-650A-2  
37 1507.5 40.1 1176 1 US-08-257-999-2  
38 1492 39.7 1157 2 US-08-532-547-5  
39 1492 39.7 1157 2 US-08-379-656B-5  
40 1492 39.7 1157 3 US-08-455-838-5  
41 1492 39.7 1157 3 US-09-019-809-5  
42 1492 39.7 1157 4 US-09-471-177-5  
43 1492 39.7 1157 4 US-09-220-806-5  
44 1486.5 39.5 1169 1 US-08-315-468-4  
45 1485.5 39.5 1156 3 US-09-002-285-72

#### ALIGNMENTS

RESULT 1  
US-08-286-870A-8  
; Sequence 8, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/286,870A  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PAUL N. KOKULIS  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 70608/220720  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-286-870A-8

Query Match 99.98; Score 3756; DB 3; Length 719;  
Best Local Similarity 99.94; Pred. No. 0; Indels 0; Gaps 0;  
Matches 718; Conservative 1; Mismatches 0;  
US-09-661-322A-42

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1 M K L K N Q D K H Q S F S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M E Y E N V E P F V S A S T I 60  
61 Q T G I G I A K I L G T L G V P P A G V A S L Y S F I L G E L W P K G N O W E I P M E H V E I I N K I S T Y A 120  
61 Q T G I G I A K I L G T L G V P P A G V A S L Y S F I L G E L W P K G N O W E I P M E H V E I I N K I S T Y A 120  
121 R N K A L T D L K G L G D A L A V H D S L E S W G N R N N T R A R S V V K S Q Y I A L E M F V Q K L P S P A V S G 180  
121 R N K A L T D L K G L G D A L A V H D S L E S W G N R N N T R A R S V V K S Q Y I A L E M F V Q K L P S P A V S G 180  
181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R O V E R A G D Y S D H C V K W Y S 240  
181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R O V E R A G D Y S D H C V K W Y S 240  
241 T G L N L R G T N A B S W R Y N Q F R D M T L M V L D L V A L P P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
241 T G L N L R G T N A B S W R Y N Q F R D M T L M V L D L V A L P P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
301 G T V H P H P S T T T W Y N N A P S F A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
301 G T V H P H P S T T T W Y N N A P S F A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
361 G G H K L E F R I G T L N I S T O G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
361 G G H K L E F R I G T L N I S T O G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
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421 V D F H K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T Q P N Y E S Y S H R L S H I G L I S 480  
481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540  
481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540  
541 T G T F G D I R V N I N P P F A Q R Y R V R I Y A S T T D L Q P H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
541 T G T F G D I R V N I N P P F A Q R Y R V R I Y A S T T D L Q P H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
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601 T F R T V G T T P P S F L D V Q S T T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
661 T A L F T S T N P R G L K T D V Q D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q L H I E R N M 719  
661 T A L F T S T N P R G L K T D V Q D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q L H I E R N M 719

RESULT 2  
US-09-661-322A-42  
; Sequence 42, Application US/09661322A  
; Patent No. 6593233  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Ruper, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo  
; FILE OF INVENTION: and Methods of Use  
; FILE REFERENCE: MECO201  
; CURRENT APPLICATION NUMBER: US/09/661,322A  
; CURRENT FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 42  
; LENGTH: 710  
; TYPE: PRT

ORGANISM: Bacillus thuringiensis  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (200)..(200)  
OTHER INFORMATION: No. 6593293-Coding  
US-09-661-322A-42

Query Match 92.58; Score 3476.5; DB 4; Length 710;  
Best Local Similarity 92.58; Pred. No. 5.5e-303;  
Matches 665; Conservative 15; Mismatches 30; Indels 9; Gaps 1;  
US-08-286-870A-4

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61 Q T G I G I A K I L G T L G V P P A G V A S L Y S F I L G E L W P K G S Q W E I P M E H V E I I N K I S T Y A 111  
52 Q T G I G I A K I L G T L G V P P A G V A S L Y S F I L G E L W P K G S Q W E I P M E H V E I I N K I S T Y A 111  
121 R N K A L T D L K G L G D A L A V H D S L E S W G N R N N T R A R S V V K S Q Y I A L E M F V Q K L P S P A V S G 180  
112 R N K A L A D L K G L G D A L A V H S L E S W I E N R N T R S V V K S Q Y I T L E M F V Q S L P S F A V S G 171  
181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R O V E R A G D Y S D H C V K W Y S 240  
172 E V P L L P I Y A Q A A N L H L L L R D A S I F G K W G L S D S E I S T F Y N R O S G K S E Y S D H C V K W Y N 231  
241 T G L N L R G T N A B S W R Y N Q F R D M T L M V L D L V A L P P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
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412 V D F H K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T Q P N Y E S Y S H R L S H I G L I S 471  
481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540  
472 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R K N 531  
541 T G T F G D I R V N I N P P F A Q R Y R V R I Y A S T T D L Q P H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
532 T G T F G D I R V N I N P P F A Q R Y R V R I Y A S T T D L Q P H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 591  
601 T F R T V G T T P P S F L D V Q S T T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
592 T F R T V G T T P P S F S D V Q S T T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E E V 651  
661 T A L F T S T N P R G L K T D V Q D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q L H I E R N M 719  
652 T A L F T S T N P R G L K T D V Q D Y H I D Q V S N L V E S L S D F Y L D E K R E L F E I V K A Q L H I E R N M 710

RESULT 3  
US-08-286-870A-4  
; Sequence 4, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN



```
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-870A-4

Query Match 90.4%; Score 3398; DB 3; Length 648;
Best Local Similarity 100.0%; Pred. No. 5.3e-236;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCLKNQKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKXSEYENVEPVSASTI 60
Db 1 MCLKNQKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKXSEYENVEPVSASTI 60

Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIEMEHVEEIIINOKISTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIEMEHVEEIIINOKISTYA 120

Qy 121 RNKALTDLKGGLDALAVYHDSLESVGNRNNTARSVVKSYIALELMFVKLPSPFVSG 180
Db 121 RNKALTDLKGGLDALAVYHDSLESVGNRNNTARSVVKSYIALELMFVKLPSPFVSG 180

Qy 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFTYNQVERAGDYSCHVKWYS 240
Db 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFTYNQVERAGDYSCHVKWYS 240

Qy 241 TGLNLRGTNAESWVRVYNOFRDMLVLDLVALPSPYDTQMPYIKTTAQLTRVYTDAL 300
Db 241 TGLNLRGTNAESWVRVYNOFRDMLVLDLVALPSPYDTQMPYIKTTAQLTRVYTDAL 300

Qy 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360

Qy 361 GGHKLEFRTIGTTLNISTQGTNTSINPTVLPFTSRDVRTESLAGLNLFTQPVNGVPR 420
Db 361 GGHKLEFRTIGTTLNISTQGTNTSINPTVLPFTSRDVRTESLAGLNLFTQPVNGVPR 420

Qy 421 VDFHWKFTVTHPIASDNFYPYAGIGTQQLQDSENLPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYPYAGIGTQQLQDSENLPEATGQPNYESYSHRLSHIGLIS 480

Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540

Qy 541 TGTEGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATWNRGSDLDYK 600
Db 541 TGTEGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATWNRGSDLDYK 600

Qy 601 TFRTVGFTTTPSFVLDVOSTFTIGAWNFSSGNEVYIDRIEFVPEVETYE 648
Db 601 TFRTVGFTTTPSFVLDVOSTFTIGAWNFSSGNEVYIDRIEFVPEVETYE 648

RESULT 4
US-09-003-217-2
; Sequence 2, Application US/09003217
; Patent No. 5986177
; GENERAL INFORMATION:
; APPLICANT: Osman, Yehia A.
; APPLICANT: Madkour, Magdy A.
; APPLICANT: Bulla, Lee A.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
; TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
; STREET: 3605 Glenwood Ave. Suite 310
; CITY: Raleigh
; STATE: NC
; COUNTRY: US
; ZIP: 27622
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,217
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 5718-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2202
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-003-217-2

Query Match 89.8%; Score 3377; DB 2; Length 719;
Best Local Similarity 89.8%; Pred. No. 4.8e-294;
Matches 646; Conservative 33; Mismatches 40; Indels 0; Gaps 0;

Qy 1 MCLKNQKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKXSEYENVEPVSASTI 60
Db 1 MCLKNPDKHTLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPPFVSASTI 60

Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIEMEHVEEIIINOKISTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIEMEHVEEIIINOKISTYA 120

Qy 121 RNKALTDLKGGLDALAVYHDSLESVGNRNNTARSVVKSYIALELMFVKLPSPFVSG 180
Db 121 RNKALTDLKGGLDALAVYHDSLESVGNRNNTARSVVKSYIALELMFVKLPSPFVSG 180

Qy 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFTYNQVERAGDYSCHVKWYS 240
Db 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFTYNQVERAGDYSCHVKWYS 240
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us-10-019-823b-55-rai

Thu Mar 10 14:26:04 2005

Db 181 EVPLLPIYAAANLHLLLRDASIFEKNGGLSASBISTFYNRQVTRDYSHYCHVKNW 240  
 Qy 241 TGLNLRGTNAESWVRVYQFRDMTLMVLDLVALFSDYDQWYPIKTTAQLTREVYTDI 300  
 Db 241 TGLNLRATNGQSWVRVYQFRKDIEMVLDLVRVFPSTLVYPIKTTSQLTREVYTDI 300  
 Qy 301 GTVHPHPSFTSTWYNNAPSFSAIAEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMMNW 360  
 Db 301 GTVDNQALRSTTWYNNAPSFSAIAEAAVVRNPHLLDFLEKVTIYSLLSRWSNTQYMMNW 360  
 Qy 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVLPTFSRDVYTESLAGNLFLTOPVNGVPR 420  
 Db 361 GGHRLSPRIGGALNTSQGSTNTSINPVLPTFSRDVYTESWAGNLFLTOPVNGVPR 420  
 Qy 421 VDFHKKFTHPIASDNFYVPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHKKFPTLPASDNFYVPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Qy 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGTGGDILRTN 540  
 Db 481 GSHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGTGGHILRTK 540  
 Qy 541 TGTFGDIRVNNPFAQRYVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLKY 600  
 Db 541 SGTFGHIRVNNPFAQRYVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLKY 600  
 Qy 601 TPTVGTFTPFSDVQSTFTTIGAWNFSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 Db 601 TPTVGTFTPFSDVQSTFTTIGAWNFSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 Qy 661 TALFTSTNPRGLTKDVKDHIQVSNLVSLSDEFLDEKRELFEIVYAKQIHIERNM 719  
 Db 661 TALFTSTNPRGLTKDVKDHIQVSNLVSLSDEFLDEKRELFEIVYAKQIHIERNM 719

RESULT 5  
 US-09-218-942-2  
 ; Sequence 2, Application US/09218942  
 ; Patent No. 6232439  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Osman, Yehia  
 ; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum  
 ; FILE REFERENCE: CryII  
 ; CURRENT APPLICATION NUMBER: US/09/218,942  
 ; EARLIER FILING DATE: 1998-12-22  
 ; EARLIER FILING DATE: 1997-01-10  
 ; EARLIER FILING DATE: 1997-01-10  
 ; EARLIER FILING DATE: 1998-01-06  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-09-218-942-2

Query Match 89.7%; Score 3372; DB 3; Length 719;  
 Best Local Similarity 89.8%; Pred. No. 1.3e-293;  
 Matches 646; Conservative 33; Mismatches 40; Indels 0; Gaps 0;

Qy 1 MKLNKQDQHSFSSNAKVDKISTDLKNETDIQLONINHECLKMSYENVEPVFSASTI 60  
 Db 1 MKLNKPKHQTLSSNAKVDKIATDSLKNETDIQLKNNNEDYLRMSHEHSDPFSASTI 60  
 Qy 61 QTGIGIAGKILGTLPVPPAGVASYSLFTGLWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 Db 61 QTGIGIAGKILGTLPVPPAGVASYSLFTGLWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 Qy 121 RNKALTDLKGLDALVYHDSLESWGNNRNTARSVVKVQVIALELMFVOKLPSFAVSG 180  
 Db 121 RNKALTDLKGLDALVYHDSLESWGNNRNTARSVVKVQVIALELMFVOKLPSFAVSG 180

Qy 181 EVPLLPIYAAANLHLLLRDASIFEKNGGLSSEISTFYNRQVERAGDYSDHCVKWS 240  
 Db 181 EVPLLPIYAAANLHLLLRDASIFEKNGGLSASBISTFYNRQVTRDYSHYCHVKNW 240  
 Qy 241 TGLNLRGTNAESWVRVYQFRDMTLMVLDLVALFSDYDQWYPIKTTAQLTREVYTDI 300  
 Db 241 TGLNLRATNGQSWVRVYQFRKDIEMVLDLVRVFPSTLVYPIKTTSQLTREVYTDI 300  
 Qy 301 GTVHPHPSFTSTWYNNAPSFSAIAEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMMNW 360  
 Db 301 GTVDNQALRSTTWYNNAPSFSAIAEAAVVRNPHLLDFLEKVTIYSLLSRWSNTQYMMNW 360  
 Qy 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVLPTFSRDVYTESLAGNLFLTOPVNGVPR 420  
 Db 361 GGHRLSPRIGGALNTSQGSTNTSINPVLPTFSRDVYTESWAGNLFLTOPVNGVPR 420  
 Qy 421 VDFHKKFTHPIASDNFYVPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHKKFPTLPASDNFYVPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Qy 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGTGGDILRTN 540  
 Db 481 GSHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGTGGHILRTK 540  
 Qy 541 TGTFGDIRVNNPFAQRYVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLKY 600  
 Db 541 SGTFGHIRVNNPFAQRYVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLKY 600  
 Qy 601 TPTVGTFTPFSDVQSTFTTIGAWNFSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 Db 601 TPTVGTFTPFSDVQSTFTTIGAWNFSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 Qy 661 TALFTSTNPRGLTKDVKDHIQVSNLVSLSDEFLDEKRELFEIVYAKQIHIERNM 719  
 Db 661 TALFTSTNPRGLTKDVKDHIQVSNLVSLSDEFLDEKRELFEIVYAKQIHIERNM 719

RESULT 6  
 US-08-286-870A-6  
 ; Sequence 6, Application US/08286870A  
 ; Patent No. 6063605  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ELY, S  
 ; APPLICANT: TAILOR, RH  
 ; APPLICANT: TIPPETT, JM  
 ; APPLICANT: BLENK, RG  
 ; TITLE OF INVENTION: BACTERIAL GENES  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CUSHMAN DAREY & CUSHMAN  
 ; ADDRESSEE: Intellectual Property Group of  
 ; ADDRESSEE: PULLSBURY, MADISON & SUTRO LLP  
 ; STREET: 1100 New York Avenue, N.W.  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; Zip: 20005-3918  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/286,870A  
 ; FILING DATE: 05-AUG-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION NUMBER: US 07/520228  
 ; FILING DATE: 09-MAY-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 8910624.9  
 ; FILING DATE: 09-MAY-1989

```

; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-870A-6

Query Match 74.6%; Score 2804; DB 3; Length 535;
Best Local Similarity 100.0%; Pred. No. 8.1e-243;
Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLNQDQHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPPFVASTI 60
Db 1 MKLNQDQHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPPFVASTI 60

Qy 61 QTGIGIAGKILGTLGVPAGOVASLYSFLGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
Db 61 QTGIGIAGKILGTLGVPAGOVASLYSFLGELWPKGNQWEIFMEHVEEIIINOKISTYA 120

Qy 121 RNKALTDLGLGDALAVYHDSLESVGNRNNTTRARSVVKSQYIALELMFVQKLPFAVSG 180
Db 121 RNKALTDLGLGDALAVYHDSLESVGNRNNTTRARSVVKSQYIALELMFVQKLPFAVSG 180

Qy 181 BEVPLLPYIAQAANLHLLLDASIFGKEWGLSSSEISTFFYNQVERAGDYSCHVKWYS 240
Db 181 BEVPLLPYIAQAANLHLLLDASIFGKEWGLSSSEISTFFYNQVERAGDYSCHVKWYS 240

Qy 241 TGLNLRCTNAESWRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTREYVYTDI 300
Db 241 TGLNLRCTNAESWRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTREYVYTDI 300

Qy 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYNNMW 360

Qy 361 GGHKLEFRTIGTLNISTQSTNTSINPVTLPFTSRDVRYESLAGNLFQTQPVNGVPR 420
Db 361 GGHKLEFRTIGTLNISTQSTNTSINPVTLPFTSRDVRYESLAGNLFQTQPVNGVPR 420

Qy 421 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

Qy 481 ASHKVLYSWTHRSADRTNTEPNSTIQTIPLVKAFNLSSGAAVVRGPGFTGGDI 535
Db 481 ASHKVLYSWTHRSADRTNTEPNSTIQTIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
; Sequence 4, Application US/08100709
; Patent No. 5322487
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia

```

```

; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,709
; FILING DATE: 19930729
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Egoif, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-100-709-4

Query Match 65.1%; Score 2446.5; DB 1; Length 1229;
Best Local Similarity 65.6%; Pred. No. 3.9e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

Qy 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCMKSEYENVEPPFVASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCAEVENNDIPFVASTVQTGINIAGRI 66

Qy 71 LGTIGVPPAGOVASLYSFLGELWPKGNQWEIFMEHVEEIIINOKISTYARKALTDLKG 130
Db 67 LGVLGVPPAGOVASLYSFLGELWPKGRDPWEIIEHVEEIIINOKISTYARKALTDLKG 126

Qy 131 LGDALAVYHDSLESVGNRNNTTRARSVVKSQYIALELMFVQKLPFAVSGVPLLPYIA 190
Db 127 LGRGYSVQQALETMDNRNDARSIIILRYVALELDITTAIPLFRNEEVPPLMYYA 186

Qy 191 QAANLHLLLDASIFGKEWGLSSSEISTFFYNQVERAGDYSCHVKWYSTGLNLRGTN 250
Db 187 QAANLHLLLDASIFGSEWGMASDVNQYQEQIRYTEEYSNHCVQYNTGLNLRGTN 246

Qy 251 AESVRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTREYVYTDIQTGIVHPHPSFT 310
Db 247 AESVRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTREYVYTDIQTGIVHPHPSFT 306

Qy 311 STTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYNNMWGCHKLEFRTI 370
Db 307 STTWYNNAPSFSAIEAAIPEPHLLDPEQVTIYSSASRWSSTQHMVYVGHRLNFRPI 366

Qy 371 GGTNLNISTQST-NTSINPVTLPFTSRDVRYESLAGNLFQTQPVNGVPRVDFHWKFVT 429
Db 367 GGTNLNISTQSTNTSINPVTLPFTSRDVRYESLAGNLFQTQPVNGVPRVDFHWKFVT 422

Qy 430 HPIASDNFYYPG-----YAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISAS 482
Db 423 --INPQNIYERGATTSYQYQGVGIGLFDSETELPPEATGQPNYESYSHRLSHIGLIIIN 480

Qy 483 HVKALVYSWTHRSADRTNTEPNSTIQTIPLVKAFNLSSGAAVVRGPGFTGGDIILRRWTG 542
Db 481 TLRAPVYSWTHRSADRTNTEPNSTIQTIPLVKALNLSGVTVVGGPGFTGGDIILRRWTG 540

Qy 543 TFGDIRVNNPPPAQRYRVRIRYASTDLOPHTSINGKAINQGNFSATMNRGEDLDYKTF 602
Db 541 TFGDIRLNNVPLSQRYRVRIRYASTDLOPHTSINGKAINQGNFSATMNRGEDLDYKTF 600

Qy 603 RTVGFPTFPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFPVPEVYEAEDYDEKAEQKVT 662
Db 601 RTAGFSTFPFNLNAQSTFTLGAQFSN-QEYVIDRVEFVPAEVTFEAYDLERAQKAVNA 659

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Db 247 AESWLRNQFRDLTLGVLDLVALFPSTRTPTINTSAQLTREIYDIDIGRTNAPSGFA 306  
Qy 311 STTYNNAPSFSAIEAAVVRNPHLLDFLOVQTYISLLSRWSNTQYMMWGGHLEFRFI 370  
Db 307 STNFFNNAPSFSAIEAAI FRPHLLDFPQLTYISASSRWSSTQHMYVWVGHRLNFRPI 366  
Qy 371 GGTLNISTQGST-NTSINPVTLPTSRDVTYRTSLAGLNLFLTQPNVGVPRVDPHMKFTV 429  
Db 367 GGTLTSTOGLTNTSINPVTLQFTSRDVTYRTESNAGTNILFTTPVNGVFWARFNF---- 422  
Qy 430 HPIASDNFYYPG-----YAGICTLODSENELPREATGQPNVYESYSHRSLHIGLISAS 482  
Db 423 --INPQNIYERGATTYQOPVQGVIGLQFDSSETLPPETTERPNVYESYSHRSLHIGLIGN 480  
Qy 483 HVKALVYSWTHRSADRTNTIETPNSITQIPLVKAPNLSSGAAVRGPGFTGCDILRRNTG 542  
Db 481 TURAPVYSWTHRSADRTNTIGPNRIQIPLVKALNLHSGVTVVGPGFTGCDILRRNTG 540  
Qy 543 TFGDIRVNINPFPQRYVRIRYASTTDLQFHTSINKAINQGNFSATMNRGELDLYKTF 602  
Db 541 TFGDIRLNLNVPLSQRYVRIRYASTTDLQFHTSINKAINQGNFSATMNRGELDLYKTF 600  
Qy 603 RTVGTTSPFLDVGOSTFTIGAMNPFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQKQVTA 662  
Db 601 RTAGFSTPFLNAOSTFTLGAQSFN-QEYVIDRVEFVPAEVTFEAYDILERAQKAVNA 659  
Qy 663 LFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKXELFEIVKAKOLHIRMN 719  
Db 660 LFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKXELFEIVKAKOLHIRMN 716

RESULT 9

US-08-474-038-4  
; Sequence 4, Application US/08474038  
; Patent No. 5679343  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yeping  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
; ADDRESSEE: Nadel  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,038  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/176,865  
; FILING DATE: 30-DEC-1993  
; APPLICATION NUMBER: US 08/100,709  
; FILING DATE: 29-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Egolf, Christopher  
; REGISTRATION NUMBER: 27633  
; REFERENCE/DOCKET NUMBER: 7205-49  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-757-1590  
; INFORMATION FOR SEQ ID NO: 4:

Qy 663 LFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKXELFEIVKAKOLHIRMN 719  
Db 660 LFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKXELFEIVKAKOLHIRMN 716  
RESULT 8  
US-08-176-865-4  
; Sequence 4, Application US/08176865  
; Patent No. 5616319  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yeping  
; APPLICANT: Gonzalez Jr., Jose M.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
; ADDRESSEE: Nadel  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/176,865  
; FILING DATE: 30-DEC-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/100,709  
; FILING DATE: 29-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Egolf, Christopher  
; REGISTRATION NUMBER: 27633  
; REFERENCE/DOCKET NUMBER: 7205-49  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-757-1590  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1229 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-176-865-4  
Query Match 65.1%; Score 2446.5; DB 1; Length 1229;  
Best Local Similarity 65.6%; Pred. No. 3.9e-210;  
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;  
Qy 13 SSNAKVDKISTDSKN-ETDTELQ-NTNHEDCKMSEYNEVPEFVSASTTQTGTGIGAKI 70  
Db 7 NENEINALSPTVSNPSTQNLSPDARIEDSLCVAEVNIDPFVSASTVQTGTGINAGRI 66  
Qy 71 LGTLGVFPAGVVASLYSIFLGELMPKKNQWEIEMNEHVEBILNOKISTYARNKALTDLKG 130  
Db 67 LGVLGVFPAGVQASLYSIFLGELMPKKNQWEIEMNEHVEBILNOKISTYARNKALTDLKG 126  
Qy 131 LGDALAVHDSLSWGVNRRNTRSVVKSOYIAELMFVOKLPSPFVSGVEEVLPLPIYA 190  
Db 127 LGRGYRSQQALETWIDNRNRRSRIILERYVALELDITAIPLFIRNEEVPFLMVA 186  
Qy 191 QAAHLHLILLRDASIFGKWSLSSEISTFTYNNRQVRAGDYSDHCVWYSTGLNLRGTN 250  
Db 187 QAAHLHLILLRDASLFGSGWGWASSDVNQYQEQIRIYEEYSNHCVQWYNTGLNLRGTN 246  
Qy 251 AESSWVRNQFRDMLMVLVDLVALFPSTRTPTINTSAQLTREIYDIDIGRTNAPSGFT 310

SEQUENCE CHARACTERISTICS:  
LENGTH: 1229 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-474-038-4

Query Match 65.1%; Score 2446.5; DB 1; Length 1229;  
Best Local Similarity 65.6%; Pred. No. 3.9e-210;  
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

Qy 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHECLKNSEYENVEPPFVSASTIQTGIGIAGKI 70  
Db 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCVAEVNNDPPFVSASTVQTGINIAGRI 66

Qy 71 LGTLGVPPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINOKISTYARKNALTDLKG 130  
Db 67 LGVLGVPPAGQLASFSYFLVGLWPSGRDPWEIFLEHVEQLIRQVTTENTARTARLEG 126

Qy 131 LGDALAVHDSLESWGNRNTRARSVVKSVQVIALELMFVKLPSPFVSGSEVPLPIYA 190  
Db 127 LGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFIRNEEVPLLMVYA 186

Qy 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTN 250  
Db 187 QAAHLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEESNHCVCQWYNTGLNNLRGTN 246

Qy 251 AESWVRYNQFRDMLTMDLVALPSPYDTQMPKTKTAQLTREYVYTDAGTVHPHPSFT 310  
Db 247 AESWLRYNQFRDMLTMDLVALPSPYDTQMPKTKTAQLTREYVYTDAGTVHPHPSFT 306

Qy 311 STTWNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRMSNTQYMMNMGHKLFEFTI 370  
Db 307 STWNNNAPSFAIEAAIFRPHLLDFPEQLTIYSASSRWSSTQHMNVYVGHRLNFRPI 366

Qy 371 GGTINISTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLFLTQPVNGVPRVDFHWKFTV 429  
Db 367 GGTINTSTQGLTNTSINPVTLPFTSRDVRVYTESLAGNLFLTQPVNGVPRVDFHWKFTV 422

Qy 430 HPIASDNFYPG-----YAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLISAS 482  
Db 423 --INPQNIYERGATTYSQYQGVGLQDFDSELTPEPTTERPNYESYSHRSLHIGLIIGN 480

Qy 483 HVKALVYSWTHRSADRTNITPNSITQIPLVKAPNLSGAAVVRGPGFTGGDILARTNTG 542  
Db 481 TLRAVYVSWTHRSADRTNITGNRITQIPLVKALNLSGVTVVGPGFTGGDILARTNTG 540

Qy 543 TFGDIRVNINPPAQRVRYRYASTTDLQFTHSINGKAINCQNSATWNGEDLDYKTF 602  
Db 541 TFGDIRLNINPLSQRYRYRYASTTDLQFTFRINGTTVNGNFSNTRMNRGDNLEYSF 600

Qy 603 RTVGFTTTPFDVOSTFTIGAMNFSNGEVYIDRIEFVPEVTVYEAAYDPEKAQEKVTA 662  
Db 601 RTAGSTTFNENFNAOSTTTLGQNSFN-QEVYIDRVFVPEVTVYEAAYDPEKAQEKVTA 659

Qy 663 LFTSTNPRGLKTDVYKHIDQVSNVLSDEFYLDKRELFPEIVKYAKQLHIERNM 719  
Db 660 LFTSTNPRRLKTDVYKHIDQVSNVACLSDDEFCLDRELFPEIVKYAKRLSDERNL 716

RESULT 10  
US-08-779-046-4  
Sequence 4, Application US/08779046  
Patent No. 5854053  
GENERAL INFORMATION:  
APPLICANT: Donovan, William P.  
APPLICANT: Tan, Yiping  
APPLICANT: Jan, Christine S.  
APPLICANT: Gonzalez Jr., Jose M.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS CYVET4 AND CYVET5  
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
ADDRESSEE: Nadel  
STREET: 1601 Market Street, 36th Floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19103

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/779,046  
APPLICATION NUMBER: 08/100,709  
FILING DATE: 29-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Egolf, Christopher  
REGISTRATION NUMBER: 27633  
REFERENCE/DOCKET NUMBER: 7205-49  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-757-1590  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1229 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-779-046-4

Query Match 65.1%; Score 2446.5; DB 2; Length 1229;  
Best Local Similarity 65.6%; Pred. No. 3.9e-210;  
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

Qy 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHECLKNSEYENVEPPFVSASTIQTGIGIAGKI 70  
Db 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCVAEVNNDPPFVSASTVQTGINIAGRI 66

Qy 71 LGTLGVPPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINOKISTYARKNALTDLKG 130  
Db 67 LGVLGVPPAGQLASFSYFLVGLWPSGRDPWEIFLEHVEQLIRQVTTENTARTARLEG 126

Qy 131 LGDALAVHDSLESWGNRNTRARSVVKSVQVIALELMFVKLPSPFVSGSEVPLPIYA 190  
Db 127 LGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFIRNEEVPLLMVYA 186

Qy 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTN 250  
Db 187 QAAHLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEESNHCVCQWYNTGLNNLRGTN 246

Qy 251 AESWVRYNQFRDMLTMDLVALPSPYDTQMPKTKTAQLTREYVYTDAGTVHPHPSFT 310  
Db 247 AESWLRYNQFRDMLTMDLVALPSPYDTQMPKTKTAQLTREYVYTDAGTVHPHPSFT 306

Qy 311 STTWNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRMSNTQYMMNMGHKLFEFTI 370  
Db 307 STWNNNAPSFAIEAAIFRPHLLDFPEQLTIYSASSRWSSTQHMNVYVGHRLNFRPI 366

Qy 371 GGTINISTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLFLTQPVNGVPRVDFHWKFTV 429  
Db 367 GGTINTSTQGLTNTSINPVTLPFTSRDVRVYTESLAGNLFLTQPVNGVPRVDFHWKFTV 422

Qy 430 HPIASDNFYPG-----YAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLISAS 482  
Db 423 --INPQNIYERGATTYSQYQGVGLQDFDSELTPEPTTERPNYESYSHRSLHIGLIIGN 480

Qy 483 HVKALVYSWTHRSADRTNITPNSITQIPLVKAPNLSGAAVVRGPGFTGGDILARTNTG 542  
Db 481 TLRAVYVSWTHRSADRTNITGNRITQIPLVKALNLSGVTVVGPGFTGGDILARTNTG 540



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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-448-170-10

Query Match 62.4%; Score 2344.5; DB 1; Length 488;
Best Local Similarity 89.7%; Pred. No. 1.2e-201;
Matches 446; Conservative 13; Mismatches 29; Indels 9; Gaps 1;

Qy 1 MKLKQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKXSEYENVEPFSASTI 60
Db 1 MKSXQNNHQSLSNATVDKNFTGSLNNTNTELQNFH-----EGIEPFSVSTI 51

Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIEMHVEEIIKISTYA 120
Db 52 QTGIGIVGKILGNLGVFPAGQVASYLSFILGELWPKGKSQWEIEMHVEEIIKISTYA 111

Qy 121 RNKALDGLGDLAVVHDSLESWGNRNTRRSVVKSOYIAELMFVKLPSPAVSG 180
Db 112 RNKALADLKLGLDALVAVHESLESWIENRNTRRSVVKSOYITLMLFVQSLSPAVSG 171

Qy 181 BEVPLLPYIAQAANLHLLLRDASIFGKXWGLSSEISTFFYNQVERAGDSDHCWKYS 240
Db 172 BEVPLLPYIAQAANLHLLLRDASIFGKXWGLSSEISTFFYNQSGKSKEYSDHCWKYN 231

Qy 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTOMYPIKTTAQTREVIYDAI 300
Db 232 TGLNRLMGNNAESWVRYNQFRDMTLMVLDLVALFPSYDTOMYPIKTTAQTREVIYDAI 291

Qy 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRMSNTQYNNMW 360
Db 292 GTVHPHPSFTSTWYNNNAPSFSIEAAVVRNPHLLDFLEQVTIYSLLSRMSNTQYNNMW 351

Qy 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFUTQPVNGVPR 420
Db 352 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFUTQPVNGVPR 411

Qy 421 VDFHWKVFTHPIASDNFYPCVAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 412 VDFHWKVFTHPIASDNFYPCVAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 471

Qy 481 ASHKVALVYSWTHRSAD 497
Db 472 ASHKVALVYSWTHRSAD 488

RESULT 13
US-08-961-803-10
; Sequence 10, Application US/08961803
; Patent No. 6150589
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
; ; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
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;
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961.803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,170
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: M/S 102DCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-961-803-10

Query Match 62.4%; Score 2344.5; DB 3; Length 488;
Best Local Similarity 89.7%; Pred. No. 1.2e-201;
Matches 446; Conservative 13; Mismatches 29; Indels 9; Gaps 1;

Qy 1 MKLKQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKXSEYENVEPFSASTI 60
Db 1 MKSXQNNHQSLSNATVDKNFTGSLNNTNTELQNFH-----EGIEPFSVSTI 51

Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIEMHVEEIIKISTYA 120
Db 52 QTGIGIVGKILGNLGVFPAGQVASYLSFILGELWPKGKSQWEIEMHVEEIIKISTYA 111

Qy 121 RNKALDGLGDLAVVHDSLESWGNRNTRRSVVKSOYIAELMFVKLPSPAVSG 180
Db 112 RNKALADLKLGLDALVAVHESLESWIENRNTRRSVVKSOYITLMLFVQSLSPAVSG 171

Qy 181 BEVPLLPYIAQAANLHLLLRDASIFGKXWGLSSEISTFFYNQVERAGDSDHCWKYS 240
Db 172 BEVPLLPYIAQAANLHLLLRDASIFGKXWGLSSEISTFFYNQSGKSKEYSDHCWKYN 231

Qy 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTOMYPIKTTAQTREVIYDAI 300
Db 232 TGLNRLMGNNAESWVRYNQFRDMTLMVLDLVALFPSYDTOMYPIKTTAQTREVIYDAI 291

Qy 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRMSNTQYNNMW 360
Db 292 GTVHPHPSFTSTWYNNNAPSFSIEAAVVRNPHLLDFLEQVTIYSLLSRMSNTQYNNMW 351
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Thu Mar 10 14:26:04 2005

Best Local Similarity 64.3%; Pred. No. 6.7e-194;  
Matches 442; Conservative 78; Mismatches 154; Indels 13; Caps 5;

Qy 361 GGKLEPRTTGGTNTSTNTSINPVTLPFTSRDVTSTSLAGNLFQTQVNGVPR 420  
Db 352 GGKLEPRTTGGTNTSTNTSINPVTLPFTSRDVTSTSLAGNLFQTQVNGVPR 411  
Qy 421 VDFHWKFTVPIASDNFYPGAGIGTQLODSNEPPEATQPNYESYSHRLSHIGLIS 480  
Db 412 VDFHWKFTVPIASDNFYPGAGIGTQLODSNEPPEATQPNYESYSHRLSHIGLIS 471  
Qy 481 ASHKALVYSWTHRSAD 497  
Db 472 ASHKALVYSWTHRSAD 488

RESULT 14  
US-07-951-715A-7  
; Sequence 7, Application US/07951715A  
; Patent No. 5625136  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/951,715A  
; FILING DATE: 25-SEP-1992  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sprulli, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: S-18805/A/COC 1577/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 541-8615  
; TELEFAX: (919) 541-8689  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1207 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-07-951-715A-7

Qy 40 BDCLKMEYENVEPVASASTIQTGIGTAGKILGTGVPPFAGQVASYSTFGLGELWPKGN 99  
Db 10 EDSLCIAGNNDPVSASTVQTGINAGRIILGVLPVFPAGQLASFVFLVGLWPRGRD 69  
Qy 100 QWELFMEHVEBIIINOKISTVARNKALTDLKGLGDALAVYHDSLESVWGNRNTRASVVK 159  
Db 70 QWELFMEHVEBIIINOKISTVARNKALTDLKGLGDALAVYHDSLESVWGNRNTRASVVK 129  
Qy 160 SOYIALELMFVOKLPSPFVSGEEVPIPIYAQAANLHLLLRDASIFGKGLWGLSSSIST 219  
Db 130 TOYIALELDFLNPMPFAIRNOEVPFLMVVAQAANLHLLLRDASIFGSEFGLTSQIQ 189  
Qy 220 FYNROVERAGDYSDHCVKWYSTGLNNLRGTNAESVRYNQPRRDMTLMVLDLVALFSDY 279  
Db 190 YFERQVTRDYSDYCVENYNTGLNLRGTNAESVRYNQPRRDLTLGLVLDLVALFSDY 249  
Qy 280 TOMYPITTAQLTREVYTDALGTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFL 339  
Db 250 TRTYPINTSAQLTREVYTDALGT--GYNMAMWNNNNNAPSFAIEAAVVRNPHLLDFL 307  
Qy 340 EQVTIYSLSRWSNTQYMMWGHKLEPRTIGTILNISTOGSTNTSINPVTLPFTSRD 399  
Db 308 EQLTIFSASSRWSNTRHMTYWGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTSRD 367  
Qy 400 RTESLAGLNL--LTQPVNGVRVDFHMKFVTHP-----IASDNFYYPGAGIGTQLODS 452  
Db 368 RTESYAGVLLWGLYLEPIHGVTVRNF---TNPQNI8DRGTANYSQP-YESPGQLKDS 423  
Qy 453 ENELPPEATQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQ 512  
Db 424 ETELPPEATQPNYESYSHRLSHIGLILQSRVNPVYSWTHRSADRTNTIEPNSITQ 483  
Qy 513 VKAFNLSSGAADVVRGPGFTGGDILRTNTGTGDIRVNIINPPPAQRYRIRYASTDLQ 572  
Db 484 VKASELPQGTTVVRGPGFTGGDILRTNTGTGDIRVNIINPPPAQRYRIRYASTDLQ 543  
Qy 573 FHTSINKKAINQGNFSAATNRGDLDTKFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNE 632  
Db 544 FVSRGCTTVNFRFLRTNMSGDELKYGMPVRRAFTPTFTTQIOIIRTSIOGLSGNGE 603  
Qy 633 VYDRIEFVPEVTEAEYDFEKAQKVTALFTSTNPRGLKTDVVDKDYHIDQVSNLVESLS 692  
Db 604 VYIDKIEIIPVATFEAEYDLERAQAVNALFTNTNPRKLTDTVDYHIDQVSNLVACLS 663  
Qy 693 DEFYLDKRELFEIVKYAKOLHIERNM 719  
Db 664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

Query Match 60.3%; Score 2265.5; DB 1; Length 1207;



; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
 ; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
 ; NUMBER OF SEQUENCES: 94  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSSEE: No. 5859336artis Corporation  
 ; STREET: Patent & Trademark Dept., 520 White Plains  
 ; STREET: Rd., POB 2005  
 ; CITY: Tarrytown  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10591-9005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/459,448A  
 ; FILING DATE: 02-JUN-1995  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/951,715  
 ; FILING DATE: 25-SEP-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/772,027  
 ; FILING DATE: 04-OCT-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Pace, Gary M.  
 ; REGISTRATION NUMBER: 40403  
 ; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (919)541-8582  
 ; TELEFAX: (919)541-8689  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1207 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-459-448A-7

Query Match 60.3%; Score 2265.5; DB 2; Length 1207;  
 Best Local Similarity 64.3%; Pred. No. 6.7e-194;  
 Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;

Qy	40	EDCLKMSYENVPEPVSASTQTGTGACIKILGTGVFPAGQVASLYSFIIGELMPKGN	99
Db	10	EDSLCIAEGNIDPVSASTVQTGINIAGRILGVLPFAGQLASFYSFLVGLMPGRD	69
Qy	100	QWEIFMEHVEIINQKISTYARNKALTDLKGGLDALAVYHDSLESWGNRNNTARSVK	159
Db	70	QWEIFLEHVEQLINQITENARNALARLQGLGDSFRAYQQSLEDWLENRDDARTSVLY	129
Qy	160	SOYTALELMFVKLPSPFAVSGEEVPLDIYAQAANLHLLLDASIFGKWLSSSEIST	219
Db	130	TOYTALELDFNLPLFAIRQVEPLLMVYAQAANLHLLLDASLFGSEFGLTSQEIQ	189
Qy	220	FYNQOVERAGDYSDHCVKWYSTGLNLRGTNAESWVRYNQFRDMTLMVLDFPSYD	279
Db	190	YERQVETRDYSDYCVWEYNTGLNSLRGTNAESWVRYNQFRDLTLGVLDLVALFPSYD	249
Qy	280	TOMYPKTTAQLTRVYTDALGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFL	339
Db	250	TRTPINTSAQLTRVYTDALGT : GVNMAWMWYNNNAPSFAIEAAIRSPHLLDFL	307
Qy	340	EQVTIYSLLSRWSNTQYNNMGCHKEPRTTGGTLNISTQSTNTSINPVTLPFTRSDVY	399
Db	308	EQLTIFSASSRWSNTRHMYRGTIQSRPIGGGLNTSTHGATNTSINPVTLPFASRDVY	367
Qy	400	RTESLAGNLNF--LTQPVNGVPRVDFHWKVTHP-----IASDNFYYPGYAGIGTQLODS	452
Db	368	RTESYAGVLLMGVLEPIHGVTVRNF---TNQPNISDRGTANYSQP-YESPGLQLKDS	423

Qy	453	ENELPPEATGQPNYESYSHRLSHLGLISASHVKALVYSWTHRSADRTNTIIPNSITQIPL	512
Db	424	ETELPPETTERPNYESYSHRLSHLGLISASHVKALVYSWTHRSADRTNTIIPNSITQIPL	483
Qy	513	VKAFNLSGAAVVRGPGFTGGDILRRNTNTGTFGDIRVNNINPPFAQRYRVRIRYASTDLQ	572
Db	484	VKASELPQGTTVVRGPGFTGGDILRRNTNTGGFGPIRVTVNGPLTQRYRIGFRYASTVDFD	543
Qy	573	PHTSINKAINQGNFSATMNRGEBLDYKTFRTVGFTTTPFSLDVQSTTTIGAWNPFSSGNE	632
Db	544	PFVSRGGTTVNNFRFLRTMNSGDBLKYNFVRRATFTTFTTQODIIRTSTIQGLSGNGE	603
Qy	633	VYIDRIEFVPVEVYBAEYDEKAEKVATLTSTNPRGLKTDVKYHIDOVSNLVESLS	692
Db	604	VYIDKIELIIPVTATFEAYDIERAQEAVALFTNTPRLKTDVTDYHIDQVSNLVACL	663
Qy	693	DEFYLDKRELFETVKYAKQLHIERNM	719
Db	664	DEFCLDEKRELEKVKYAKRLSDERNL	690

Search completed: March 9, 2005, 17:27:40  
 Job time : 25.1512 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 9, 2005, 17:18:14 ; Search time 23.1512 Seconds  
(without alignments)  
2318.356 Million cell updates/sec

Title: US-10-019-823B-56

Perfect score: 3762

Sequence: 1 MKLKNQKHQSFSNAKVDK.....KRELFEIVKYANELHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3739	99.4	719	3	US-08-286-870A-8
2	3459.5	92.0	710	4	US-09-661-322A-42
3	3389	90.1	648	3	US-08-286-870A-4
4	3379	89.8	719	2	US-09-003-217-2
5	3374	89.7	719	3	US-09-218-942-2
6	2795	74.3	535	3	US-08-286-870A-6
7	2437.5	64.8	1229	1	US-08-100-709-4
8	2437.5	64.8	1229	1	US-08-176-865-4
9	2437.5	64.8	1229	1	US-08-474-038-4
10	2437.5	64.8	1229	2	US-08-779-046-4
11	2437.5	64.8	1229	2	US-08-881-340-4
12	2335.5	62.1	488	1	US-08-448-170-10
13	2335.5	62.1	488	3	US-08-961-803-10
14	2250.5	59.8	1207	1	US-07-951-715A-7
15	2250.5	59.8	1207	2	US-08-459-448A-7
16	2250.5	59.8	1207	3	US-08-459-595A-7
17	2250.5	59.8	1207	3	US-08-459-504B-7
18	2250.5	59.8	1207	3	US-08-459-444-7
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21	2250.5	59.8	1207	4	US-09-988-462-7
22	2249.5	59.8	1227	3	US-09-053-549-2
23	2180.5	58.0	1227	1	US-08-448-170-8
24	2180.5	58.0	1227	3	US-08-961-803-9
25	2171.5	57.7	1227	4	US-09-661-322A-63
26	2156.5	57.3	1186	3	US-09-178-252-23
27	2156.5	57.3	1186	4	US-09-826-660-23

28 2101 55.8 1228 4 US-09-661-322A-38 Sequence 38, Appl  
29 1923.5 51.1 643 3 US-09-178-252-25 Sequence 25, Appl  
30 1923.5 51.1 643 4 US-09-826-660-25 Sequence 25, Appl  
31 1891 50.3 380 5 PCT-US91-02560-4 Sequence 4, Appl  
32 1678.5 44.6 653 4 US-09-661-322A-6 Sequence 6, Appl  
33 1655.5 44.0 1157 1 US-07-876-280-30 Sequence 30, Appl  
34 1655.5 44.0 1157 1 US-07-812-180A-2 Sequence 2, Appl  
35 1655.5 44.0 1157 1 US-08-315-468-2 Sequence 2, Appl  
36 1655.5 44.0 1157 3 US-07-941-650A-2 Sequence 2, Appl  
37 1492.5 39.7 1176 1 US-08-257-999-2 Sequence 2, Appl  
38 1483 39.4 1157 2 US-08-532-547-5 Sequence 5, Appl  
39 1483 39.4 1157 2 US-08-379-656B-5 Sequence 5, Appl  
40 1483 39.4 1157 3 US-08-455-838-5 Sequence 5, Appl  
41 1483 39.4 1157 3 US-09-019-809-5 Sequence 5, Appl  
42 1483 39.4 1157 4 US-08-471-177-5 Sequence 5, Appl  
43 1483 39.4 1157 4 US-09-220-806-5 Sequence 5, Appl  
44 1476.5 39.2 1156 3 US-09-002-285-72 Sequence 72, Appl  
45 1476.5 39.2 1156 4 US-09-589-477-72 Sequence 72, Appl

## ALIGNMENTS

## RESULT 1

US-08-286-870A-8  
; Sequence 8, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENN, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DAREY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PAUL N. KOKULIS  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 70608/220720  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-286-870A-8

Thu Mar 10 14:26:04 2005

Query Match		99.48;	Score 3739;	DB 3;	Length 719;
Best Local Similarity		99.44;	Pred. No. 0;		
Matches 715;		Conservative	2;	Mismatches	2; Indels 0; Gaps 0;
ORGANISM: Bacillus thuringiensis					
FEATURE:					
NAME/KEY: misc_feature					
LOCATION: (200)..(200)					
OTHER INFORMATION: No. 6593293-Coding					
US-09-661-322A-42					
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Best Local Similarity		92.14;	Pred. No. 2.4e-301;		
Matches 662;		Conservative	16;	Mismatches	32; Indels 9; Gaps 1;
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Db	61	QTGIGIAGKIILGTGLVPPAGQVASYLFIKELMFKGKNOWEIIFMEHVEEIIINQKISTYA	120		
Qy	121	RNKALTDLKGLDALAVVHDSLEWGNRNNTARSVVKSYQYIALELMFVKQLPSPAVSG	180		
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Qy	181	BEVPLPIPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNROVERAGDYSYHCVKWS	240		
Db	181	BEVPLPIPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNROVERAGDYSYHCVKWS	240		
Qy	241	TGANNLRGTNAESWRYNQFRDMLMVLDLVALPSPYDTQMPYIKTTAQLTREVTDAI	300		
Db	241	TGANNLRGTNAESWRYNQFRDMLMVLDLVALPSPYDTQMPYIKTTAQLTREVTDAI	300		
Qy	301	GTVHPHPSFTTWTYNNNAPSFAEAAVVRNPHLLDFLEQVTIYSLSRMSNTQYNNMW	360		
Db	301	GTVHPHPSFTTWTYNNNAPSFAEAAVVRNPHLLDFLEQVTIYSLSRMSNTQYNNMW	360		
Qy	361	GGHKLFRITGTLNISTOGSTNTSINPVTLPFTSRDVRTSLAGNLFTLPQVNGVPR	420		
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Qy	421	VDHFWKFTVTHPIASDNFYFPGYAGICTQDSNELPPEATQPNYESYSHRLSHIGLIS	480		
Db	421	VDHFWKFTVTHPIASDNFYFPGYAGICTQDSNELPPEATQPNYESYSHRLSHIGLIS	480		
Qy	481	ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN	540		
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Db	541	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSATMNGEDLDYK	600		
Qy	601	TFRTVGFTTSPFLDVOSTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV	660		
Db	601	TFRTVGFTTSPFLDVOSTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV	660		
Qy	661	TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM	719		
Db	661	TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM	719		
RESULT 2					
US-09-661-322A-42					
Sequence 42, Application US/09661322A					
Patent No. 6593293					
GENERAL INFORMATION:					
APPLICANT: Baum, James A.					
APPLICANT: Chu, Chih-Rei					
APPLICANT: Donovan, William P.					
APPLICANT: Gilmer, Amy J.					
APPLICANT: Rudar, Mark J.					
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos					
FILE REFERENCE: MEC0201					
CURRENT APPLICATION NUMBER: US/09/661,322A					
CURRENT FILING DATE: 2000-09-13					
NUMBER OF SEQ ID NOS: 63					
SOFTWARE: PatentIn version 3.0					
SEQ ID NO 42					
LENGTH: 710					
TYPE: PRT					
RESULT 3					
US-08-286-870A-4					
Sequence 4, Application US/08286870A					
Patent No. 6063605					
GENERAL INFORMATION:					
APPLICANT: ELY, S					
APPLICANT: TAILOR, RH					
APPLICANT: TIPPETT, JM					
APPLICANT: BLENN, RG					
TITLE OF INVENTION: BACTERIAL GENES					
NUMBER OF SEQUENCES: 10					
CORRESPONDENCE ADDRESS:					
ADDRESSEE: CUSHMAN DABBY & CUSHMAN					

```

; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-870A-4

Query Match 90.1%; Score 3389; DB 3; Length 648;
Best Local Similarity 99.8%; Pred. NO. 4.4e-295;
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 181 E E V P L L P T Y A Q A A N H L L L L D A S I F G K E W G L S S E I S T F Y N Q R V E R A G D Y S Y H C V K W Y S 240

Qy 241 T G L N N L R G T N A E S W R Y N Q F R D M T L M V L D V A L P P S Y D T Q M P I K T T A Q L T R E V Y T D A I 300
Db 241 T G L N N L R G T N A E S W R Y N Q F R D M T L M V L D V A L P P S Y D T Q M P I K T T A Q L T R E V Y T D A I 300

Qy 301 G T V H P H P S F T T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R N S N T Q Y M N W 360
Db 301 G T V H P H P S F T T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R N S N T Q Y M N W 360

Qy 361 G C H K L E P R T I G G T L N I S T Q G S T N T S I N P V T L P P T S R D V Y R T E S L A G L N L F T Q P V G V P R 420
Db 361 G C H K L E P R T I G G T L N I S T Q G S T N T S I N P V T L P P T S R D V Y R T E S L A G L N L F T Q P V G V P R 420

Qy 421 V D F H W K F V T H P I A S D N F Y P G V A G I G T Q L Q D S E N L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480
Db 421 V D F H W K F V T H P I A S D N F Y P G V A G I G T Q L Q D S E N L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480

Qy 481 A S H V K A L V Y S W T H S A D R T N T I E P N S I T O I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540
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Qy 601 T F R T V G T T P P S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E 648
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RESULT 4
US-09-003-217-2
; Sequence 2, Application US/09003217
; Patent No. 5986177
; GENERAL INFORMATION:
; APPLICANT: Osman, Yehia A.
; APPLICANT: Madkour, Magdy A.
; APPLICANT: Bulla, Lee A.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
; TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: W. Murray Sprull (Alston & Bird, LLP)
; STREET: 3605 Glenwood Ave. Suite 310
; CITY: Raleigh
; STATE: NC
; COUNTRY: US
; ZIP: 27622
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,217
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprull, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 5718-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2202
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-003-217-2

Query Match 89.8%; Score 3379; DB 2; Length 719;
Best Local Similarity 89.7%; Pred. No. 4.1e-294;
Matches 645; Conservative 34; Mismatches 40; Indels 0; Gaps 0;

Qy 1 M L K N Q D K H Q S F S S N A K V D K I S T S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60
Db 1 M L K N P D K H Q T L S S N A K V D K I A T D S L K N E T D I E L K N M N N E D Y L R M S E H S I D P F V S A S T I 60

Qy 61 Q T G I G I A K I L G T L G V P F A G Q V A S I Y S F I L G E L M P K G N Q W E I F M E H V E E I I N Q K I S T Y A 120
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Qy 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180
Db 121 R N K A L T D L K G L G D A L A V Y H S L E S W G N R N N T R A R S V V K Q Y I A L E M F V Q K L P S F A V S G 180

Qy 181 E E V P L L P T Y A Q A A N H L L L L D A S I F G K E W G L S S E I S T F Y N Q R V E R A G D Y S Y H C V K W Y S 240
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 181 EVVPLPIYAAANLHLLLDASIFKCKWGLSSSEISTFYNRQVERADYSHCVKWS 240  
 241 TGLNLRGTNAESVVRVYQFRDMTLMVLDFVALFSPYDTOMYPIKTTAQLTREVYTDI 300  
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 301 GTVHPHSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMMNW 360  
 361 GGHKLEPFTIGTLNISTQGSTNTSINPVTLPFTSRDVTYTESLAGLNLFTOPVNGVPR 420  
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 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
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 601 TPTVGTFTPFGLDVQSTFTTICAWNFSGNEVYIDRIEFVPEVVEVYAEYDFEKAQEKV 660  
 601 TPTVGTFTPFGLDVQSTFTTICAWNFSGNEVYIDRIEFVPEVVEVYAEYDFEKAQEKV 660  
 661 TALFTSTNPRGLKTDVKDHYDOVSNLVSLSDEFLDEKRELFEIVKYAKIHIERNM 719  
 661 TALFTSTNPRGLKTDVKDHYDOVSNLVSLSDEFLDEKRELFEIVKYAKIHIERNM 719

RESULT 6  
 US-08-286-870A-6  
 ; Sequence 6, Application US/08286870A  
 ; Patent No. 6063605  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ELY, S  
 ; APPLICANT: TAILOR, RH  
 ; APPLICANT: TIPPETT, JM  
 ; APPLICANT: BLENK, RG  
 ; TITLE OF INVENTION: BACTERIAL GENES  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
 ; ADDRESSEE: Intellectual Property Group of  
 ; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
 ; STREET: 1100 New York Avenue, N.W.  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005-3918  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/286,870A  
 ; FILING DATE: 05-AUG-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/520228  
 ; FILING DATE: 09-MAY-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 8910624.9  
 ; FILING DATE: 09-MAY-1989

181 EVVPLPIYAAANLHLLLDASIFKCKWGLSSSEISTFYNRQVERADYSHCVKWS 240  
 241 TGLNLRGTNAESVVRVYQFRDMTLMVLDFVALFSPYDTOMYPIKTTAQLTREVYTDI 300  
 241 TGLNLRGTNAESVVRVYQFRDMTLMVLDFVALFSPYDTOMYPIKTTAQLTREVYTDI 300  
 301 GTVHPHSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMMNW 360  
 301 GTVHPHSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMMNW 360  
 361 GGHKLEPFTIGTLNISTQGSTNTSINPVTLPFTSRDVTYTESLAGLNLFTOPVNGVPR 420  
 361 GGHKLEPFTIGTLNISTQGSTNTSINPVTLPFTSRDVTYTESLAGLNLFTOPVNGVPR 420  
 421 VDFHWKFTPIASDNFYVYAGIGTQLODSENELPEATGQPNYESYSHRSLSHIGLIS 480  
 421 VDFHWKFTPIASDNFYVYAGIGTQLODSENELPEATGQPNYESYSHRSLSHIGLIS 480  
 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 541 TGTGDIRVNIAPPFAQRYRVRIRYASTTDLOFHTSINGKAINQCNFSATMNRGCDLYK 600  
 541 TGTGDIRVNIAPPFAQRYRVRIRYASTTDLOFHTSINGKAINQCNFSATMNRGCDLYK 600  
 601 TPTVGTFTPFGLDVQSTFTTICAWNFSGNEVYIDRIEFVPEVVEVYAEYDFEKAQEKV 660  
 601 TPTVGTFTPFGLDVQSTFTTICAWNFSGNEVYIDRIEFVPEVVEVYAEYDFEKAQEKV 660  
 661 TALFTSTNPRGLKTDVKDHYDOVSNLVSLSDEFLDEKRELFEIVKYAKIHIERNM 719  
 661 TALFTSTNPRGLKTDVKDHYDOVSNLVSLSDEFLDEKRELFEIVKYAKIHIERNM 719

RESULT 5  
 US-09-218-942-2  
 ; Sequence 2, Application US/09218942  
 ; Patent No. 6232439  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Osman, Yehia  
 ; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum  
 ; TITLE OF INVENTION: Activity  
 ; FILE REFERENCE: CryII  
 ; CURRENT APPLICATION NUMBER: US/09/218,942  
 ; CURRENT FILING DATE: 1998-12-22  
 ; EARLIER APPLICATION NUMBER: 60/035,361  
 ; EARLIER FILING DATE: 1997-01-10  
 ; EARLIER APPLICATION NUMBER: 09/003,217  
 ; EARLIER FILING DATE: 1998-01-06  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 ; ORGANISM: Bacillus thuringiensis  
 ; US-09-218-942-2  
 Query Match 89.7%; Score 3374; DB 3; Length 719;  
 Best Local Similarity 89.7%; Pred. No. 1.2e-293;  
 Matches 645; Conservative 34; Mismatches 40; Indels 0; Gaps 0;  
 1 MKLNKDKHOSFSSNAKVDKISTDLKNETDIELQNIHEDCLKMSVENVEPVSASTI 60  
 1 MKLNKDKHOSFSSNAKVDKISTDLKNETDIELQNIHEDCLKMSVENVEPVSASTI 60  
 61 QTGIGIAGKILGTLPVPPAGVASYLSFTLGLWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 61 QTGIGIAGKILGTLPVPPAGVASYLSFTLGLWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 121 RNKALTDLKGDLALAVYHDSLESYWGNGNRRNTRARSVVKVSYIALELMFVQKLPFAVSG 180  
 121 RNKALTDLKGDLALAVYHDSLESYWGNGNRRNTRARSVVKVSYIALELMFVQKLPFAVSG 180

```

; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-870A-6

Query Match 74.3%; Score 2795; DB 3; Length 535;
Best Local Similarity 99.8%; Pred. No. 6.5e-242;
Matches 534; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKQDKHQSFSSNAKVDKISTDSLKNETDIELQINHHEDCLKXSEYENVEPFSASTI 60
Db 1 MKLKQDKHQSFSSNAKVDKISTDSLKNETDIELQINHHEDCLKXSEYENVEPFSASTI 60

Qy 61 QTGIGIAGKILGTGVPAGQVASLYSFIILGELMPKGNQWEIEMEHVEEIIINOKISTYA 120
Db 61 QTGIGIAGKILGTGVPAGQVASLYSFIILGELMPKGNQWEIEMEHVEEIIINOKISTYA 120

Qy 121 RNKALTDLKGIDGALAVVHDSLESWVGNNRNNTRARSVVKSQYIALELMFVKLPFAVSG 180
Db 121 RNKALTDLKGIDGALAVVHDSLESWVGNNRNNTRARSVVKSQYIALELMFVKLPFAVSG 180

Qy 181 EEVPLLPYIAQAANLHLLLDASIFGKEWGLSSSEISTFTNQRVERAGDYSHCVKWS 240
Db 181 EEVPLLPYIAQAANLHLLLDASIFGKEWGLSSSEISTFTNQRVERAGDYSHCVKWS 240

Qy 241 TGLANLRGTAESWVRYNQFRRDMLVLDLVALFPSTDTOMYPIKTTAQLTREYITDAI 300
Db 241 TGLANLRGTAESWVRYNQFRRDMLVLDLVALFPSTDTOMYPIKTTAQLTREYITDAI 300

Qy 301 GTVHPHPSFTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360

Qy 361 GGHKLEFRTIGTGLNISTQSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420
Db 361 GGHKLEFRTIGTGLNISTQSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420

Qy 421 VDFHWKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

Qy 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDI 535
Db 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
; Sequence 4, Application US/08100709
; Patent No. 5322687
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Janv, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia

```

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; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,709
; FILING DATE: 19930729
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-100-709-4

Query Match 64.8%; Score 2437.5; DB 1; Length 1229;
Best Local Similarity 65.4%; Pred. No. 3.1e-209;
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

Qy 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHHEDCLKXSEYENVEPFSASTIQTGGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCAEVNINIDPFVSASTVQTGINIAGRI 66

Qy 71 LGTLGVPPAGQVASLYSFIILGELMPKGNQWEIEMEHVEEIIINOKISTYANKALTDLKG 130
Db 67 LGVLGVPPAGQVASLYSFIILGELMPKGNQWEIEMEHVEEIIINOKISTYANKALTDLKG 126

Qy 131 LGDALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVKLPFAVSGEVPPLPIYA 190
Db 127 LGRGYRSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNESEVPLLMVYA 186

Qy 191 QAANLHLLLDASIFGKEWGLSSSEISTFTNQRVERAGDYSHCVKWSYGLNLRGTN 250
Db 187 QAANLHLLLDASIFGSEMGMASSDVNQYQEQIRIYTEESNHCVOYNTGLNLRGTN 246

Qy 251 AESWVRYNQFRRDMLVLDLVALFPSTDTOMYPIKTTAQLTREYITDAIGTVHPHPSFT 310
Db 247 AESWVRYNQFRRDMLVLDLVALFPSTDTOMYPIKTTAQLTREYITDAIGTVHPHPSFT 306

Qy 311 STTWYNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMWGSHKLEPRTI 370
Db 307 STWYNNAPSFAIEAAI FRPHLLDFPEQVTIYSLLSRWSNTQYNNMWVGHRLNFRPI 366

Qy 371 GGTGLNISTQST-NTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPRDHFHWKFT 429
Db 367 GGTGLNISTQST-NTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPRDHFHWKFT 422

Qy 430 HPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISAS 482
Db 423 --INPQNIYERGATYTSQYQGVGIGLFDSETELPETTERPNERPYESYSHRLSHIGLIIGN 480

Qy 483 HVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDIILRRWTG 542
Db 481 TLRAVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDIILRRWTG 540

Qy 543 TFGDIRVNNPPFAQRVVRIRYASTTDLQPHFTSINGKAINQGNFSATMNRGEBLDYKTF 602
Db 541 TFGDIRVNNPPFAQRVVRIRYASTTDLQPHFTSINGKAINQGNFSATMNRGEBLDYKTF 600

Qy 603 RTVGFPTTFPSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDEKAEQKYTA 662
Db 601 RTAGFSTFPFLNAQSTFTLGAQGSFN-QEYVIDRVEFPVPAEVTFEAEYDLERAQKAYNA 659

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[illegible]

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RESULT 8
US-08-176-865-4
; Sequence 4, Application US/08176865
; Patent No. 5616319
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yeping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryETS
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/176,865
; APPLICATION NUMBER: 30-DEC-1993
; FILING DATE: 30-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-176-865-4
Query Match 64.8%; Score 2437.5; DB 1; Length 1229;
Best Local Similarity 65.4%; Pred No. 3.1e-209;
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTSLKN-ETDIELQ-NINHEDECLKMSYENVVEPFFVSASTIOTGTGIAGKI 70
DB 7 NENEINALSIPTVSNPSTQMNLSPDARIEDSLCAEVANNIDPFFVSASTVOTGTGINIAGRI 66

QY 71 LGTLGVPPAGOVASLSFYLGLWPKGKNOWEIFVEHVEEIIINQKISYARNKALTDLKG 130
DB 67 LGVLGVPPAGQLASFYSFLVGLWPSGRDPWFIFLEHVEQLIRQQVTENTNTAARLEG 126

QY 131 LGDALAVYHDSLSBSWGNRRNTRARSVVKVSQYIALELMFVQKLPSPFVSGEVPLLPIYA 190
DB 127 LGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEEVPULMWYA 186

QY 191 QAAHLLILLRDASIECKEGLSSRSISFTYNQROVERAGDYSVHCVKWYSTGLNNLRGTN 250
DB 187 QAAHLLILLRDASLFGSEGMWMASSDNNQYQEQIRYETSEYSHCFQWNTGLNNLRGTN 246

QY 251 AESWVRYNQFRDWTMLMVLDLVALFPSTQMYPIKTKTAQLTRVYTDAGIVTHPHPSFT 310

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247	Db	AEBSRLYNQPRRDLTGVLDLVALFPSTYDTRYYPINTSAQLTREITYDPIGRNTAPSGFA	306
311	QY	STTWNNNAPSFAISAAVVRPHLLDPLFLEQVTVISLLSRWSNTQYMMWGGCHKLEPFI	370
307	Db	STWNNNAPSFAISAAVVRPHLLDPLFLEQVTVISLLSRWSNTQYMMWGGCHKLEPFI	366
371	QY	GGTLNISTQGST-NTSINPVTLPFTSRDYVRYESLAGLNLFTQPVNGVPRVDFHWKFVT	429
367	Db	GGTLNISTQGLTNNTSINPVTLPFTSRDYVRYESLAGLNLFTQPVNGVPRVDFHWKFVT	422
430	QY	HPIASDNFYYPG-----YAGICTQLQDSENELPPEATGQPNYESYSHRLSHIGLISAS	482
423	Db	--INPQNIYERGATTSYQPGVGIQLFDSETEPLPETTERPNYESYSHRLSHIGLIIGN	480
483	QY	HVKALVYSWTHRSADRNTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDLTRNTNG	542
481	Db	TLRAPVYSWTHRSADRNTNTEPNSITQIPLVKALNLHSGVTVVGGPGFTGGDLTRNTNG	540
543	QY	TFGDIRUNINPPFAQRYRVRIRYASTTDLQFHTSINGKALNQCNFSATMNRGEBLDYKFT	602
541	Db	TFGDIRUNINPVLQSRYRVRIRYASTTDLQFHTSINGKALNQCNFSATMNRGEBLDYKFT	600
603	QY	RTVGFTTTPFSLDQSTFTTCIAMNFSGSEVYIDRIEFVVEVTVYDAEYDFEKAQEKVTA	662
601	Db	RTAGSTFTFNLNAQSTFTTLGAQGSFN-QEYVIDRVEFVPAEVTFEAYDLERAQAKVNA	659
663	QY	LFTSTNPNGLKTDVKDHIQVSNLVESLSDEFVLDEKRELFEILVKYANELHLEIRNM	719
660	Db	LFTSTNPNRLKTDVTDHIQVSNVACLSDFECLDEKRELFEKVYAKESIDERNL	716

## RESULT 9

US-08-474-038-4  
; Sequence 4, Application US/08474038  
; Patent No. 5679343  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yeping  
; APPLICANT: Jany, Christine S.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS c1yE4 AND c1yE5  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
; ADDRESSEE: Nadel  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,038  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/176,865  
; FILING DATE: 30-DEC-1993  
; APPLICATION NUMBER: US 08/100,709  
; FILING DATE: 29-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Egolf, Christopher  
; REGISTRATION NUMBER: 27633  
; REFERENCE/POCKET NUMBER: 7205-49  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-757-1590  
; INFORMATION FOR SEQ ID NO: 4:



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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-038-4

Query Match      64.8%; Score 2437.5; DB 1; Length 1229;
Best Local Similarity 65.4%; Pred. No. 3.1e-209;
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPTVSNPSTQMLSPDARIEDSLCAEVNNDIPFVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
DB 67 LGVLGVPPAGQLASFSYFLVGLWPSGRDPWEIFLEHVEQLIRQQVTENTTAIRLEG 126
QY 131 LGDALAVTHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFVSGEVPPLPIYA 190
DB 127 LGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPLFRNBEVPLLMVYA 186
QY 191 QAAHLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRGTN 250
DB 187 QAAHLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEEYSNHCVMQYNTGLNNLRGTN 246
QY 251 AESWRYNQFRDRLTMVLVDLVALPSPYDTQMPYIKTTAQLTREYVTDAGTVHPHPSFT 310
DB 247 AESWLRYNQFRDRLTMVLVDLVALPSPYDTQMPYIKTTAQLTREYVTDAGTVHPHPSFT 310
QY 311 STTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGHGKLEFRTI 370
DB 307 STNWFNNAPSFAIEAAI FRPPHLLDPPEQLTIYSSASSRWSSTQHMWYVGHRLNFRPI 366
QY 371 GGTLNISTQGST-NTSINPVTLPFTSRDVRYESLAGLNLFLOTPVNGVPRVDFHWKFTV 429
DB 367 GGTLNISTQGLTNNTSINPVTLPFTSRDVRYESLAGLNLFLOTPVNGVPRVDFHWKFTV 422
QY 430 HPIASDNFYYPG-----YAGIGTQLQDSNELPPEATGPNYESYSHRSLHIGLISAS 482
DB 423 --INPQNIYERGATTYSQPYQGVGLQDFDSELPETTERPNYESYSHRSLHIGLIIGN 480
QY 483 HVKALVSWTHRSADRTNTEPNSTIQLVKAFNLSSGAAVVRGPGTGGDILARTNTG 542
DB 481 TLRAPVYSWTHRSADRTNTIGPNRITQPLVKALNLSHSGVTVVGPGFTGGDILARTNTG 540

Query Match      64.8%; Score 2437.5; DB 2; Length 1229;
Best Local Similarity 65.4%; Pred. No. 3.1e-209;
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPTVSNPSTQMLSPDARIEDSLCAEVNNDIPFVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
DB 67 LGVLGVPPAGQLASFSYFLVGLWPSGRDPWEIFLEHVEQLIRQQVTENTTAIRLEG 126
QY 131 LGDALAVTHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFVSGEVPPLPIYA 190
DB 127 LGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPLFRNBEVPLLMVYA 186
QY 191 QAAHLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNNLRGTN 250
DB 187 QAAHLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEEYSNHCVMQYNTGLNNLRGTN 246
QY 251 AESWRYNQFRDRLTMVLVDLVALPSPYDTQMPYIKTTAQLTREYVTDAGTVHPHPSFT 310
DB 247 AESWLRYNQFRDRLTMVLVDLVALPSPYDTQMPYIKTTAQLTREYVTDAGTVHPHPSFT 310
QY 311 STTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGHGKLEFRTI 370
DB 307 STNWFNNAPSFAIEAAI FRPPHLLDPPEQLTIYSSASSRWSSTQHMWYVGHRLNFRPI 366
QY 371 GGTLNISTQGST-NTSINPVTLPFTSRDVRYESLAGLNLFLOTPVNGVPRVDFHWKFTV 429
DB 367 GGTLNISTQGLTNNTSINPVTLPFTSRDVRYESLAGLNLFLOTPVNGVPRVDFHWKFTV 422
QY 430 HPIASDNFYYPG-----YAGIGTQLQDSNELPPEATGPNYESYSHRSLHIGLISAS 482
DB 423 --INPQNIYERGATTYSQPYQGVGLQDFDSELPETTERPNYESYSHRSLHIGLIIGN 480
QY 483 HVKALVSWTHRSADRTNTEPNSTIQLVKAFNLSSGAAVVRGPGTGGDILARTNTG 542
DB 481 TLRAPVYSWTHRSADRTNTIGPNRITQPLVKALNLSHSGVTVVGPGFTGGDILARTNTG 540
QY 543 TFGDIRVNINPPAQRVRYRYASTTDLQPHTSINGKAIQGNFSATWNGEDLDYKTF 602
DB 541 TFGDIRVNINPVSQRVRYRYASTTDLQPHTSINGKAIQGNFSATWNGEDLDYKTF 600
QY 603 RTVGFTTFFSLDVOSTFTIGAWNPFSSGNEVVYDRIEFVVPVETVEAEYDPEKAQKVTA 662
DB 601 RTAGSTTFNPLNAQSTTFLGAQSFN-QEYVIDRVEFVPAEYVFEAEYDPEKAQKAVNA 659
QY 663 LFTSTNPRGLKTDVXDYHIDQVSNLVSDEFYLDKRELFELVYKIANELHIERNM 719
DB 660 LFTSTNPRRLKTDVXDYHIDQVSNMVACLSDEFCLDKRELFELVYKAKRLSDERNL 716

RESULT: 10
US-08-779-046-4
; Sequence 4, Application US/08779046
; Patent No. 5854053
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jan, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
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QY 543 TFGDIRVNPBPAQRYVRIRVASTTDLQFHTSINGKAINQGNFSATWNRGEDIYKTF 602  
Db 541 TFGDIRVNPBPAQRYVRIRVASTTDLQFHTSINGKAINQGNFSATWNRGEDIYKTF 600  
QY 603 RTVGFTTFPGFLDVQSTFTIGANNFSSGNNVYIDRIEFVPEVTEAEYDFEKAQEKVTA 662  
Db 601 RTAGFSTPFNLAQSTFTLGAQSFN-QEYVIDRVEFPAEVTFAEYDLERAQKAVNA 659  
QY 663 LFTSTNPRGLKTDVYHIDQVSNVACLSDDEFVLDKRELFEIVKYANLHIERNM 719  
Db 660 LFTSTNPRGLKTDVYHIDQVSNVACLSDDEFVLDKRELFEIVKYANLHIERNM 716  
RESULT 11  
US-08-881-340-4  
; Sequence 4, Application US/08881340  
; Patent No. 5942658  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yiping  
; APPLICANT: Jan, Christine S.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CIYET4 AND CIYET5  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
; ADDRESS: Nadel  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,340  
; FILING DATE: 24-JUN-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/100,709  
; FILING DATE: 29-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Egolf, Christopher  
; REGISTRATION NUMBER: 27633  
; REFERENCE/DOCKET NUMBER: 7205-49  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-757-1590  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1229 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-881-340-4  
Query Match 64.8%; Score 2437.5; DB 2; Length 1229;  
Best Local Similarity 65.4%; Pred. NO. 3.1e-209;  
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;  
QY 13 SSNAKVDKISTSLKN-ETDIELQ-NINHECLMKSEYENVEPVFSASTTQTGTGIAGKI 70  
Db 7 NENEINSLIPTNSPTQMLSPDARIESLCAEVANNIDPFVSASTVQTGINIAGRI 66  
QY 71 LGTLGVFPAGQVASYLFIKGLWPKGNQKQWEIFMHEVEELINQKISTYARNKALDTLKG 130  
Db 67 LGVLGVFPAGQVASYLFIKGLWPKGNQKQWEIFMHEVEELINQKISTYARNKALDTLKG 126  
QY 131 LGDALAVYHDSLESVWGNRNTFRASVYKVSQVIALELMFVQKLPSFAVSGEEVPLPIYA 190

Db 127 LGRYRSYQQALETWLDNRNDAERSIILERYVALELDITTAIPLRIRNEEYVPLLMVYA 186  
QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTEYFNQVRAGDYSYHCVKWYSTGLNLRGTN 250  
Db 187 QAAHLHLLLRDASIFGKEWGLSSSEISTEYFNQVRAGDYSYHCVKWYSTGLNLRGTN 246  
QY 251 AESWRYNQFRDRLTGLVLDLVALFPDSTQMPPIKTAQITREVVYTDATGTVHPHSET 310  
Db 247 AESWRYNQFRDRLTGLVLDLVALFPDSTQMPPIKTAQITREVVYTDATGTVHPHSET 306  
QY 311 STTWYNNAPSAEAAVAVENPHLLDLEQVTTIYLLSRWSNTQYNNMGGHKLERTI 370  
Db 307 STTWYNNAPSAEAAVAVENPHLLDLEQVTTIYLLSRWSNTQYNNMGGHKLERTI 366  
QY 371 GGTNLISQGST-NTSINPVTLPFTSRDVRATESLAGNLPLETOPVNGVPRVDFHKEFT 429  
Db 367 GGTNLISQGST-NTSINPVTLPFTSRDVRATESLAGNLPLETOPVNGVPRVDFHKEFT 422  
QY 430 HPIASDNFYPG-----YAGIGTQLODSENELPPEATGPNYSEYSHRLSHIGLISAS 482  
Db 423 --INPQNIYERGATTYSQYQGVGQLDSELPPEATGPNYSEYSHRLSHIGLISAS 480  
QY 483 HVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTNTG 542  
Db 481 TLRAPVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTNTG 540  
QY 543 TFGDIRVNPBPAQRYVRIRVASTTDLQFHTSINGKAINQGNFSATWNRGEDIYKTF 602  
Db 541 TFGDIRVNPBPAQRYVRIRVASTTDLQFHTSINGKAINQGNFSATWNRGEDIYKTF 600  
QY 603 RTVGFTTFPGFLDVQSTFTIGANNFSSGNNVYIDRIEFVPEVTEAEYDFEKAQEKVTA 662  
Db 601 RTAGFSTPFNLAQSTFTLGAQSFN-QEYVIDRVEFPAEVTFAEYDLERAQKAVNA 659  
QY 663 LFTSTNPRGLKTDVYHIDQVSNVACLSDDEFVLDKRELFEIVKYANLHIERNM 719  
Db 660 LFTSTNPRGLKTDVYHIDQVSNVACLSDDEFVLDKRELFEIVKYANLHIERNM 716  
RESULT 12  
US-08-448-170-10  
; Sequence 10, Application US/08448170  
; Patent No. 5723758  
; GENERAL INFORMATION:  
; APPLICANT: Payne, Jewel  
; APPLICANT: Cummings, David A.  
; APPLICANT: Cannon, Raymond J.C.  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Stelman, Steve  
; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted  
; TITLE OF INVENTION: B.t. PSI58C2, Active Against Lepidopteran Pests, and Genes  
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/448,170  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/069,902  
; FILING DATE: 01-JUNE-1993  
; CLASSIFICATION: 424

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-448-170-10

Query Match 62.1%; Score 2335.5; DB 1; Length 488;
Best Local Similarity 89.5%; Pred. No. 9.6e-201;
Matches 445; Conservative 13; Mismatches 30; Indels 9; Gaps 1;

Qy 1 MCLKNODKHQFSSNAKVDKISTDLKNETDIELQNIHEDCLKMSYENVEPFFVSASTI 60
Db 1 MCKSNQNMHQSLSNATVDKNFTGSLNNTNTELFQNFH-----EGIEPPFVSASTI 51

Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIEMHVEEIIINOKISTYA 120
Db 52 QTGIGIVGKILGNLGVFPAGQVASYLSFILGELMPKGSQWEIEMHVEEELINOKISTYA 111

Qy 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNRTRSVVKSQYIALELMFVQKLPFAVSG 180
Db 112 RNKALADLKGLDALAVYHDSLESWVGNNRNRTRSVVKSQYITLLELMFVQSLPFAVSG 171

Qy 181 BEVPLLPYIAQAANLHLLLRDASIFGKMGWLSSEISTFYNRQVERAGDYSYHCVKWS 240
Db 172 BEVPLLPYIAQAANLHLLLRDASIFGKMGWLSSEISTFYNRQSGKSEISDHCVRWYN 231

Qy 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREYVTDAT 300
Db 232 TGLNLRGNNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREYVTDAT 291

Qy 301 GTVHPHPSFTTWNNNAPSFSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMNW 360
Db 292 GTVHPHPSFTTWNNNAPSFSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMNW 351

Qy 361 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDYRTESLAGLNLFTQPVNGVPR 420
Db 352 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDYRTESLAGLNLFTQPVNGVPR 411

Qy 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 412 VDFHWKFTVTHPIASDNFYYPGAGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLIS 471

Qy 481 ASHKVLYSWNTHRSAD 497
Db 472 ASHKVLYSWNTHRSAD 488

RESULT 13
US-08-961-803-10
; Sequence 10, Application US/08961803
; Patent No. 6150589
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.C. PS158C2, Active Against Lepidopteran Pests, and Genes
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; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961.803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,170
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: M/S 102DCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-961-803-10

Query Match 62.1%; Score 2335.5; DB 3; Length 488;
Best Local Similarity 89.5%; Pred. No. 9.6e-201;
Matches 445; Conservative 13; Mismatches 30; Indels 9; Gaps 1;

Qy 1 MCLKNODKHQFSSNAKVDKISTDLKNETDIELQNIHEDCLKMSYENVEPFFVSASTI 60
Db 1 MCKSNQNMHQSLSNATVDKNFTGSLNNTNTELFQNFH-----EGIEPPFVSASTI 51

Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIEMHVEEIIINOKISTYA 120
Db 52 QTGIGIVGKILGNLGVFPAGQVASYLSFILGELMPKGSQWEIEMHVEEELINOKISTYA 111

Qy 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNRTRSVVKSQYIALELMFVQKLPFAVSG 180
Db 112 RNKALADLKGLDALAVYHDSLESWVGNNRNRTRSVVKSQYITLLELMFVQSLPFAVSG 171

Qy 181 BEVPLLPYIAQAANLHLLLRDASIFGKMGWLSSEISTFYNRQVERAGDYSYHCVKWS 240
Db 172 BEVPLLPYIAQAANLHLLLRDASIFGKMGWLSSEISTFYNRQSGKSEISDHCVRWYN 231

Qy 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREYVTDAT 300
Db 232 TGLNLRGNNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREYVTDAT 291

Qy 301 GTVHPHPSFTTWNNNAPSFSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMNW 360
Db 292 GTVHPHPSFTTWNNNAPSFSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMNW 351
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Best Local Similarity 64.0%; Pred. No. 1.8e-192; Caps 5;  
Matches 440; Conservative 77; Mismatches 157; Indels 13;

QY 361 GGKLEERTIGTINISGTSTNTSINPVLPTSDVYRTESLAGNLFLLTOPVNGVPR 420  
DB 352 GGKLEERTIGTINISGTSTNTSINPVLPTSDVYRTESLAGNLFLLTOPVNGVPR 411  
QY 421 VDFHWKVFTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480  
DB 412 VDFHWKVFTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 471  
QY 481 ASHKALVYSWTHRSAD 497  
DB 472 ASHKALVYSWTHRSAD 488

RESULT 14  
US-07-951-715A-7  
; Sequence 7, Application US/07951715A  
; Patent No. 5625136  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07951,715A  
; FILING DATE: 25-SEP-1992  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sprulli, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: S-18805/A/COC 1577/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8615  
; TELEFAX: (919)541-8669  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1207 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-951-715A-7

Query Match 59.8%; Score 2250.5; DB 1; Length 1207;

QY 40 EDCLEMEYENVEPVASASTIQTGIGTAGKILGTGLVPPAGQVASYLSFILGELWPKGN 99  
DB 10 EDSICIAEGNNDIPFVSASTVQTGINIAGILGVLPVPPAGQLASFYSFLVGLWPRGRD 69  
QY 100 QWEIFMEHVERIINQKISTYARNKALTDLKLGDALAVYHDSLESWVGNNRNTARSVVK 159  
DB 70 QWEIFLEHVEQLNQITENARTALARQLQDGSFRAYQQSLDMLWLENDDARTSRVLY 129  
QY 160 SQYIALELMFVKQLPSFAVSGEYVPLPIYAQAANLHLLLRDASIRKGEKWLSSSSBI 219  
DB 130 TQYIALELDLFLNAPLFAIRNQEVPLLVYAQAANLHLLLRDASLFGSEFGLTSQEIQR 189  
QY 220 FYNROVERAGDYSYHCVKWTYSTGLNNLRGTNAESWRYNQPRRDMTLMVLDLVALF 279  
DB 190 YIERQVTRTDYSDYCVWEYNTGLNLRGTNAESWRYNQPRRDLTLGLVLDLVALF 249  
QY 280 TQMPYIKTTAQLTRVYTDATGTVHPHPSFTSTWYNNAPSAIAEAAVVRNPHLLD 339  
DB 250 TRTYPINTSAQLTRVYTDATGAT--GYNMAMWYNNNAPSAIAEAAVVRNPHLLD 307  
QY 340 EQVTIYSLSRWSNTQYMMMGHKLPRITIGTIGTINISGTSTNTSINPVLPTSDVY 399  
DB 308 EQLTIPSASSRWSNTRHTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVLPTSDVY 367  
QY 400 RTESLAGLNF--LTQPVNGVPRVDFHMKFVTHP-----IASDNFYPGYAGIGTQLO 452  
DB 368 RTESYAGVLLGWLYLEPIHGVTVRNF---TNPQNI8DRGTANYSQP-YESPGQLKDS 423  
QY 453 ENELPEATGQPNYESYSHRSLSHIGLISASHVKALVYSWTHRSADRTNTPNSITQ 512  
DB 424 ETELPPETTERPNYESYSHRSLSHIGLILQSRVNVVYSWTHRSADRTNTPNSITQ 483  
QY 513 VKAPNLSSGAAVVRGPGFTGGDILRRTNTGTGDIRVNNINPPFAQRYRIRYASTT 572  
DB 484 VKASELPQGTTVVRGPGFTGGDILRRTNTGTGDIRVNNINPPFAQRYRIRYASTT 543  
QY 573 FHTSINKKAINQGNFATNMGEDLDYKTRFTVGTFTTFFSFLDVOSTFTIGAWNFSS 632  
DB 544 FVSRGCTTVNFRFLRTNMGSDGELKGNFVRRAFTTFTTFTTQIDIIIRTSIOGLSG 603  
QY 633 VYDRIEFVPEVTEAEYDFEKAQKVTALFTSTNPRGLKTDVXDYHIDQVSNLVESLS 692  
DB 604 VYIDKIEIIPVTATFEAEYDLERAQAVNALFTNTNPRKLTDTVDYHIDQVSNLV 663  
QY 693 DEFYLDKRELFEIVKYANLHIERNM 719  
DB 664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 15  
US-08-459-448A-7  
; Sequence 7, Application US/08459448A  
; Patent No. 5859336  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.

Search completed: March 9, 2005, 17:27:43  
Job time : 26.1512 secs

Query Match	59.8%;	Score	2250.5;	DB	2;	Length	1207;
Best Local Similarity	64.0%;	Pred. No.	1.8e-152;				
Matches	440;	Conservative	77;	Mismatches	157;	Indels	13;
Gaps	5;						

  

Qy	40	EDCLKMEYENVRPFVSASTIQTGIGTAGKITGLTGVFPFAGQVASLYSFILGELWPMRGKN	99
Db	10	EDSLCIAEGNNIDPFVSASIVQTGINIAGRILGVLGVFPFAGQLASFVSLFVGEUWPMRGDR	69
Qy	100	QWEIFMEHVEIINQKISTYARNKALTDLKGGLDALAVYTHDSLESVGNRNNTREARSVVK	159
Db	70	QWEIFLEHVEQLINQKITENARNALTARLQGLGDSFRAYQQSLDLEWLRDDARTRSVLY	129
Qy	160	SOYIALELMPVQKLPSFAVSGEEVPLPIYVAAQANLHLLLRDASITGKEWGLSSSIIST	219
Db	130	TOYIALELDPLNAPLFAIRNQEVPLVMYVAAQANLHLLLRDASLFGSGFGLTSQBIR	189
Qy	220	FYNQVRERAGDYSVHCVKWYSTGLNNLRGTNAESWVRYNQPRRDMTLMVLDLVALFPSYD	279
Db	190	YIERQVERTRDYSYCYVEWYNTGLNSLRGTNAASWVRYNQPRRDLTLGVLDLVALFPSYD	249
Qy	280	TMQYPIKTTAQLTREVTDAIGTVHPHPSFTSTTWYNNAPSPSAIEAAVVRNPHLLDPL	339
Db	250	TRTYPINTSAQLTREVTDAIGAT--GVNWSAMNMYNNAPSPSAIEAAAIRSPHLLDPL	307
Qy	340	EQVTIYGLLSRWSNTQYMNWGGHKLFRITGGTLNISTOGSTNTSINPVTLPFTSRDXY	399
Db	308	EQLTIFASGRWSNTRHWYVRGHTIOSRPICGGINTSTHGATNTSINPVTLPFASRDXY	367
Qy	400	RTESLAGLNIUF--LTQPVNGVPRVDFHWKFVTHP-----IASDNFYYPGAGIGTQLQDS	452
Db	368	RTESYAGVLWGIYLEDIHGVPTVRVNF---TNPONTSDRGNTANYSP--YESPGLQKDS	423

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QY	421	VDFHKKFVTHPIASDNFYPGYAGIGTQLODSNELPPEATGPNVYESYSHRLSHIGLIS	480
DB	421	VDFHKKFVTHPIASDNFYPGYAGIGTQLODSNELPPEATGPNVYESYSHRLSHIGLIS	480
QY	481	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDIILRTN	540
DB	481	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDIILRTN	540
QY	541	TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINOGNFSATMNRGDLDYK	600
DB	541	TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINOGNFSATMNRGDLDYK	600
QY	601	TFRVTGFTTPEFLDVQSTFTIGAWNFSSGNEVVIDRIEFVPEVVTYEAEDFEKAQEKV	660
DB	601	TFRVTGFTTPEFLDVQSTFTIGAWNFSSGNEVVIDRIEFVPEVVTYEAEDFEKAQEKV	660
QY	661	TALFTSTNPRGLKTDVQHYDQVSNLVESLSDFFYLDEKRELFEIVKYANELHIERNM	719
DB	661	TALFTSTNPRGLKTDVQHYDQVSNLVESLSDFFYLDEKRELFEIVKYANELHIERNM	719
RESULT 2			
S25383			
parasporal crystal protein cryIIa1 - Bacillus thuringiensis			
N:Alternate names: delta-endotoxin; parasporal crystal protein cryV			
C:Species: Bacillus thuringiensis			
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004			
C:Accession: S25383			
R:Tailor, R.; Tippett, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.			
Mol. Microbiol. 6, 1211-1217, 1992			
A:Title: Identification and characterization of a novel Bacillus thuringiensis delta-end			
A:Reference number: S25383; MUID:92269582; PMID:1588820			
A:Accession: S25383			
A:Molecule type: DNA			
A:Residues: 1-719 <TAI>			
A:Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:G40289; PIDN:CAA44633.1; PID:G40290			
C:Gene: cryV			
C:Superfamily: parasporal crystal protein			
C:Keywords: delta-endotoxin			
Query Match 99.8%; Score 3753; DB 2; Length 719;			
Best Local Similarity 99.7%; Pred. No. 5.2e-251;			
Matches 717; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
QY	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEHEDCLKSEYENVEPVSASTI	60
DB	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEHEDCLKSEYENVEPVSASTI	60
QY	61	QTGIGIAGKILGTLGVPPAGQVASYLSYFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA	120
DB	61	QTGIGIAGKILGTLGVPPAGQVASYLSYFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA	120
QY	121	RNKALTDLKLGDALAVYHDSLSWGNRNNTARSVVKVSKQYIALELMFVQKLPSPFVSG	180
DB	121	RNKALTDLKLGDALAVYHDSLSWGNRNNTARSVVKVSKQYIALELMFVQKLPSPFVSG	180
QY	181	EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSVHCVKWYS	240
DB	181	EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSVHCVKWYS	240
QY	241	TGLNNLKGTAESWVRNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDI	300
DB	241	TGLNNLKGTAESWVRNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDI	300
QY	301	GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTOYNNMW	360
DB	301	GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTOYNNMW	360
QY	361	GGHKLKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVTESLAGNLFLTQPVNGVPR	420
DB	361	GGHKLKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVTESLAGNLFLTQPVNGVPR	420

QY	421	VDFHKKFVTHPIASDNFYPGYAGIGTQLODSNELPPEATGPNVYESYSHRLSHIGLIS	480
DB	421	VDFHKKFVTHPIASDNFYPGYAGIGTQLODSNELPPEATGPNVYESYSHRLSHIGLIS	480
QY	481	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDIILRTN	540
DB	481	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDIILRTN	540
QY	541	TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINOGNFSATMNRGDLDYK	600
DB	541	TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINOGNFSATMNRGDLDYK	600
QY	601	TFRVTGFTTPEFLDVQSTFTIGAWNFSSGNEVVIDRIEFVPEVVTYEAEDFEKAQEKV	660
DB	601	TFRVTGFTTPEFLDVQSTFTIGAWNFSSGNEVVIDRIEFVPEVVTYEAEDFEKAQEKV	660
QY	661	TALFTSTNPRGLKTDVQHYDQVSNLVESLSDFFYLDEKRELFEIVKYANELHIERNM	719
DB	661	TALFTSTNPRGLKTDVQHYDQVSNLVESLSDFFYLDEKRELFEIVKYANELHIERNM	719
RESULT 3			
I39815			
insecticidal protein cryV - Bacillus thuringiensis			
C:Species: Bacillus thuringiensis			
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004			
C:Accession: I39815			
R:Gleaves, A.P.; Williams, R.; Hedges, R.J.			
Appl. Environ. Microbiol. 59, 1683-1687, 1993			
A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for			
ensis subsp. kurstaki.			
A:Reference number: I39815; MUID:93298009; PMID:8517758			
A:Accession: I39815			
A:Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: DNA			
A:Residues: 1-719 <RES>			
A:Cross-references: UNIPROT:Q45752; GB:M98544; NID:gl42767; PIDN:AAA22354.1; PID:gl42768			
C:Gene: cryV			
C:Superfamily: parasporal crystal protein			
Query Match 99.5%; Score 3743; DB 2; Length 719;			
Best Local Similarity 99.6%; Pred. No. 2.6e-250;			
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;			
QY	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEHEDCLKSEYENVEPVSASTI	60
DB	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEHEDCLKSEYENVEPVSASTI	60
QY	61	QTGIGIAGKILGTLGVPPAGQVASYLSYFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA	120
DB	61	QTGIGIAGKILGTLGVPPAGQVASYLSYFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA	120
QY	121	RNKALTDLKLGDALAVYHDSLSWGNRNNTARSVVKVSKQYIALELMFVQKLPSPFVSG	180
DB	121	RNKALTDLKLGDALAVYHDSLSWGNRNNTARSVVKVSKQYIALELMFVQKLPSPFVSG	180
QY	181	EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSVHCVKWYS	240
DB	181	EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSVHCVKWYS	240
QY	241	TGLNNLKGTAESWVRNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDI	300
DB	241	TGLNNLKGTAESWVRNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDI	300
QY	301	GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTOYNNMW	360
DB	301	GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTOYNNMW	360
QY	361	GGHKLKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVTESLAGNLFLTQPVNGVPR	420
DB	361	GGHKLKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVTESLAGNLFLTQPVNGVPR	420



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QY 421 VDFHKKFVTHPIASDNFYYPGVAGITGLQDSENELPPEATQOPNYESYSHRLSHIGLIS 480
Db 421 VDFHKKFVTHPIASDNFYYPGVAGITGLQDSENELPPEATQOPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVRGPGFTGCDILLRNN 540
Db 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVRGPGFTGCDILLRNN 540
QY 541 TGTFGDIRVINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600
Db 541 TGTFGDIRVINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600
QY 601 TPRTVGFTPPFSFLDVQSTFTIGAMNFGSGNEVYIDRIEFVPEVYEAEDYFEKAQEKV 660
Db 601 TPRTVGFTPPFSFLDVQSTFTIGAMNFGSGNEVYIDRIEFVPEVYEAEDYFEKAQEKV 660
QY 661 TALFTSTNPRGLTKTDVKDHYHIDQVSNLVESLDEFLDEKRELFEIVKYANLSLHIERNM 719
Db 661 TALFTSTNPRGLTKTDVKDHYHIDQVSNLVESLDEFLDEKRELFEIVKYANLSLHIERNM 719

RESULT 4
I40590
Cryv465 protein - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40590
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A:Title: Distribution of cryv-type insecticidal protein genes in Bacillus thuringiensis
tomocidus.
A:Reference number: I39814; MUID:95314293; PMID:7793960
A:Accession: I40590
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-719 <RES>
A:Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:G467234; PIDN:AAA82114.1; PID:G4672
C:Genetics:
A:Gene: cryv465
C:Superfamily: paraaporal crystal protein

Query Match 93.1%; Score 3503; DB 2; Length 719;
Best Local Similarity 92.5%; Pred. No. 9.5e-234;
Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;
QY 1 MKLNQDKHQSPSSNAKVDKISTDSLKNETDTELQNIHEDCLKMEYENVPFVSASTI 60
Db 1 MKLNQDKHQSPSSNAKVDKISTDSLKNETDTELQNIHEDCLKMEYENVPFVSASTI 60
QY 61 QTGIGIAGKILGTVPPAGQVASYLSFILGELWPKGKNQWEIFMEHVBEIINQKISTYA 120
Db 61 QTGIGIAGKILGTVPPAGQVASYLSFILGELWPKGKNQWEIFMEHVBEIINQKILTYA 120
QY 121 RNKALTDLKGDLAAYVHDSLESVGNRNNTARSVVKVQYIALBELMFVKLPSPAVSG 180
Db 121 RNKALTDLKGDLAAYVHDSLESVGNRNNTARSVVKVQYIALBELMFVKLPSPAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSVHCVKWYS 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSVHCVKWYS 240
QY 241 TGLNNLRGTNAESWVRYNQFRDMLTLMVLDLVALFPSPYDTQMPYIKTTAQLTREVVYDAI 300
Db 241 TGLNNLRGTNAESWVRYNQFRDMLTLMVLDLVALFPSPYDTQMPYIKTTAQLTREVVYDAI 300
QY 301 GTVHPHPSFTSTWYNNAPSPSAIAA VVRNPHLLDFLEQVTIYSLLSRWNSQTQMNW 360
Db 301 GTVHPHPSFTSTWYNNAPSPSAIAA VVRNPHLLDFLEQVTIYSLLSRWNSQTQMNW 360
QY 361 GGHKLEFRITGGTNTSTOGSTNTSINPVTLPFTSRDVYRTESLAGNLFLTPQVNGVPR 420
Db 361 GGHKLEFRITGGTNTSTOGSTNTSINPVTLPFTSRDVYRTESLAGNLFLTPQVNGVPR 420
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QY 421 VDFHKKFVTHPIASDNFYYPGVAGITGLQDSENELPPEATQOPNYESYSHRLSHIGLIS 480
Db 421 VDFHKKFVTHPIASDNFYYPGVAGITGLQDSENELPPEATQOPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVRGPGFTGCDILLRNN 540
Db 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVRGPGFTGCDILLRNN 540
QY 541 TGTFGDIRVINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600
Db 541 TGTFGDIRVINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600
QY 601 TPRTVGFTPPFSFLDVQSTFTIGAMNFGSGNEVYIDRIEFVPEVYEAEDYFEKAQEKV 660
Db 601 TPRTVGFTPPFSFLDVQSTFTIGAMNFGSGNEVYIDRIEFVPEVYEAEDYFEKAQEKV 660
QY 661 TALFTSTNPRGLTKTDVKDHYHIDQVSNLVESLDEFLDEKRELFEIVKYANLSLHIERNM 719
Db 661 TALFTSTNPRGLTKTDVKDHYHIDQVSNLVESLDEFLDEKRELFEIVKYANLSLHIERNM 719

RESULT 5
S00873
paraaporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis
N:Alternate names: paraaporal crystal protein cryA4
C:Species: Bacillus thuringiensis subsp. thuringiensis
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S00873
R:Brizzard, B.L.; Whiteley, H.R.
Nucleic Acids Res. 16, 2723-2724, 1988
A:Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus
A:Reference number: S00873; MUID:88203216; PMID:3362680
A:Accession: S00873
A:Molecule type: DNA
A:Residues: 1-1228 <BRI>
A:Cross-references: UNIPROT:P05517; EMBL:X06711; NID:G40264; PIDN:CAA29898.1; PID:G58084;
C:Genetics:
A:Gene: cryA4
A:Start codon: TTG
C:Superfamily: paraaporal crystal protein
C:Keywords: delta-endotoxin

Query Match 60.1%; Score 2262.5; DB 2; Length 1228;
Best Local Similarity 62.4%; Pred. No. 9.6e-148;
Matches 447; Conservative 79; Mismatches 165; Indels 25; Gaps 6;
QY 23 TDSLKNETDIELQNTNH-----EDCLKMEYENVPFVSASTIQTGIGTAGKI 70
Db 2 TSNRNKNEIINAVNSHAQMDLLPDARIEDSLCIAEGNNIDPFVSASTIQTGINTAGRI 61
QY 71 LGTLGVPPAGQVASYLSFILGELWPKGKNQWEIFMEHVBEIINQKISTYARNKALTDLKG 130
Db 62 LGVLGVPPAGQLASFYSLVGLWPRGRDQWEIFLEHVEQLINQITENARNALTALRQG 121
QY 131 LGDALAVYHDSLESVGNRNNTARSVVKVQYIALBELMFVKLPSPAVSGEVPPLPIYA 190
Db 122 LGDSFRAYQOQSLDLENDRDARTSVLYTQYIALELDFLNAFLFAIRNQSVPLMWYA 181
QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSVHCVKWYSTGLNNLRGTN 250
Db 182 QAANLHLLLRDASIFGSEFGLTSQEIQRYSRQVERTRDYSQVCEWNTGLNSURGTN 241
QY 251 AESWVRYNQFRDMLTLMVLDLVALFPSPYDTQMPYIKTTAQLTREVVYDAIGTVHPHPSFT 310
Db 242 AASWVRYNQFRDMLTLMVLDLVALFPSTYTRYPINTSAQLTREVVYDAIGAT--GVNMA 299
QY 311 STWYNNAPSPSAIAA VVRNPHLLDFLEQVTIYSLLSRWNSQTQMNWGGHKLFRIT 370
Db 300 SMWYNNAPSPSAIAA VVRNPHLLDFLEQVTIYSLLSRWNSQTQMNWGGHKLFRIT 359
QY 371 GGTINISTOGSTNTSINPVTLPFTSRDVYRTESLAGNLFL--LTQPVNGVPRVDHMKFV 428
Db 360 GGLTNTSTHGATNTSINPVTLPFTSRDVYRTESLAGNLFL--LTQPVNGVPRVDHMKFV 416
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Db 709 YGHDKQMLLEAVRAAKRLSRNL 732

## RESULT 8

S32645  
parasporal crystal protein cryIgal - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S32645  
R:Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A:Reference number: S32645  
A:Accession: S32645  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1166 <LAW>  
A:Cross-references: UNIPROT:Q45746; EMBL:Z22510; NID:g295861; PIDN:CAA80233.1; PID:g2958  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 39.0%; Score 1467.5; DB 2; Length 1166;  
Best Local Similarity 45.8%; Pred. No. 6.8e-93;  
Matches 323; Conservative 100; Mismatches 207; Indels 75; Gaps 17;  
QY 41 DCLKMEYE---NVEPFVASTIQTGIGIAGKILGTGVFPAGQVASYSLFELWPK 96  
DB 13 NCLNPESEIFNARNNSFGLVQSSGL---TRFLLEAAVPEAGPALGLFDIIGAL--- 66  
QY 97 GKNQWEIFMEHVEEIIINQKISTYARNKALTDLKGDLALAVYHDSLESWGNTRARS 156  
DB 67 GVDQNSLFRQEQLEIRITELERNRATAILTGLSSYNLYVEALREWENDFNPNPASQE 126  
QY 157 VVKSVIALELMFVQKLPFAVSGEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSE 216  
DB 127 RVTRFRLTDDALVTGLPTLAIRNLEVNLSVYQAANLHLLLRDASVYFGERWGLTQAN 186  
QY 217 ISTFYNRQVERAGDYSYHCVKVYSTGLNLRGTNAESWVRYNQFRDMTLVLDVALPP 276  
DB 187 IEDLYTRLTNSIQEYSDHCARWYNQGLNEIGGISR---RYLDFQRLDTISVLDIVALPP 242  
QY 277 SYDTQMYPIKTTAQLTREYVTDAL--GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNH 334  
DB 243 NYDIRTYPIPTQSOLTRITYSPVAGNI-----NFGLSIANVLRAHP 285  
QY 335 LLDPLFQVITYSLLRSWNTQYMMNGHKLFRITIG-GTLN-----ISTQGSTNTS 385  
DB 286 LMDFDIRIVYTNVR--STPY---WAGHEVISRRTGQOGHEIRPPLYGVANAEPVPT 340  
QY 386 INPVTLPFTSRDVRTESS-----LAGNLFLTPQVNGVPRVDFHWKVFVTHPIASDNFY 439  
DB 341 IRPTGFTDEQORWYRARSRVSPRSQDFSLVDAVG-----FLT-IFSAVSIYR 389  
QY 440 PGVAGIGTQLODSENELPPEATQCPNYESYSHRLSHIGLISAS-----HVKALVSWTHR 494  
DB 390 NGF-GPNT---DTIDRPIEGTDP--FTGYSHRLCHVGFLASSPFTISQYARAPIFSWTHR 443  
QY 495 SADRTWTIBPNSITQIPLKAFNLSCAAVVRGPGFTGCDILRRWTGTGFDIRVNNINPP 554  
DB 444 SATLTWTIAPDVITQIPLKAFNLHSGAIVKGPFTGCDILRRWVSGFGDMRVNITAP 503  
QY 555 PAQRYVRIRYASTTDLOFHTSINGKAINQGNFSAITMRGEDLDYKTPRTVGTFTTSPSEL 614  
DB 504 LSQRVVRIRYASTTDLOFVTNINGTTINIGFSSMTSDGDDLOQGRFVAGFTTFTFTFS 563  
QY 615 DVQSTTTICANFPSSGNEVYIDRIEFPVVEVYAEYDEKAQEKVTALFTSTNPRGLKT 674  
DB 564 DANSTFTIGAFGSPNNEVYIDRIEFPVPAEVTFAEYDLEKAQAYNALFTSSNQIGLKT 623  
QY 675 DVKDYHIDQVNLVESLSEFYLDEKRELFELIVKYANELHIERNM 719  
DB 624 DVTDYHIDKVNLYVECLSEDFCLDEKRELSKVKHAKRLSDERNL 668

## RESULT 9

S32649  
parasporal crystal protein cryIpa3 - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S32649  
R:Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A:Reference number: S32645  
A:Accession: S32649  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1174 <LAW>  
A:Cross-references: UNIPROT:Q45749; EMBL:Z22512; NID:g295865; PIDN:CAA80235.1; PID:g2958  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 38.8%; Score 1461; DB 2; Length 1174;  
Best Local Similarity 44.6%; Pred. No. 1.9e-92;  
Matches 324; Conservative 101; Mismatches 205; Indels 96; Gaps 17;  
QY 36 NINHE---DCLKMEYENVEPFVSASTIQTGIGIA-GKILGTGVFPAGQVASYSLF 90  
DB 4 NIONQCVNCLNSNEVEILSEERSTGRPLDISLSLTRFLSEFVPGVGVAFGLDLIW 63  
QY 91 GELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKGDLALAVYHDSLESWGNRN 150  
DB 64 GFITP---SEWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEVYLEALREWEENPN 120  
QY 151 NTRARSVVKSVIALELMFVQKLPFAVSGEVPLPIYAQAANLHLLLRDASIFGKEW 210  
DB 121 NAQLREYRIARPDDDALITAINNFTLSFEIPLSVYVQAANLHLLLRDASVFGQGM 180  
QY 211 GLSSSEISTFYNRQVERAGDYSYHCVKVYSTGLNLRGTNAESWVRYNQFRDMTLVLD 270  
DB 181 GUDIATVNNHNLINLHRYTECHCDTYNQGLENLRTNTRQNSRFQFRELTLTVLD 240  
QY 271 LVALPSPDYDTQMYPIKTTAQLTREYVTDALGTVHPHPSFTSTWYNNAPSPSAIEAAV 329  
DB 241 IVALFPNYDARAYPIQTSQSLTREYTSV--IEDSP-----VSANIPNGFNRAEFG- 290  
QY 330 VNPHELLFLEQVITYSLLRSWNTQYMMNGHKLFRITIGTGLNISTQGSTNTSINPV 389  
DB 291 VRPPLHMDFMN-----SLFVTAETVRSQTVMGHVLV-----SSRTAGNP 331  
QY 390 TLPP-----TSRDVYRTESLAGNLFLTPQVNGVPRVDFHWKVFVTHPIAS 434  
DB 332 NPTIYGINPGAIWIAEDDPFPFRT-----LSDPV-----FVRGGFGN 371  
QY 435 DNFFYPGAGIGTQLQ-----DSENELPPEATQCPNYESYSHRLSHI----- 476  
DB 372 PH-YVLGLRGVAFQQTGTNHTTRFNSGTIDSLDEIPQDNSGAPWNDYSHVLNHVTVR 430  
QY 477 --GLISASHV-KALVYVSWTHRSADRTNIEPNSITQIPLKAFNLSSGAUVRGPGFTGG 533  
DB 431 WFEIAGSDSWRAPMFSWTHRSADRTNINPNIITQIPAVKAHNLHSGSTVVRGPGFTGG 490  
QY 534 DTLRETTNGTGDIRVNNIPPEAQRVYRIRYASTTDLOFHTSINGKAINQGNFSAITMR 593  
DB 491 DLURRTNGTGFADIRVNTGPLSQRYRIRYASTTDLOFTRINGTSVQNQNFQRTMNR 550  
QY 594 GEDLDYKTPRTVGTFTTSPSELVDVQSTFTTIGAMNFSGNEVYIDRIEFPVVEVYAEYDF 653  
DB 551 CGNLSSGNFRTAGFTSPFSNAQSTFTLTGTQAFSN-QEYVIDRIEFPVPAEVTFAESDL 609  
QY 654 EKAQSKVTALFTSTNPRGLKTDVKDHYHIDQVNLVESLSEFYLDEKRELFELIVKYANEL 713  
DB 610 ERAQKAVNALFTSTSQLGLKTNVTGYHIDQVNLVACLSEDFCLDEKRELSKVKHAKRL 669  
QY 714 HIERNM 719  
DB 670 SDRNL 675

RESULT 10

A26513  
parasporal crystal protein - Bacillus thuringiensis (strain aizawai)  
C:Species: Bacillus thuringiensis  
C>Date: 11-Mar-1988 #sequence\_revision 11-Mar-1988 #text\_change 09-Jul-2004  
C:Accession: A26513  
R:Oeda, K.; Oehie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, H.  
Gene 53, 113-119, 1987  
A:Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis  
A:Reference number: A26513; MUID:87248103; PMID:3297927  
A:Accession: A26513  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1155 <OE>  
A:Cross-references: UNIPROT:P06578; GB:M16463; NID:G143098; PIDN:AAA22551.1; PID:G143098  
A:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match		38.8%;	Score 1459;	DB 2;	Length 1155;
Best Local Similarity		44.1%;	Pred. No. 2.6e-92;		
Matches		313;	Conservative 112;	Mismatches 230;	Indels 54; Gaps 12;
Qy	36	NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTIGVFPAGQVASLYS	87		
Db	4	NPINNECIPYNCLSNPEVEVLGGRIETGTPIDISLSLTQFLISEF-VPGAGFVLGLVD	62		
Qy	88	FILGELPQKQKQWEIEMHEVVEIINQKISTYARNKALTDLKGGLDALAVYHDSLESMVG	147		
Db	63	IIWGIF---GPSQWDAFLVQIEQLINQRIEFARNQAIISLEGSLNLYQIYAESFRWEA	119		
Qy	148	NNNTRARSVVKSVQVIALELMFVKLPSPFAVSSEVPLLPITYAANLHLLLRDASIFG	207		
Db	120	DPTPALREEMRIQFNDMNSALTTPALPLFAVQVQVPLSVYVQAANLHLSVLREDVSFVG	179		
Qy	208	KEWGLSSEISTFYNRQVERAGSYHCVKWYSTGLNNLRQTNASWVRYNQFRDWTLM	267		
Db	180	QRWGDAATINSRYNDLTRIGNVTDAVRVYNTGLERVWGPDSGRDWIRYNQFRRELTLT	239		
Qy	268	VLDLVALPSPVDTQWYPIKTTAQTAEVVTYDAIGVHPHPSFTSTTWNNAFSAIEA	327		
Db	240	VLDIVSLSPNDVDSRTYPIRTVSQLTREIYTPV-----LENPDGSFRALAQ	285		
Qy	328	AV---VRNPHLLDFEQVTIYSLLSR-----WSNTQYMMN---WGHKLEFRTIGTILNIS	377		
Db	286	GIEGSIKSPHLMIDLNSITITVDAHRGEYVWSGHQIMASPVGSGPEPTFPLYGTMGNA	345		
Qy	378	TQGSTNTSINPVTLPFTGRDVYRTESLAGNLFLTOPVNGVPRVDPHKFWTHFIASDNF	437		
Db	346	PQQRIVAGLQGVYRTLSSTLYRRPFINGIN---NQQLSVLDGTGEFAYG-----TSSNL	396		
Qy	438	YYPGAGIGTQDQSENELPPEATQPNVESVSHRLSHIGLI-----SASHVKALVYS	490		
Db	397	PSAVTRKSGT--VDSLDEIPPNVNPVPRQFSHRLSHVSPFRSFSNVSIIIRAPMFS	454		
Qy	491	WTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRNTNTGTGDIRVN	550		
Db	455	WTHRSAEFNIIIPSSQITQIPLTKNLGSGTSVVKGPFTGGDILRNTSPQISTLRVN	514		
Qy	551	INPPAQRYVRIRVASTTDLQFHTSINGKAINQGNFSATNRGEDLDYKTFRTVGTFTTP	610		
Db	515	ITAPLSQRYVRIRVASTTNLQFHTSIDGRPINQGNFSATMSSGNLSQSGSFRVGTFTTP	574		
Qy	611	RFSLDVQSTFTTIGANFSGNEVYIDRIEFVPEVVEYEAEDYDEKAQKVATLFTSTNPR	670		
Db	575	FNFSNGSVFTLSAHVFNSGNEVYIDRIEFVPAETTPAEYDLEBAQKAVNELFTSSNQI	634		
Qy	671	GLKTDVKQYHIDQVSNLVESLSEFYLDKRELFEIVKYANELHITERNM	719		
Db	635	GLKTDVTDVHIDQVSNLVESLSEFYLDKRELFEIVKYANELHITERNM	719		

RESULT 11

JD00002  
parasporal crystal protein cryIAb3 - Bacillus thuringiensis  
N:Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal prot  
C:Species: Bacillus thuringiensis  
C>Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 09-Jul-2004  
C:Accession: A90025; A91560; A90955; S14555; A26461; A24172; A29043; JD00002  
R:Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.  
Agric. Biol. Chem. 51, 455-463, 1987  
A:Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from  
A:Reference number: A90025  
A:Accession: A90025  
A:Molecule type: mRNA  
A:Residues: 1-1155 <KON>  
A:Cross-references: UNIPROT:P06578  
A:Experimental source: subsp. kurstaki  
R:Geiser, M.; Schweitzer, S.; Grimm, C.  
Gene 48, 109-118, 1986  
A:Title: The hypervariable region in the genes coding for entomopathogenic crystal prote:  
A:Reference number: A91560; MUID:87163505; PMID:3557124  
A:Accession: A91560  
A:Molecule type: DNA  
A:Residues: 1-1155 <GEI>  
A:Cross-references: GB:M15271; NID:G143123; PIDN:AAA22561.1; PID:G143124  
A:Experimental source: subsp. kurstaki  
R:Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.  
DNA 5, 305-314, 1986  
A:Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product anal;  
A:Reference number: A90955; MUID:86300092; PMID:3743328  
A:Accession: A90955  
A:Molecule type: DNA  
A:Residues: 1-1155 <WAB>  
A:Cross-references: GB:M13898; NID:G142719; PIDN:AAA22330.1; PID:G142720  
A:Experimental source: subsp. berliner  
R:Chak, K.F.; Jen, J.C.  
submitted to the EMBL Data Library, October 1990  
A:Description: Complete nucleotide sequence and expression in Escherichia coli of a cry  
A:Reference number: S14555  
A:Accession: S14555  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1155 <CHA>  
A:Cross-references: EMBL:X54939; NID:G40272; PIDN:CAA38701.1; PID:G40273  
R:Hofte, H.; de Greve, H.; Seurinck, J.; Janssens, S.; Mahillon, J.; Ampe, C.; Vandekerckh  
Eur. J. Biochem. 161, 273-280, 1986  
A:Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thur  
A:Reference number: A26461; MUID:87054036; PMID:3023091  
A:Accession: A26461  
A:Molecule type: DNA  
A:Residues: 1-730, 'L', 732-784, 'R', 786-1155 <HOF>  
A:Cross-references: GB:X04698; NID:G40254; PIDN:CAA28405.1; PID:G40255  
A:Experimental source: strain berliner 1715  
C:Comment: This toxin is lethal to the larvae of lepidoptera and dipterans.  
C:Genetics:  
A:Gene: cry-1-2; bt2  
A:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin  
F:82-586/Product: toxic peptide #status predicted <TXP>  
F:82-300/Region: toxic #status predicted  
F:300-586/Region: insecticidal #status predicted

Query Match		38.6%;	Score 1452;	DB 2;	Length 1155;
Best Local Similarity		44.2%;	Pred. No. 7.8e-92;		
Matches		314;	Conservative 111;	Mismatches 229;	Indels 56; Gaps 13;
Qy	36	NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTIGVFPAGQVASLYS	87		
Db	4	NPINNECIPYNCLSNPEVEVLGGRIETGTPIDISLSLTQFLISEF-VPGAGFVLGLVD	62		
Qy	88	FILGELPQKQKQWEIEMHEVVEIINQKISTYARNKALTDLKGGLDALAVYHDSLESMVG	147		
Db	63	IIWGIF---GPSQWDAFLVQIEQLINQRIEFARNQAIISLEGSLNLYQIYAESFRWEA	119		
Qy	148	NNNTRARSVVKSVQVIALELMFVKLPSPFAVSSEVPLLPITYAANLHLLLRDASIFG	207		

Db 120 DPTNPALREEMRIQFNDMNSALTATTAIPFAVQNYQVPLLSVYVQAANHLSLVLRDVSFG 179  
QY 208 KEWGLSSSEISTFYNRQVERAGDYSVHCVKWYSTGLNNLRGTNAESWVRYNQFRDMLTLM 267  
Db 180 QRWGFDATINSRYNDLTRIGNYTDHVRWYNTGLERVMGPDSDRWIRYNOFRRELTIT 239  
QY 268 VLDLVALPSPDYQMPYPIKTAQLTREVYTDAGTVVHPHPSFTSTTWYNNAPSF-----S 323  
Db 240 VLDIVSLFPNDSRTYPIRTVSQLTREIYTNPV-----LENFGDSFRGSAQ 285  
QY 324 ATEAAVVRNPHLLDFLEQVTIYSLLSR-----WSNTQYMM-----WGHKLEPRTIGTGLNI 376  
Db 286 GIEGS-IRSPHLMIDLNSITITDAHGEYVWSGHQIMASPVGFGPEFTFPLYGTMGNA 344  
QY 377 STQGSNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPRVDFHVKFVTHPIASN 436  
Db 345 APQORIVAOLGGQVYRTLSLTYRRPFNIGIN---NQLSVLDGTEFAYG-----TSSN 395  
QY 437 FYPYGAGITQLQDSNELPPEATQPNYESYSHRLSHIGLI-----SASHVKALYV 489  
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPROGFSHRLSHVSMFRSGFSNVSIIIRAPMF 453  
QY 490 SWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRLRTNTGTGDIRV 549  
Db 454 SWHRSAEFNNIPSSQITQIPLTKSTNLGSGTSVVGPGFTGGDILRLRTSPQOISTLRV 513  
QY 550 NINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYKTFRTVGFTT 609  
Db 514 NITAPLSQRYRIRYASTTNLQFHTSIDGRINQGNFSATMSSGNLQSGSFRIVGFTT 573  
QY 610 PFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFPVPEVTEAEYDFEKAQKVTALTFTSTNP 669  
Db 574 PNFNSNGSVFTLSAHVFNSGNEVYIDRIEFPVPAEVTFEAEYDLERAQKAVNELFTSSNQ 633  
QY 670 RGLKTDVQDHYHDQVSNLVESLSDEFYLDKELFEIVKYANLHIERNM 719  
Db 634 IGLKTDVTDYHDQVSNLVESLSDEFYLDKELFEIVKYANLHIERNM 683

## RESULT 12

A29125  
parasporal crystal protein Bc2 - Bacillus thuringiensis subsp. kurstaki (strain HD-1)  
C:Species: Bacillus thuringiensis subsp. kurstaki  
C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 09-Jul-2004  
C:Accession: A29125  
R:Pischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme  
Bio/technology 5, 807-813, 1987  
A:Title: Insect tolerant transgenic tomato plants.  
A:Reference number: A29125  
A:Accession: A29125  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-1156 <FIS>  
A:Cross-references: UNIPROT:Q9F296; UNIPROT:Q93T21  
A:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 38.6%; Score 1452; DB 2; Length 1156;  
Best Local Similarity 44.2%; Pred. No. 7.8e-92;  
Matches 314; Conservative 111; Mismatches 229; Indels 56; Gaps 13;

QY 36 NINHECLKMSYENVE-PFVSASTIQTG-----IGIAGKILGTGLVPPFAGQVASLYS 87  
Db 4 NPNINECIYPNCLSNPEVEVLGGERIETGYTIDISLSLTQFLSEF-VPGAGFVLGLVD 62  
QY 88 FILGELWPKGNQWEIFMEHVEEIIINQISTYARNKALTDLKGDLALAVYHDSLSWVG 147.  
Db 63 IIWGIEF---GPSQWDAFLVQIEQLNRIEFPARNQAIISRLGSLNLYQIYAESFREWEA 119  
QY 148 NRNNTARSVVKSQYTALELMFVKQLPSFAGSVEVPILLPIYAQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMNSALTATTAIPFAVQNYQVPLLSVYVQAANHLSLVLRDVSFG 179

QY 208 KEWGLSSSEISTFYNRQVERAGDYSVHCVKWYSTGLNNLRGTNAESWVRYNQFRDMLTLM 267  
Db 180 QRWGFDATINSRYNDLTRIGNYTDHVRWYNTGLERVMGPDSDRWIRYNOFRRELTIT 239  
QY 268 VLDLVALPSPDYQMPYPIKTAQLTREVYTDAGTVVHPHPSFTSTTWYNNAPSF-----S 323  
Db 240 VLDIVSLFPNDSRTYPIRTVSQLTREIYTNPV-----LENFGDSFRGSAQ 285  
QY 324 ATEAAVVRNPHLLDFLEQVTIYSLLSR-----WSNTQYMM-----WGHKLEPRTIGTGLNI 376  
Db 286 GIEGS-IRSPHLMIDLNSITITDAHGEYVWSGHQIMASPVGFGPEFTFPLYGTMGNA 344  
QY 377 STQGSNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPRVDFHVKFVTHPIASN 436  
Db 345 APQORIVAOLGGQVYRTLSLTYRRPFNIGIN---NQLSVLDGTEFAYG-----TSSN 395  
QY 437 FYPYGAGITQLQDSNELPPEATQPNYESYSHRLSHIGLI-----SASHVKALYV 489  
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPROGFSHRLSHVSMFRSGFSNVSIIIRAPMF 453  
QY 490 SWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRLRTNTGTGDIRV 549  
Db 454 SWHRSAEFNNIPSSQITQIPLTKSTNLGSGTSVVGPGFTGGDILRLRTSPQOISTLRV 513  
QY 550 NINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYKTFRTVGFTT 609  
Db 514 NITAPLSQRYRIRYASTTNLQFHTSIDGRINQGNFSATMSSGNLQSGSFRIVGFTT 573  
QY 610 PFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFPVPEVTEAEYDFEKAQKVTALTFTSTNP 669  
Db 574 PNFNSNGSVFTLSAHVFNSGNEVYIDRIEFPVPAEVTFEAEYDLERAQKAVNELFTSSNQ 633  
QY 670 RGLKTDVQDHYHDQVSNLVESLSDEFYLDKELFEIVKYANLHIERNM 719  
Db 634 IGLKTDVTDYHDQVSNLVESLSDEFYLDKELFEIVKYANLHIERNM 683

## RESULT 13

I39838  
parasporal crystal protein - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I39838  
R:Hefford, M.A.; Brousseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J.A.; Lau, P.C.K.  
J. Biotechnol. 6, 307-322, 1987  
A:Title: Sequence of a lepidopteran toxin gene of Bacillus thuringiensis subsp kurstaki  
A:Reference number: I39838  
A:Accession: I39838  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-1155 <RES>  
A:Cross-references: UNIPROT:P06578; GB:M37263; NID:gl42885; PIDN:AAA22420.1; PID:gl42886  
A:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 38.4%; Score 1443; DB 2; Length 1155;  
Best Local Similarity 44.1%; Pred. No. 3.3e-91;  
Matches 313; Conservative 111; Mismatches 230; Indels 56; Gaps 13;

QY 36 NINHECLKMSYENVE-PFVSASTIQTG-----IGIAGKILGTGLVPPFAGQVASLYS 87  
Db 4 NPNINECIYPNCLSNPEVEVLGGERIETGYTIDISLSLTQFLSEF-VPGAGFVLGLVD 62  
QY 88 FILGELWPKGNQWEIFMEHVEEIIINQISTYARNKALTDLKGDLALAVYHDSLSWVG 147  
Db 63 IIWGIEF---GPSQWDAFLVQIEQLNRIEFPARNQAIISRLGSLNLYQIYAESFREWEA 119  
QY 148 NRNNTARSVVKSQYTALELMFVKQLPSFAGSVEVPILLPIYAQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMNSALTATTAIPFAVQNYQVPLLSVYVQAANHLSLVLRDVSFG 179  
QY 208 KEWGLSSSEISTFYNRQVERAGDYSVHCVKWYSTGLNNLRGTNAESWVRYNQFRDMLTLM 267

Db 180 QRGFDDAATINSRYNDLTRIGNYTDHVAWYNTGLERVWGPDSRDWIRYNOFRRELTILT 239  
QY 268 VLDLVALFPSSYDTOMYPIKTTAQLTREVVYDAIGTVHPHPSFTSTTWYNNNAPSFAIEA 327  
Db 240 VLDIVLFSNDSRYRPIRVTSQLTREIYNPV-----LENFDGSRGSAQ 285  
QY 324 AIEAAVRNPHLLDFLEQVITYSLLSR-----WSNTQYMMN---WGHKLEFTIGTGLNI 376  
Db 286 GIEGS-IRSPHLDILNSIIITDAHGEYVWSGHQIMASPGVSGPEFTFPLYGTMGNA 344  
QY 377 STQSGTNTSNPVLTPTSDRVRTESLAGLNFLTPQVNGVPRVDFHMKFVTHPTASDN 436  
Db 345 APOQRIVAQLGQGYRTLSLTLYRRPNIGIN---NQQLSVLDGTBFAYG-----TSSN 395  
QY 437 FYPYAGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHITGLI-----SASHVKALVY 489  
Db 396 LPSAVYRKSGLT--VDSLDEIPQNNVPPROGFSHRLSHVSMFRSGFSNVSIIIRAPMF 453  
QY 490 SWTHRSADRTNTIIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRLRTNTGTFGDIRV 549  
Db 454 SWIHSRANFNIIIPSSQITQIPLTKSTNLGSGTGVKPGFTGGDILRLRTSPGOISTLRV 513  
QY 550 NINPPAQRVRYRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKYKTFRTVGF 609  
Db 514 NITAPLSQRVRYRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKYKTFRTVGF 573  
QY 610 PFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQKVTALFTSTNP 669  
Db 574 PNFNSGSSVFTLSAHVNSGNEVYIDRIEFVPAEVTFAEYDILERAQKAVNELFTSSNQ 633  
QY 670 RLKTKTDVYDHIDQVNSLVESLDEFYDKRELFEIVKYANLHIERNM 719  
Db 634 IGLKTDVTDYDHIDQVNSLVESLDEFYDKRELFEIVKYANLHIERNM 683

RESULT 14  
A22798  
parasporal crystal protein - Bacillus thuringiensis  
C;Species: Bacillus thuringiensis  
C;Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 09-Jul-2004  
C;Accession: A22798  
R;Shibano, Y.; Yamagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, M.  
Gene 34, 243-251, 1985  
A;Title: Nucleotide sequence coding for the insecticidal fragment of the Bacillus thuringiensis  
A;Reference number: A22798; MUID:85232070; PMID:2989108  
A;Accession: A22798  
A;Molecule type: DNA  
A;Residues: 1-934 <SHI>  
A;Cross-references: UNIPROT:Q9S5V8; GB:M10917; NID:G143100; PIDN:AAA22552.1; PID:g551713  
C;Comment: The authors translated the codon ACA for residue 264 as Ser.  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 38.3%; Score 1439.5; DB 2; Length 934;  
Best Local Similarity 43.3%; Pred. No. 4.1e-91;  
Matches 308; Conservative 118; Mismatches 225; Indels 61; Gaps 12;

QY 36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGLTVGPAGQVASLYS 87  
Db 4 NPNINECIPYCNLSNPEVEVLGGRIETGTPIDISLITQFLSEF-VPGAGFVLGLVD 62

QY 88 FILGELWPKGNQWEIFMEHVEEIIINQISTYARNKALTDLKGDLALAVYHDSLESVWG 147  
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEBAFARNOAISRLGSLNLYQIYAESPREWEA 119

QY 148 NRNTRARSVVKSQYIALELMFVKQLPSFAVSGEEVPLLPYQAANLHLLRLDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYQAANLHLSVLVDVSFG 179

QY 208 KEWGLSSEISTFYNQVERAGDYSYHCWKYSTGLNLRGTNAESWRYNQFRDRTLM 267  
Db 180 QRWGFDATINSRYNDLTRIGNYTDVAVRWYNTGLERVWGPDSRDWRVYNOFRRELTILT 239

QY 268 VLDLVALFPSSYDTOMYPIKTTAQLTREVVYDAIGTVHPHPSFTSTTWYNNNAPSFAIEA 327  
Db 240 VLDIVLFSNDSRYRPIRVTSQLTREIYNPV-----LENFDGSRGSAQ 285  
QY 328 AV---VRNPHLLDFLEQVITYSLLSRNTQYMMNMGHKLKLEFTTIGCT---LNISTQGS 381  
Db 286 RIEQNIQRPHLMDILNRTIYDVHRG-----FNWMSGHQITASPGVSGPEFAFPLFGN 340  
QY 382 TMTSINPVLTPTSDRVYRTESL-----AGLNFLTPQVNGVPRVDFHMKFVTHPT 432  
Db 341 AGNAAPPVLSLTGLGIFRTLSPLRYRIILGSGPN---NQLEFVLDTGTFSPASLTNLT 397  
QY 433 ASDNFPYCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHITGLISAS-----HYKAL 487  
Db 398 PSTYRQRTV-----DSLDDVIPQDQNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP 450  
QY 488 VYSWTHRSADRTNTIIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRLRTNTGTFGDI 547  
Db 451 TFSWQHRSAGFNNIIPSSQITQIPLTKSTNLGSGTGVKPGFTGGDILRLRTSPGOISTLT 510  
QY 548 RVNINPPAQRVRYRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKYKTFRTVGF 607  
Db 511 RVNITAPLSQRVRYRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKYKTFRTVGF 570  
QY 608 TTPFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQKVTALFTST 667  
Db 571 TTPFNSGSSVFTLSAHVNSGNEVYIDRIEFVPAEVTFAEYDILERAQKAVNELFTSS 630  
QY 668 NFRGLKTDVYDHIDQVNSLVESLDEFYDKRELFEIVKYANLHIERNM 719  
Db 631 NQIGLTKTDVTDYDHIDQVNSLVESLDEFYDKRELFEIVKYANLHIERNM 682

RESULT 15  
JT0241  
parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)  
N;Alternate names: 135K insecticidal protein  
C;Species: Bacillus thuringiensis  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C;Accession: JT0241  
R;Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.  
Agric. Biol. Chem. 52, 1565-1573, 1988  
A;Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein  
A;Reference number: JT0241  
A;Accession: JT0241  
A;Molecule type: DNA  
A;Residues: 1-1176 <SHI>  
A;Cross-references: UNIPROT:P02965  
A;Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal protein  
C;Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 38.2%; Score 1438.5; DB 2; Length 1176;  
Best Local Similarity 43.3%; Pred. No. 6.9e-91;  
Matches 308; Conservative 117; Mismatches 226; Indels 61; Gaps 12;

QY 36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGLTVGPAGQVASLYS 87  
Db 4 NPNINECIPYCNLSNPEVEVLGGRIETGTPIDISLITQFLSEF-VPGAGFVLGLVD 62

QY 88 FILGELWPKGNQWEIFMEHVEEIIINQISTYARNKALTDLKGDLALAVYHDSLESVWG 147  
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEBAFARNOAISRLGSLNLYQIYAESPREWEA 119

QY 148 NRNTRARSVVKSQYIALELMFVKQLPSFAVSGEEVPLLPYQAANLHLLRLDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYQAANLHLSVLVDVSFG 179

QY 208 KEWGLSSEISTFYNQVERAGDYSYHCWKYSTGLNLRGTNAESWRYNQFRDRTLM 267  
Db 180 QRWGFDATINSRYNDLTRIGNYTDVAVRWYNTGLERVWGPDSRDWRVYNOFRRELTILT 239



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2005, 17:22:50 ; Search time 70.6029 Seconds  
(without alignments)  
3350.901 Million cell updates/sec

Title: US-10-019-823B-56

Perfect score: 3762

Sequence: 1 MCLKNQKHQSFSSNAKVDK.....KRELFIVKYANELHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubaa/US07\_PUBCOMB.pep.\*

2: /cgn2\_6/ptodata/1/pubaa/PCT\_NEW\_PUB.pep.\*

3: /cgn2\_6/ptodata/1/pubaa/US06\_NEW\_PUB.pep.\*

4: /cgn2\_6/ptodata/1/pubaa/US06\_PUBCOMB.pep.\*

5: /cgn2\_6/ptodata/1/pubaa/US07\_NEW\_PUB.pep.\*

6: /cgn2\_6/ptodata/1/pubaa/PCTUS\_PUBCOMB.pep.\*

7: /cgn2\_6/ptodata/1/pubaa/US08\_NEW\_PUB.pep.\*

8: /cgn2\_6/ptodata/1/pubaa/US08\_PUBCOMB.pep.\*

9: /cgn2\_6/ptodata/1/pubaa/US09A\_PUBCOMB.pep.\*

10: /cgn2\_6/ptodata/1/pubaa/US09B\_PUBCOMB.pep.\*

11: /cgn2\_6/ptodata/1/pubaa/US09C\_PUBCOMB.pep.\*

12: /cgn2\_6/ptodata/1/pubaa/US09\_NEW\_PUB.pep.\*

13: /cgn2\_6/ptodata/1/pubaa/US10A\_PUBCOMB.pep.\*

14: /cgn2\_6/ptodata/1/pubaa/US10B\_PUBCOMB.pep.\*

15: /cgn2\_6/ptodata/1/pubaa/US10C\_PUBCOMB.pep.\*

16: /cgn2\_6/ptodata/1/pubaa/US10D\_PUBCOMB.pep.\*

17: /cgn2\_6/ptodata/1/pubaa/US10\_NEW\_PUB.pep.\*

18: /cgn2\_6/ptodata/1/pubaa/US11\_NEW\_PUB.pep.\*

19: /cgn2\_6/ptodata/1/pubaa/US60\_NEW\_PUB.pep.\*

20: /cgn2\_6/ptodata/1/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3743	99.5	719	US-10-782-020-10	Sequence 10, Appl
2	3743	99.5	719	US-10-782-141-8	Sequence 8, Appl
3	3459.5	92.0	710	US-10-428-961-42	Sequence 42, Appl
4	2263.5	60.2	1228	US-10-809-953-10	Sequence 10, Appl
5	2260.5	59.8	1207	US-09-988-462-7	Sequence 7, Appl
6	2171.5	57.7	1227	US-10-428-961-63	Sequence 63, Appl
7	2156.5	57.3	1186	US-09-826-660-23	Sequence 23, Appl
8	2101	55.8	1228	US-10-428-961-38	Sequence 38, Appl
9	1923.5	51.1	643	US-10-614-524-2	Sequence 2, Appl
10	1923.5	51.1	643	US-09-826-660-25	Sequence 25, Appl
11	1707.5	45.4	1167	US-10-089-678-1	Sequence 1, Appl
12	1678.5	44.6	653	US-10-428-961-6	Sequence 6, Appl
13	1655.5	44.0	1157	US-10-782-141-16	Sequence 16, Appl

14	1496	39.8	1206	13	US-10-032-717-2	Sequence 2, Appl
15	1496	39.8	1206	14	US-10-414-637-2	Sequence 2, Appl
16	1496	39.8	1206	15	US-10-606-320-2	Sequence 2, Appl
17	1480	39.3	1210	13	US-10-032-717-4	Sequence 4, Appl
18	1480	39.3	1210	14	US-10-414-637-4	Sequence 4, Appl
19	1480	39.3	1210	15	US-10-606-320-4	Sequence 4, Appl
20	1476.5	39.2	1156	14	US-10-099-285-72	Sequence 72, Appl
21	1476.5	39.2	1156	15	US-10-428-961-28	Sequence 28, Appl
22	1452	38.6	1155	9	US-09-756-643-2	Sequence 2, Appl
23	1452	38.6	1155	10	US-09-988-462-9	Sequence 9, Appl
24	1452	38.6	1155	15	US-10-136-998A-2	Sequence 2, Appl
25	1452	38.6	1177	14	US-10-035-060-6	Sequence 6, Appl
26	1452	38.6	1181	10	US-09-988-462-11	Sequence 11, Appl
27	1452	38.6	1181	10	US-09-988-462-13	Sequence 13, Appl
28	1452	38.6	1181	10	US-09-988-462-15	Sequence 15, Appl
29	1452	38.6	1181	10	US-09-988-462-17	Sequence 17, Appl
30	1452	38.6	1181	10	US-09-988-462-28	Sequence 28, Appl
31	1452	38.6	1181	15	US-10-136-998A-4	Sequence 4, Appl
32	1452	38.6	1181	15	US-10-136-998A-8	Sequence 8, Appl
33	1452	38.6	1181	15	US-10-136-998A-10	Sequence 10, Appl
34	1452	38.6	1181	15	US-10-136-998A-12	Sequence 12, Appl
35	1447	38.5	1177	14	US-10-035-060-2	Sequence 2, Appl
36	1445	38.4	1177	14	US-10-035-060-8	Sequence 8, Appl
37	1444	38.4	1177	14	US-10-102-469-24	Sequence 24, Appl
38	1428.5	38.0	1176	16	US-10-782-141-6	Sequence 6, Appl
39	1416.5	37.7	1176	11	US-09-837-961-2	Sequence 2, Appl
40	1416.5	37.7	1176	16	US-10-825-751-2	Sequence 2, Appl
41	1385	36.8	1167	15	US-10-428-961-40	Sequence 40, Appl
42	1364	36.3	1177	9	US-09-873-873-26	Sequence 26, Appl
43	1364	36.3	1177	10	US-09-916-956A-26	Sequence 26, Appl
44	1364	36.3	1177	10	US-09-997-914-26	Sequence 26, Appl
45	1364	36.3	1177	14	US-10-365-645-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1

US-10-782-020-10

Sequence 10, Application US/10782020

Publication No. US20040197916A1

GENERAL INFORMATION:

APPLICANT: Carozzi, Nadine

APPLICANT: Hargiss, Tracy

APPLICANT: Koziel, Michael G.

APPLICANT: Duck, Nicholas B.

APPLICANT: Carr, Brian

TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and

TITLE OF INVENTION: Methods for Its Use

FILE REFERENCE: 045600/274139

CURRENT APPLICATION NUMBER: US/10782.020

PRIOR FILING DATE: 2004-02-19

PRIOR APPLICATION NUMBER: 60/448,810

PRIOR FILING DATE: 2003-02-20

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10

LENGTH: 719

TYPE: PRT

ORGANISM: Bacillus thuringiensis

US-10-782-020-10

Query Match	99.5%	Score 3743;	DB 16;	Length 719;
Best Local Similarity	99.6%	Pred. No. 8.2e-308;		
Matches 716;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	MCLKNQKHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKNSEVENPEFVSASTI	60	
Db	1	MCLKNQKHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKNSEVENPEFVSASTI	60	
Qy	61	QTGGIAGKILGTGVFPAGOVASLYSFLGELPKGNQWEIEMFHVHEEIIINQKISTYA	120	
Db	61	QTGGIAGKILGTGVFPAGOVASLYSFLGELPKGNQWEIEMFHVHEEIIINQKISTYA	120	

QY	121	RNKALTDLKGIGDALAVYHDSLSWGNRNNTARSVVKSOYIALELMFVQKLPSPAVSG	180
DB	121	RNKALTDLKGIGDALAVYHDSLSWGNRNNTARSVVKSOYIALELMFVQKLPSPAVSG	180
QY	181	BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVRAGDYSVHCVKWYS	240
DB	181	BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVRAGDYSVHCVKWYS	240
QY	241	TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSTQMPYPIKTTAQLTREVTYDAI	300
DB	241	TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSTQMPYPIKTTAQLTREVTYDAI	300
QY	301	GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW	360
DB	301	GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW	360
QY	361	GGHKLFEFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFITQPVNGVPR	420
DB	361	GGHKLFEFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFITQPVNGVPR	420
QY	421	VDFHMKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLIS	480
DB	421	VDFHMKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLIS	480
QY	481	ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN	540
DB	481	ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN	540
QY	541	TGTFGDIRVNNPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDLKY	600
DB	541	TGTFGDIRVNNPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDLKY	600
QY	601	TFTVTGFTTFFSFLDQSTFTIGAMNFFSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV	660
DB	601	TFTVTGFTTFFSFLDQSTFTIGAMNFFSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV	660
QY	661	TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDREKRELFEIVKYAKQLHIERNM	719
DB	661	TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDREKRELFEIVKYAKQLHIERNM	719
RESULT 2			
US-10-782-141-8			
; Sequence 8, Application US/10782141			
; Publication No. US20040197917A1			
; GENERAL INFORMATION:			
; APPLICANT: Carozzi, Nadine			
; APPLICANT: Hargies, Tracy			
; APPLICANT: Koziel, Michael G.			
; APPLICANT: Duck, Nicholas B.			
; APPLICANT: Carr, Brian			
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and			
; TITLE OF INVENTION: Methods for Its Use			
; FILE REFERENCE: 045600/274143			
; CURRENT APPLICATION NUMBER: US/10782.141			
; CURRENT FILING DATE: 2004-02-20			
; PRIOR FILING DATE: 2004-02-20			
; NUMBER OF SEQ ID NOS: 23			
; SOFTWARE: FASTSEQ for Windows Version 4.0			
; SEQ ID NO 8			
; LENGTH: 719			
; TYPE: PRT			
; ORGANISM: Bacillus thuringiensis			
US-10-782-141-8			
Query Match 99.5%; Score 3743; DB 16; Length 719;			
Best Local Similarity 99.6%; Pred. No. 8.2e-308;			
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;			
QY	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLMKSEYENVPFVSASTI	60

NAME/KEY: misc feature  
LOCATION: (2007..(200)  
OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid  
US-10-428-961-42

Query Match 92.0%; Score 3459.5; DB 15; Length 710;  
Best Local Similarity 92.1%; Pred. No. 8.5e-284; Indels 9; Gaps 1;  
Matches 662; Conservative 16; Mismatches 32

QY 1 MKLKNQKHQSSNAKVDKIDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60  
DB 1 MKSKNQNHQSLNNATVDKNFTGSLNNTNTELFQNFH-----EGIEPVSASTI 51  
QY 61 QTGIGIAGKILGTLPVAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISYA 120  
DB 52 QTGIGIAGKILGNLGPVAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISYA 111  
QY 121 RNKALDGLGDLAVVHDSLESWGNRNTRRSVVKSOYIALELMFVOKLPFAVSG 180  
DB 112 RNKALADLKGDLAVVHDSLESWGNRNTRRSVVKSOYITULELMFVOKLPFAVSG 171  
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSEYSDHCWKYN 231  
DB 172 BEVPLLPPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSEYSDHCWKYN 231  
QY 241 TGLNLRGTNAESWRYNQFRDMLMVLVDLVALPSPYDTQMPYIKTTAQLTREVTDAI 300  
DB 232 TGLNLRGTNAESWRYNQFRDMLMVLVDLVALPSPYDTQMPYIKTTAQLTREVTDAI 291  
QY 301 GTVHPHPSFTSTWNNNAPSFAEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMNW 360  
DB 292 GTVHPHPSFTSTWNNNAPSFAEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMNW 351  
QY 361 GCHKLEPFTIGTLNISTQSGTNTSINPVTLPFTSRDVRYESLAGNLFQTPVNGVPR 420  
DB 352 GCHKLEPFTIGTLNISTQSGTNTSINPVTLPFTSRDVRYESLAGNLFQTPVNGVPR 411  
QY 421 VDFHWKFTVTHPIASNFYYPGAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480  
DB 412 VDFHWKFTVTHPIASNFYYPGAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 471  
QY 481 ASHKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
DB 472 ASHKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 531  
QY 541 TGTGDIRVNINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFATWNRGDDLYK 600  
DB 532 TGTGDIRVNINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFATWNRGDDLYK 591  
QY 601 TFRVGTFTTSPFLDQSTFTTIGAWNPSGNEVYIDRIEFVPEVYEAEDFEKAQEV 660  
DB 592 TFRVGTFTTSPFLDQSTFTTIGAWNPSGNEVYIDRIEFVPEVYEAEDFEKAQEV 651  
QY 661 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDFEYLDKRELFEIVKYANELHIERNM 719  
DB 652 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDFEYLDKRELFEIVKYANELHIERNM 710

RESULT 4

US-10-809-953-10  
Sequence 10, Application US/10809953  
Publication No. US20040181825A1  
GENERAL INFORMATION:  
APPLICANT: Botterman, Herman  
APPLICANT: Van Mellaert, Johan  
APPLICANT: Van Rie, Jeroen  
APPLICANT: Joos, Henk  
TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTICIDAL PROTEINS  
FILE REFERENCE: 021565-078  
CURRENT APPLICATION NUMBER: US/10/809,953  
CURRENT FILING DATE: 2004-03-26  
PRIOR APPLICATION NUMBER: US/09/661,016

PRIOR FILING DATE: 2000-09-13  
PRIOR APPLICATION NUMBER: PCT/EP90/00905  
PRIOR FILING DATE: 1990-05-30  
PRIOR APPLICATION NUMBER: GB 89401499.2  
PRIOR FILING DATE: 1989-05-31  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 1228  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis  
US-10-809-953-10

Query Match 60.2%; Score 2263.5; DB 16; Length 1228;  
Best Local Similarity 62.4%; Pred. No. 4.3e-182;  
Matches 447; Conservative 79; Mismatches 165; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQNH-----ECLKMEYENVEPVSASTIQTGIGIAGKI 70  
DB 2 TSNRKNENEIINAVNSHSAQMDLLPDKARIEDSLCIAEGNNDIPFVSASTVQTGINIAGRI 61  
QY 71 LGTLGVFPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130  
DB 62 LGVLGVFPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 121  
QY 131 LGDLAVYHDSLESWGNRNTRRSVVKSOYIALELMFVOKLPFAVSGEVPPLPIYA 190  
DB 122 LGDSFRAYQQSLEDWLENRDDARTSVLHTQYIALELDFLNAMPLFAIRNOEVPPLMYYA 181  
QY 191 QAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSEYSDHCWKYNSTGLNLRGTN 250  
DB 182 QAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSEYSDHCWKYNSTGLNLRGTN 241  
QY 251 AESWRYNQFRDMLMVLVDLVALPSPYDTQMPYIKTTAQLTREVTDAIQTGHPHPSFT 310  
DB 242 AASWRYNQFRDMLMVLVDLVALPSPYDTQMPYIKTTAQLTREVTDAIQTGHPHPSFT 299  
QY 311 STWYNNNAPSFAEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMNWGHKLEPFTI 370  
DB 300 SMWYNNNAPSFAEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMNWGHKLEPFTI 359  
QY 371 GGTINISTQSGTNTSINPVTLPFTSRDVRYESLAGNLF--LTPQVNGVPRVDFHMKFV 428  
DB 360 GGTINISTQSGTNTSINPVTLPFTSRDVRYESLAGNLF--LTPQVNGVPRVDFHMKFV 416  
QY 429 THP-----IASDNFYPCYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLISASH 483  
DB 417 TNPQNSDRGTANYSQP--YESPGLQKXDETELPETTERPNYESYSHRLSHIGLISASH 475  
QY 484 VKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 543  
DB 476 VNVFVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 535  
QY 544 FGDIRVNINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFATWNRGDDLYK 603  
DB 536 FGDIRVNINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFATWNRGDDLYK 595  
QY 604 TVGFTTSPFLDQSTFTTIGAWNPSGNEVYIDRIEFVPEVYEAEDFEKAQEV 663  
DB 596 RRAFTTFTTQIDQVSNLVESLSDFEYLDKRELFEIVKYANELHIERNM 655  
QY 664 FTSTNPRGLKTDVYHIDQVSNLVESLSDFEYLDKRELFEIVKYANELHIERNM 719  
DB 656 FTSTNPRGLKTDVYHIDQVSNLVESLSDFEYLDKRELFEIVKYANELHIERNM 711

RESULT 5

US-09-988-462-7  
Sequence 7, Application US/09988462  
Publication No. US20030046726A1  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
APPLICANT: Desai, Nalini M.

Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Launis, Karen L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Syngenta Biotechnology, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/988,462  
FILING DATE: 20-NO. US20030046726A1-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/547,422  
FILING DATE: 11-APR-2000  
APPLICATION NUMBER: US 08/459,504  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Weigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-188051  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7  
Query Match 59.8%; Score 2250.5; DB 10; Length 1207;  
Best Local Similarity 64.0%; Pred. No. 5.3e-181;  
Matches 440; Conservative 77; Mismatches 157; Indels 13; Gaps 5;

40 EDLCIKSEYENVEPVASSTIQIGTAGKILGTGVFPAGOVASLYSFIIGELMPKGN 99  
10 EDLSLCAEAGNNIDPFVASTVQGINIAGILGTGVFPAGQLASFSFLVGLMPGRGD 69  
100 QWEIFMEHVEEINQKISTYARNKALTDLKGDLALAVYHDSLESWVGNNNTARSVVK 159  
70 QWEIFLEHVEQLNQITENARNTALARLQGLGDSFRAYQQSLDLEWLRDDARTSVLY 129  
160 SQYIALBELMFVKQLPSFVSGEEVPLPIYAQANLHLILLRDLASIFGKEWGLSSSEIST 219  
130 TQYIALDELFLNAPLFAIRNQEVPLLMVYAQANLHLILLRDLASLFGSEFGLTSEIOR 189  
220 FYNQVERAGDYSYHCVKWTSTGLNNLRGTNAESWVRYNQFRDRMTLMVLDLVALPSPYD 279  
190 YFERQVERTRDYSYCVWNTGLNLRGTNAESWVRYNQFRDRMTLMVLDLVALPSPYD 249  
280 TQMPYPIKTAQLTREVYTDAGTGVHPPHSTSTTWYNNAPSFSAEAAVVRNPHLLDFL 339

250 TRTYPIINTSAQLTREVYTDAGTGVHPPHSTSTTWYNNAPSFSAEAAVVRNPHLLDFL 307  
340 EQVTIYSLLSWSNTQYNNMGHKLKERTTIGTGLNISTOGSTNTSINPVTLPFTSRDYY 399  
308 EQLTIFSSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTSRDYY 367  
400 RTESLAGLNLF-LTQPVNGVPRVDFHMKFVTHP-----IASDNFYPGYAGIGTQLODS 452  
368 RTESVAGVLLGYLEPIHGVTFRNF--TNPQNISDRGTANYSQP-YESPGQLKDS 423  
453 ENELPEATGQPNYESYSHRLSHIGLISASHKALVYSWTHRSADRTNIBNSITQIPL 512  
424 ETELPEETTERPNYESYSHRLSHIGLISASHKALVYSWTHRSADRTNIBNSITQIPL 483  
513 VKAFNLSSCAAUVVRGPGFTGGDILRRTNTGTGDIRVNVINPPFAQRYRVRAYATTDIQ 572  
484 VKASELPQGTTVVRGPGFTGGDILRRTNTGTGDIRVNVINPPFAQRYRVRAYATTDIQ 543  
573 FHTSINGKAINQGNFSATNMGEDLDYKTRFTVGTFTTTPSFSLDVQSTFTIGAWNFSSGNE 632  
544 FVSRGTTVNNFRFLRTMNSGDELKYGNFVRAFTTPTFTQIQDIIRTSIQLSGNGE 603  
633 VIIDRIEFVPEVTEAEYDFEKAQEKVTALETSTNPRGLKTDVDYHIDQVSNLVESLS 692  
604 VIIDKIEIIPVTATFEAYDLEAQAQAVNALFTNTNPRKLDVTDYHIDQVSNLVACLS 663  
693 DEFYDLKRELPEIVKYANELHIERNM 719  
664 DEFCLDEKRELLEKVKYAKELSDERNL 690

RESULT 6  
US-10-428-961-63  
Sequence 63 Application US/10428961  
Publication No. US2003023711A1  
GENERAL INFORMATION:  
APPLICANT: Baum, James A.  
APPLICANT: Chu, Chih-Rei  
APPLICANT: Donovan, William P.  
APPLICANT: Gilmer, Amy J.  
APPLICANT: Ruper, Mark J.  
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
FILE REFERENCE: MECO201--1  
CURRENT APPLICATION NUMBER: US/10/428,961  
CURRENT FILING DATE: 2003-05-02  
PRIOR APPLICATION NUMBER: 09/661,322  
PRIOR FILING DATE: 2000-09-13  
PRIOR APPLICATION NUMBER: 60/153,995  
PRIOR FILING DATE: 1999-09-15  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: Patent In version 3.2  
SEQ ID NO 63  
LENGTH: 1227  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis  
US-10-428-961-63

Query Match 57.7%; Score 2171.5; DB 15; Length 1227;  
Best Local Similarity 59.0%; Pred. No. 2.7e-174;  
Matches 421; Conservative 104; Mismatches 176; Indels 13; Gaps 3;  
13 SSNAKVDKISTDSLKN-----ETDIELQNNHEDCLKMESEYENVEPVASSTIQIGIG 65  
7 NENEIINALSIPAVSNHSAQNNLSLTDARI-----EDSLCIAEAGNNIDPFVASTVQGIN 61  
66 TAGKILGTGVFPAGOVASLYSFIIGELMPKGNQWEIFMEHVEEINQKISTYARNKAL 125  
62 IAGRLGLVGLVFPAGQIASFSFLVGLMPGRDPWEIFLEHVEHRLRQQVTENTRTAL 121  
126 TDLKGLGDALAVYHDSLESWVGNNNTARSVVKSQYIALBELMFVKQLPSFVSGEEVPL 185



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; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; US-10-614-524-2

Query Match      55.8%; Score 2101; DB 15; Length 1228;
Best Local Similarity 59.2%; Pred. No. 2.5e-168;
Matches 422; Conservative 97; Mismatches 184; Indels 10; Gaps 7;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCMKSEYENVEPVFSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66
QY 71 LGTGVPPAGQVASYLSFILGELMPKGNQWEIIFMEHVEELINOKISTYARNKALTDLKG 130
Db 67 LGVLGVPPAGQIASFYSLVGLWLPGRDQWEIIFLEHVEQLINQOITENARNATALARLQ 126
QY 131 LGDALAVYHDSLESWGNRNTRARSVVKSYQYIALELMFVQKLPFAVSGSEVPLLIYA 190
Db 127 LGDSFRAYQQSLEDWLENRDDARTSVLYTQYIALELDLFLNAMPFAIRNQEVPLLMVYA 186
QY 191 QAAHLHLLLDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWYSTGLNNLRGTN 250
Db 187 QAAHLHLLLDASIFGSEFGLTSQEIQRYERQVEQTRDYSYDVCVEWYNTGLNSLRGTN 246
QY 251 AESWVRNQFRDMLVLDLVALFPSYDTOMYPIKTTAQLTREVTYDAIGAT--GVNMA 304
Db 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMWGGHKLERTI 370
QY 305 SNWYNNAPSFSAIETAVIRSPHLLDFLEQVTIYSLLSRWSTQYMMWGGHKLERTI 364
QY 371 GGTLMISTQGSTNTSINPVTLPFTSRDYRTESLAGLNL--LTQPVNGVPRVDFHWKFV 428
Db 365 GGLNTSTHGSTNTSINPVLSPFSRDVYVYTESYAGVLLWGIYLEPIHGVTFRFNRNP 424
QY 429 --THPIASDNFYPGYAGIGTQLODSNELPPEATQPNYESYSHRLSHGLISASHVKA 486
Db 425 QNTFERGTANYSQP--YESPGLQKDSSETLPETTERPNYESYSHRLSHGLISASHV 483
QY 487 LVYSWTHRSADRTNIENPSITQIPLVKAFNLSSGAAVVRGPGFTGGDILARTNTGTG 546
Db 484 PVSWTHRSADRTNISDSITQIPLVKSFNLNGSTSVSGFGFTGGDIIRTNVNGSVLS 543
QY 547 IRVINPFPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSAATNRGEDIYKTFRTVG 606
Db 544 MGLNFNNTSLQRYRVRVRYAASQTMVLRTVTVGGSTTFDQGPSTMSANESLTSQSFRAE 603
QY 607 FTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKVTALPTS 666
Db 604 FVVGISAGSQ--TAGISISNNAGRTQTHFDKIEFIPITATFEAYDLERAQEVNVALFTN 662
QY 667 TNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVVKYANELHIERNM 719
Db 663 TNPRRLKTDVTDYHIDQVSNLVACLSDDEFCLDEKRELLKVKYAKRLSDERNL 715

RESULT 9
US-10-614-524-2
; Sequence 2, Application US/10614524
; Publication No. US20040016020A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva
; APPLICANT: Vanneste, Strijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
; FILE REFERENCE: NEWBTSUS2
; CURRENT APPLICATION NUMBER: US/10/614,524
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/739,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28

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; PRIOR APPLICATION NUMBER: 09/178,252  
 ; PRIOR FILING DATE: 1998-10-23  
 ; PRIOR APPLICATION NUMBER: 60/065,215  
 ; PRIOR FILING DATE: 1997-11-12  
 ; PRIOR APPLICATION NUMBER: 60/076,445  
 ; PRIOR FILING DATE: 1998-03-02  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn ver. 2.0  
 ; SEQ ID NO 25  
 ; LENGTH: 643  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene  
 US-09-826-660-25

Query Match 51.1%; Score 1923.5; DB 9; Length 643;  
 Best Local Similarity 57.5%; Pred. No. 1e-153;  
 Matches 370; Conservative 100; Mismatches 160; Indels 13; Gaps 3;

Qy	13	SSNAKVDKISTSLKN-----ETDIELQNIHEDCLKMSYENVEPFPVSASTIQTGIG	65
Dd	7	NEINEIINALSIPAVSNHSAQWNLSTDARI-----EDSLCIAEGNNIDPFPVSASTVQTGIN	61
Qy	66	IACKILGTGVPPAGQVASYISFPLGBLMPKGNQWEIFMEHVEEIIINQISTYARNKAL	125
Dd	62	IAGRILGVLGVPAGQIASFYSFLVGBLMPGRDPEIFLEHVEQLIRQQWENTRTDAL	121
Qy	126	TDLKGIGDALAVYHDSLESVGNRNTRASVVKSVQYIALELMFVOKLPSFAVSGEVP	185
Dd	122	ARLOGLGNSPRAYQOQSLDEWLENRDDARTRSVLYQYIALELDFLNAMPLFAIRNOEVP	181
Qy	186	LPITYAQAANLHLLLRDLASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNN	245
Dd	182	LMVYQAQAANLHLLLRDLASIFGSEFGLTSQEIQRYERYQVEKTRREYSDYCARWYNTGLNN	241
Qy	246	LRGTNAESVRYNQFRDMLTLMVLDLVALPFSYDTQMPYIKTTAQLTREYVYTDAGTVHP	305
Dd	242	LRGTNAESWLRYNQFRDRLTLGLVLDLVALPFSYDTRVYPMNTSAQLTREYVYTDPIGRNA	301
Qy	306	HPFSTSTWYNNNAPSFAEAAVRNPHLLDLEQVTIYSLSRWSNTQYMNWGGHKL	365
Dd	302	PSGFASNTWNNNAPSFAEAAVIRPHLLDPPEQLTIFSVLSRWSNTQYMNWYVGHRL	361
Qy	366	EFRITGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTQPVNGVPRVDFHW	425
Dd	362	ESRTIRGSLSTHGNTNTSINPVTLOFTSRDVRVYTESFAGINILLTTPVNGVPRVDFHW	421
Qy	426	KFVTHPIASDNFYYPGAGTGLQDSENELPPEATQPNYESSYHRLSHIGHISASHVK	485
Dd	422	RNPLNSLRGSLLYTIGTVGVGTQDFDSELTPELTPETTERPNYESSYHRLSNIRLISGNLTLR	481
Qy	486	ALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTGTGFG	545
Dd	482	APVYSWTHRSADRNTIISDSTIQLPLVKSFNLSGTSVVSFGFTGGDILRRNTGTGFG	541
Qy	546	DIRVINPPFAQRVVRVIRVASTTDLQFHTSINGKAINQGNFSAATNRRGEDLDYKKTFRV	605
Dd	542	SMGLNFNTSLQRVVRVIRVTAAGTQVLRVTVGSGSTTFDQGFSTMSANESLTSQSRFA	601
Qy	606	GFTTPFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVYTYE	648
Dd	602	EPFVGISASGSQ-TAGISISNNAGRQTFHFDKIEFIPITATLE	643

RESULT 11  
 US-10-089-678-1  
 ; Sequence 1, Application US/10089678  
 ; Publication No. US20030017967A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ASANO, Shinichiro  
 ; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A  
 ; TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD

RESULT 12

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US-10-428-961-6
; Sequence 6, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201-1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-6

Query Match      44.6%; Score 1678.5; DB 15; Length 653;
Best Local Similarity 51.5%; Pred. No. 5.9e-133; Indels 47; Gaps 14;
Matches 346; Conservative 105; Mismatches 174;

QY 13 SSNAKDKISTDLSKN---ETDIEIQNHEDCLMKSEYENVEPVFVSASTIQTGTGIGAGK 69
DB 2 NENEINALSIPAVNSHNSQMDLSL-DARIEDSLCIAEGNNINPLVSASTVQTGINAGR 60

QY 70 ILGTGVPPAGVASYLSFILGELMPKGNQKQWEIEMHVEELINOKISTYARNKALTDLK 129
DB 61 ILGLVGPAGQASFPYSLVGLWPGSDPWEIFLEYEQIRIQOVTNRTAIBALE 120

QY 130 GLGDALAVYHDSLESVGNRNTRARSVVKSQVIALELMFVQKLPSPFVSGEVEPLPIY 189
DB 121 GLGRGYSRQQALETWLDNRNDARSIILEYVALELDITTAIPLFIRNEEVLPMVY 180

QY 190 AQAAHLHLLLRDASIFGKESLSSEISTFTYNNQVERAGDYSHCVKXWYSTGLNNLRT 249
DB 181 AQAAHLHLLLRDASIFGSEWGMASDVNQYQEQIRIYEEYSNCHVCQWYNTGLNNLRT 240

QY 250 NAEWRYNQFRDWTLMVLVDLVALPSPYDTQMPYPIKTTAQLTREVYTDALGTVHPHPSF 309
DB 241 NAEWRLRYNQFRDLTLGLVDLVALPSPYDTRTPINTSAQUTREIYTDPIGRTNAPSGF 300

QY 310 TSTTWNNAAPSFAIEAAVVRNPHLLDLEQVITYSLLSRWSNTQYMMMGCHLEFRT 369
DB 301 ASTNWNNAAPSFAIEAAIFRPHLLDPEQLTIYSASSRWSSTOHMNYWVGHRLNRP 360

QY 370 IGGTLNISTOGST--NTSINPVTLPF--TSRDVRYTESLAGNLFLTOPVNGVRPVDHVKF 427
DB 361 IGGTLNISTOGLTNNTSINPVTLYHVSRRDVRYTESNAGTNILFTTPVNGVWPARN--F 418

QY 428 VTHPIASDNPYP-----GYAGICTQLQDSENELPPEATGQPNVESYSHRLSHIG-- 477
DB 419 ITRIRFKEAPLTVNRIRELGNLYLIQKLYHQK-----QQDQIMHIVIDISYR 470

QY 478 LISASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGDILR 537
DB 471 LIIGNTLRAPVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGDILR 529

QY 538 -RTNWTGTF--GDIRVNNIN--PPFAQRYRVRIRASITDLDQFHTSINGKAINQCNFSAWN 592
DB 530 LNRNNGNIQNGRYEIVPQITSTSTRYRVRVRYASVTSIELNVLNNGSSIFTNTPATAA 589

QY 593 RGEDLDYKTRTVGTGFTPPSFLDVOSTFT-----IGAMNFSSGNEVYIDRIEFVPEVT 646
DB 590 SLDNLQ-----SGDFGYVEINNAFTSATGNIVGARNFSAAEVIIDRFEFIPVTAT 640

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QY 647 YEAYDFEKAQE 658
DB 641 FEVEYDLERAQK 652

RESULT 13
US-10-782-141-16
; Sequence 16, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1157
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-16

Query Match      44.0%; Score 1655.5; DB 16; Length 1157;
Best Local Similarity 48.8%; Pred. No. 1.3e-130; Indels 57; Gaps 18;
Matches 369; Conservative 97; Mismatches 233;

QY 1 MCLKNODKSHFSSNAKVDKISTDS---LKNETDIEIQNHEDCLMKSEYE-----N 50
DB 1 MSPNNQNEYIIDATPST-SVSSDSNRYPPANEPTDALQNMNYKDYLKMSGGENPELFGN 59

QY 51 VEPFVSASTIQTGTGIGAGKILGTLPVFPAGQVAVSLYSFILGELMP-KGKNQWEIEMHVE 109
DB 60 PETFISSSTIQTGTGIGVIRILGALGVFPASQIASFYFVIGQLWPSKSDVIMGEIMERVE 119

QY 110 EIIINOKISTYARNKALTDLGLGDALAVYHDSLESVGNRNTRARSVVKSQVIALELMF 169
DB 120 ELVDQKIEKVYKDKALAEKGLGNALDVYQOSLEDWLENENDARTSRVSVNQFIADLNF 179

QY 170 VQKLPSPFVSGEVEPLPIYAAANLHLLLRDASIFGKESLSSEISTFTYNNQVERAG 229
DB 180 VSSIPSPFVSGHEVLLAVYAQAVNLHLLLRDASIFGEEWGTTPGEISRYNRQVQJTA 239

QY 230 DYSYHCVKXWYSTGLNNLRTNAGTNAESWRYNQFRDWTLMVLVDLVALPSPYDTQMPYPIKTTA 289
DB 240 EYSDYCVKXWYKIGLDKLGTTSKSLWNYHQPRREMTLLVDLVALFPNYDTHMYPETTA 299

QY 290 QLTREVYTDALGTVHPHPSFTST---TWYNNNAAPSFAIEAAVVRNPHLLDLEQVITY 345
DB 300 QLTREVYTDPIA----FNIVTSTGFCNPWSTHSGILFVEVENNVIRPHLPFDILSSVEIN 355

QY 346 SLLSR-----WSTQYMMMGCHLEFR-----TGGLTNISTOGSTNTSINPVTLPFTR 396
DB 356 T--SRGGITLNDAYINWWSGHTLKRYRTADSTVTYTYANYGRITSEKNS-----FALEDR 408

QY 397 DVYRTESLAGNLFLTOPVNGVRPVDHVKFVTHPIASDNPY-----YPGVAGICTQLQD 451
DB 409 DIFEINSTVANLANYQKAYGVPGSWFH--MWKGTSTTAYLYSKTHALQGC-TQVYE 465

QY 452 SENELPPEATGQPNVESYSHRLSHI-----GLISASHVKALVSWTHRSADRTNTE 503
DB 466 SDEIPLDRT-VPVAESYSHRLSHITSHFSKNG--SAYYGSFPVFWVWTHSTADLNNTIY 522

QY 504 PNSTQIPLVKAFNLSSGAAVVRGPGTGDILARTNTEGDIRVNNINPPFAQRYRVR 563
DB 504 PNSTQIPLVKAFNLSSGAAVVRGPGTGDILARTNTEGDIRVNNINPPFAQRYRVR 563

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Db 523 SDKITQIPAVKGMVYLGSSVVGPGFTGGDILKRTNPSILGTFAVTNVSLSQRYRVI 582  
Qy 564 RYASTTDLQFHTSINGKAINQGNFATMNRGDLDYKTRTVGTFTPFSLDVQSTFTIG 623  
Db 583 RYASTTDPF-LYLGDITKRNFKNTMDNGASLTETFKFASFTIDFQFRETQDKILLS 641  
Qy 624 ANNFSSGNEVYIDRIEFVPEVTEYAEYDFEAKQKVTALFTSTNPRGLKTDVQDHYDQ 683  
Db 642 MGFSSGQEVYIDRIEFVPEVTEYAEQDLAAKAVNALFTNKD-GLRPGVTGYEVNQ 700  
Qy 684 VSNLVESLDEFYLDKRELFEIVKYANELHIERNM 719  
Db 701 AANLVECLSDDLLYPNEKRLLFDAVREAKRLSARNL 736  
RESULT 14  
US-10-032-717-2  
; Sequence 2, Application US/10032717  
; Publication No. US20020151709A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With  
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/032,717  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1206  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-032-717-2  
Query Match 39.8%; Score 1496; DB 13; Length 1206;  
Best Local Similarity 44.1%; Pred. No. 4.4e-117;  
Matches 335; Conservative 129; Mismatches 232; Indels 64; Gaps 22;  
Qy 1 MKLKNQDKHQSFSSNAKVDKISTDS----LKNETDIELQINHEDECLM-----SEYE-N 50  
Db 1 MSPNNQNEVEIIDATPST-SVNSDNRYPFPANEPTNALQNDYKDYLNKSNAGNASEYPGS 59  
Qy 51 VEPFVSA-STIQTGIGIAGKILGTIGVPPAGQVASYLSFILGELWPKG-KNQWEIFMEHV 108  
Db 60 PEVLVSGQDAKAAIDIVGKLGLGVFPVGPVIVSLYTLQILDILWPSGEKSKQWEIFMEQV 119  
Qy 109 EEIINOKISTYARNKALTDLKGLDALAVYHDSLESWGNRNNTARSVVKSOYTALEIM 168  
Db 120 EELINOKIAEYARNKALSELEGLNNYQLYLTALAEENPNPNSALRDVRNRFILDSL 179  
Qy 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVRA 228  
Db 180 FTQMPSPRVNTFVFPFLTVYAMAANLHLLLRDASIFGEEWGWSTTTINNYDQMKLT 239  
Qy 229 GDYSYHCVKWTSTGLNNLRGTNAESWRYNQPRRDMTLVLDLVALFPSTQYPMPIKTT 288  
Db 240 AEYSDHCVKVETGLAKLGTSKQWVDYDQPRRMTLAVLDVVALFPYDTRTPMETK 299  
Qy 289 AQLTRVYTDALGTGTHPSPFTSTTYNNNAPSFAIEAAVVRNPHLLDFLEQVITYILL 348  
Db 300 AQLTRVYTDPLGAVNV-----SIGSWY-DKAPSGFVIESSVIRPPHVFYDITGLTYTQS 355  
Qy 349 SRWSNTQYNNMGHKLFRFTIGTGLNISTQGSTNTSNPV-TLPFTSRDVRVRESLAGL 407  
Db 356 RSISARIYRHWAGHGISVHRVSRGSLNQMYGTGNLHLSSTFTFDYIDYIKLUSKQAV 415

Qy 408 NLFLTQP-----VNGVPRVDFHWKFVTHPIASDN---FYYPGAYIGTQLQDSENELPPE 459  
Db 416 LLDIVYPGYTTFIFCGMEVEF---FMVQLANTRKTLKYNPVVSKDIIASTRDSLELPPE 472  
Qy 460 ATGQNVYESYSHRLSHIGLISAS-HVKAL--VYSWTHESADRTNTEPNSITQIPLVKAF 516  
Db 473 TSDQNVYESYSHRLCHITSIFATGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKWC 532  
Qy 517 NLSSGAAVVRGPGFTGGDILR-RTNLTGTFGDI---RVNINPPFAQRYRVRIRYASTTDLQ 572  
Db 533 DNLFPVPVVGPGHTGGDLQVNRSTGSGVTLFLARYGLALEKAGKYRVLRYATDADIV 592  
Qy 573 FHTSINGKAINQGNFATMNRGDLDYKTR-----TVGFTTTPSF------DVQST 619  
Db 593 LH--VNDQA1---QMPKTMNFCEDLTSKTFKVADAITTLNLATDSSLKALKNLGEDPNST 647  
Qy 620 FTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEAKQKVTALFTSTNPRGLKTDVQDY 679  
Db 648 LS-----GIVYVDRIEFIPVDEYEAQDLAAKAVNALFTNKD-GLRPGVTDY 697  
Qy 680 HIDQVSNLVESLDEFYLDKRELFEIVKYANELHIERNM 719  
Db 698 EVNQAAANLVECLSDDLLYPNEKRLLFDAVREAKRLSARNL 737  
RESULT 15  
US-10-414-637-2  
; Sequence 2, Application US/10414637  
; Publication No. US20030177528A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With  
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/414,637  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: US/10/032,717  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/242,838  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1206  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-414-637-2  
Query Match 39.8%; Score 1496; DB 14; Length 1206;  
Best Local Similarity 44.1%; Pred. No. 4.4e-117;  
Matches 335; Conservative 129; Mismatches 232; Indels 64; Gaps 22;  
Qy 1 MKLKNQDKHQSFSSNAKVDKISTDS----LKNETDIELQINHEDECLM-----SEYE-N 50  
Db 1 MSPNNQNEVEIIDATPST-SVNSDNRYPFPANEPTNALQNDYKDYLNKSNAGNASEYPGS 59  
Qy 51 VEPFVSA-STIQTGIGIAGKILGTIGVPPAGQVASYLSFILGELWPKG-KNQWEIFMEHV 108  
Db 60 PEVLVSGQDAKAAIDIVGKLGLGVFPVGPVIVSLYTLQILDILWPSGEKSKQWEIFMEQV 119  
Qy 109 EEIINOKISTYARNKALTDLKGLDALAVYHDSLESWGNRNNTARSVVKSOYTALEIM 168  
Db 120 EELINOKIAEYARNKALSELEGLNNYQLYLTALAEENPNPNSALRDVRNRFILDSL 179  
Qy 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVRA 228  
Db 180 FTQMPSPRVNTFVFPFLTVYAMAANLHLLLRDASIFGEEWGWSTTTINNYDQMKLT 239



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:11:42 ; Search time 81.1112 Seconds  
(without alignments)  
4539.261 Million cell updates/sec

Title: US-10-019-823B-56  
Perfect score: 3762  
Sequence: 1 MKLKNQKHQSFSSNAKVDK.....KRELFEIVKYANELHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3743	99.5	719	1	C1IA_BACTK
2	3743	99.5	719	2	Q6X181
3	3738	99.4	719	2	Q93NJ5
4	3737	99.3	719	2	O85796
5	3608	95.9	719	2	O8KY61
6	3534	93.9	719	2	Q9F0P8
7	3503	93.1	719	1	C1IB_BACTE
8	3380	89.8	719	1	C1ID_BACTU
9	3379	89.8	719	1	C1IC_BACTU
10	2437.5	64.8	1229	1	C1BE_BACTU
11	2437.5	64.8	1229	1	C1BC_BACTM
12	2263.5	60.2	1228	2	Q93T75
13	2262.5	60.1	1228	2	C1BA_BACTK
14	2254.5	59.9	1228	2	Q93NM5
15	2180.5	58.0	849	2	Q6PYW8
16	2180.5	58.0	1227	1	C1BE_BACTU
17	2103.5	55.9	1231	2	O8KNY2
18	2098.5	55.8	1231	1	C1BD_BACTZ
19	1979.5	52.6	1215	1	C1KA_BACTM
20	1895	50.4	381	2	Q45740
21	1655.5	44.0	1157	1	C8AA_BACUK
22	1643	43.7	1144	2	O8KZL7
23	1493	39.4	1157	1	C9CA_BACTO
24	1471.5	39.1	1169	1	C8BN_BACUK
25	1469	39.0	1167	1	C1JA_BACTU
26	1467.5	39.0	1166	1	C1GA_BACTU
27	1467	39.0	1169	1	C1FB_BACTM
28	1461	38.8	1174	2	Q45749
29	1452	38.6	1155	1	C1AB_BACTK
30	1452	38.6	1155	2	Q7BE98
31	1452	38.6	1155	2	Q9F296

RESULT 1				
C1IA_BACTK				
ID	C1IA_BACTK	STANDARD;	PRT;	719 AA.
AC	Q45752;	P71092;	Q45750;	Q45751;
DT	30-MAY-2000	(Rel. 39, Created)		
DT	30-MAY-2000	(Rel. 39, Last sequence update)		
DT	05-JUL-2004	(Rel. 44, Last annotation update)		
DE	Pesticidial crystal protein cryIIa (Insecticidal delta-endotoxin)			
GN	CryII(a) (Crystalline entomocidal protoxin) (81 kDa crystal protein).			
DE	Name-cryIIa; Synonyms-CGCryV, cryII(a), cryV, cryVI;			
OS	Bacillus thuringiensis (subsp. kurstaki).			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=29339;			
RN	[1] SEQUENCE FROM N.A.			
RP	STRAIN=DSIR732;			
RC	MEDLINE=93298009; PubMed=8517758;			
RX	Gleaves A.P., Williams R., Hedges R.J.;			
RA	"Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for the presence of cryV-like insecticidal protein genes and characterization of a cryV gene cloned from B. thuringiensis subsp. kurstaki";			
RT	Appl. Environ. Microbiol. 59:1683-1687(1993).			
RL	[2] SEQUENCE FROM N.A.			
RN	STRAIN=JHCC4835;			
RC	MEDLINE=92269582; PubMed=1588820;			
RX	Tailor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;			
RA	"Identification and characterization of a novel Bacillus thuringiensis delta-endotoxin entomocidal to coleopteran and lepidopteran larvae";			
RT	Mol. Microbiol. 6:1211-1217(1992).			
RL	[3] SEQUENCE FROM N.A.			
RN	STRAIN=HD-1;			
RC	MEDLINE=95314293; PubMed=7793960;			
RX	Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;			
RA	"Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis and cloning of cryV-type genes from Bacillus thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp. entomocidus";			
RT	Appl. Environ. Microbiol. 61:2402-2407(1995).			
RL	[4] SEQUENCE FROM N.A.			
RN	STRAIN=AB88;			
RC	MEDLINE=96178985; PubMed=8606196;			
RX	Kostichka K., Warren M.G., Mullins M., Mullins A.D., Palekar N.V., Craig J.A., Koziel M.G., Estruch J.J.;			
RA	"Cloning of a cryV-type insecticidal protein gene from Bacillus thuringiensis: the cryV-encoded protein is expressed early in stationary phase";			
RT	J. Bacteriol. 178:2141-2144(1996).			
RL	[5] SEQUENCE FROM N.A.			
RN	STRAIN=61;			
RC				

32	1450	38.5	1118	2	Q9AM83	Q9am83 bacillus th
33	1447	38.5	1156	2	Q6CUA7	Q6cuA7 bacillus th
34	1442	38.3	1177	2	Q6EIX3	Q6eIX3 bacillus th
35	1440	38.3	1155	2	Q93T21	Q93t21 bacillus th
36	1439.5	38.3	793	2	Q6PYW7	Q6pyW7 bacillus th
37	1439.5	38.3	1180	2	Q9S5V8	Q9s5V8 bacillus th
38	1438.5	38.2	1176	2	Q7WZT9	Q7wzt9 bacillus th
39	1434.5	38.1	1181	1	C1AE_BACTL	Q03748 bacillus th
40	1432.5	38.1	1176	2	Q45736	Q45736 bacillus th
41	1428.5	38.0	1169	2	Q8GHE8	Q8ghe8 bacillus th
42	1428.5	38.0	1176	1	C1AA_BACTK	P02965 bacillus th
43	1428.5	38.0	1176	2	Q9RC30	Q9rc30 bacillus th
44	1421.5	37.8	1169	1	C1GB_BACTZ	Q92a26 bacillus th
45	1416.5	37.7	1179	1	C1AD_BACTA	Q03744 bacillus th

ALIGNMENTS

b	361	GGHKLKLEPTIGTGLNISTQGSNTWTSINFTVTLFTFSRDIYRTESLAGUNLFLTQPVNGVPR	420
y	421	VDHFHKVFTPIASDNFFYPGVAGTGTQLODSENLPEATQGNYESYSHRLSHIGLIS	480
b	421	VDHFHKVFTPIASDNFFYPGVAGTGTQLODSENLPEATQGNYESYSHRLSHIGLIS	480
y	481	ASHVKALVYSWTHRSADRTNTTIEPNSITQIPLVKAFNLSGAAVVRGGFTGGDILRRTN	540
b	481	ASHVKALVYSWTHRSADRTNTTIEPNSITQIPLVKAFNLSGAAVVRGGFTGGDILRRTN	540
y	541	TGTFGDIRVNIINPPFAQRVVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK	600
b	541	TGTFGDIRVNIINPPFAQRVVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK	600
y	601	TPRTVGTFTPTSFLDVQSTFTIGAMFSSGNEVYIDRIFVPVEVTVYEAEDFEKAQEKV	660
b	601	TPRTVGTFTPTSFLDVQSTFTIGAMFSSGNEVYIDRIFVPVEVTVYEAEDFEKAQEKV	660
y	661	TALFTSTNPRGLKTDVVDXHYHDVSNLVSLSDEFYLDKRELFELVIKYANLHIERNM	719
b	661	TALFTSTNPRGLKTDVVDXHYHDVSNLVSLSDEFYLDKRELFELVIKYANLHIERNM	719
RESULT 2			
PRELIMINARY; PRT; 719 AA.			
b	Q6X181	Q6X181	
AC	Q6X181; 2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	CryII.		
GN	Name=cryII;		
OS	Bacillus thuringiensis.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
CC	NCBI_TaxID=1428;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RP	Espondola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;		
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.		
RL	EMBL; AY262167; AAP86782.1;		
DR	GO; GO:0005102; F:receptor binding; IEA.		
DR	GO; GO:0006952; P:defense response; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin_C.		
DR	InterPro; IPR005639; endotoxin_N.		
DR	InterPro; IPR008979; Gal_bind_like.		
DR	Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		
DR	SEQUENCE 719 AA; 81215 MW; 3627E5A6C25DAFF5 CRC64;		
QY	Query Match	99.58; Score 3743; DB 2; Length 719;	
Db	Best Local Similarity	99.6%; Pred. No. 1.9e-251;	
QY	Matches 716; Conservative	1; Mismatches 2; Indels 0; Gaps 0;	
QY	1	MKLKQDKHQFSFNKAVDKISTDSLKNETDIQLQINHEDCLKMSYENVPFVSASTI	60
Db	1	MKLKQDKHQFSFNKAVDKISTDSLKNETDIQLQINHEDCLKMSYENVPFVSASTI	60
QY	61	QTGIGIAGKILGTGVPPAQVASLYSFTILGELWPKGNQWEI FMEHV EEEIINQISTYA	120
Db	61	QTGIGIAGKILGTGVPPAQVASLYSFTILGELWPKGNQWEI FMEHV EEEIINQISTYA	120
QY	121	RKALTDLKLGDALAVVHDSLESWGVRNNTARSVVKVSQVIALELMFVKQLSPFVSG	180
Db	121	RKALTDLKLGDALAVVHDSLESWGVRNNTARSVVKVSQVIALELMFVKQLSPFVSG	180
QY	181	EEVPLLPYIAOANLHLLILDASIFCKEGLSSSEISTFTYNQVERAGDYSYHCWKYS	240
Db	181	EEVPLLPYIAOANLHLLILDASIFCKEGLSSSEISTFTYNQVERAGDYSYHCWKYS	240

QY	241	TGLNNLRGTVNAESWRYNQFRDMDLMLVDLVALPSPSYDTQMPYIKTTAQLTREVYTDAI	300
Db	241	TGLNNLRGTVNAESWRYNQFRDMDLMLVDLVALPSPSYDTQMPYIKTTAQLTREVYTDAI	300
QY	301	GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDLEQVTIYSLLSRWNTQYMMNW	360
Db	301	GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDLEQVTIYSLLSRWNTQYMMNW	360
QY	361	GGHKLFRITIGTGLNISTQGSTNTSINPVTLPFTSRDVRVYRTSLAGLNLFLTPQVNGVPR	420
Db	361	GGHKLFRITIGTGLNISTQGSTNTSINPVTLPFTSRDVRVYRTSLAGLNLFLTPQVNGVPR	420
QY	421	VDHFKFVTHPTIASDNFYYPGVAGIGTQDSENELPPEATQPNVYESYSHRLSHIGLIS	480
Db	421	VDHFKFVTHPTIASDNFYYPGVAGIGTQDSENELPPEATQPNVYESYSHRLSHIGLIS	480
QY	481	ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
Db	481	ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
QY	541	TGTFGDIRVINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK	600
Db	541	TGTFGDIRVINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK	600
QY	601	TTRTVGFTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDYFEKAQEKV	660
Db	601	TTRTVGFTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDYFEKAQEKV	660
QY	661	TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDDEFYLDKRELFELVKYAKQLHIERNM	719
Db	661	TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDDEFYLDKRELFELVKYAKQLHIERNM	719
RESULT 3			
Q93NJ5		PRELIMINARY; PRT; 719 AA.	
AC	Q93NJ5		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	CryIa.		
GN	Name=cryIa;		
OS	Bacillus thuringiensis.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1428;		
RN	[1]_SEQUENCE FROM N.A.		
RP	SEQUENCE FROM N.A.		
RA	Song F., Zhang J., Gu A., Huang D., Li G.;		
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF373207; AAK66742.1; -.		
DR	HSSP; P02965; 1CIV.		
DR	GO; GO:0005102; F:receptor binding; IEA.		
DR	GO; GO:0006952; P:defense response; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin_C.		
DR	InterPro; IPR005639; endotoxin_N.		
DR	InterPro; IPR008979; Gal bind like.		
DR	Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		
SQ	SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;		
Query Match 99.4%; Score 3738; DB 2; Length 719;			
Best Local Similarity 99.4%; Pred. No. 4.1e-251; Gaps 0;			
Matches 715; Conservative 1; Mismatches 3; Indels 0;			
QY	1	MKLKQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVPFVFASTI	60
Db	1	MKLKQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVPFVFASTI	60
QY	61	QTGIGIAGKILGTVLPFAGQVVASLYSIFLGBLMPKGNQWEIFMEHVBEIINQKISTYA	120

Db	61	QTGIGIAGKILGTVLPFAGQVVASLYSIFLGBLMPKGNQWEIFMEHVBEIINQKISTYA	120
QY	121	RNKALTDLKLGDALAVYHDSLESWVGNRNNTARSVVKSOYIALELMFVQKLPSFAVSG	180
Db	121	RNKALTDLKLGDALAVYHDSLESWVGNRNNTARSVVKSOYIALELMFVQKLPSFAVSG	180
QY	181	BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNRQVERAGDYSYHCVKWYS	240
Db	181	BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNRQVERAGDYSYHCVKWYS	240
QY	241	TGLNNLRGTVNAESWRYNQFRDMDLMLVDLVALPSPSYDTQMPYIKTTAQLTREVYTDAI	300
Db	241	TGLNNLRGTVNAESWRYNQFRDMDLMLVDLVALPSPSYDTQMPYIKTTAQLTREVYTDAI	300
QY	301	GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDLEQVTIYSLLSRWNTQYMMNW	360
Db	301	GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDLEQVTIYSLLSRWNTQYMMNW	360
QY	361	GGHKLFRITIGTGLNISTQGSTNTSINPVTLPFTSRDVRVYRTSLAGLNLFLTPQVNGVPR	420
Db	361	GGHKLFRITIGTGLNISTQGSTNTSINPVTLPFTSRDVRVYRTSLAGLNLFLTPQVNGVPR	420
QY	421	VDHFKFVTHPTIASDNFYYPGVAGIGTQDSENELPPEATQPNVYESYSHRLSHIGLIS	480
Db	421	VDHFKFVTHPTIASDNFYYPGVAGIGTQDSENELPPEATQPNVYESYSHRLSHIGLIS	480
QY	481	ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
Db	481	ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
QY	541	TGTFGDIRVINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK	600
Db	541	TGTFGDIRVINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK	600
QY	601	TTRTVGFTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDYFEKAQEKV	660
Db	601	TTRTVGFTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDYFEKAQEKV	660
QY	661	TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDDEFYLDKRELFELVKYANLHIERNM	719
Db	661	TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDDEFYLDKRELFELVKYAKQLHIERNM	719
RESULT 4			
085796		PRELIMINARY; PRT; 719 AA.	
ID	085796		
AC	085796		
DT	01-NOV-1998 (TrEMBLrel. 08, Created)		
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Insecticidal protein.		
GN	Name=crvV101;		
OS	Bacillus thuringiensis (subsp. kurstaki).		
OC	Plasmid large plasmid.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=29339;		
RN	[1]_SEQUENCE FROM N.A.		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-S101;		
RA	Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;		
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF076953; AAC26910.1; -.		
DR	HSSP; P02965; 1CIV.		
DR	GO; GO:0005102; F:receptor binding; IEA.		
DR	GO; GO:0006952; P:defense response; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin_C.		
DR	InterPro; IPR005639; endotoxin_N.		
DR	InterPro; IPR008979; Gal bind like.		
DR	Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		

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Tue Feb 15 10:07:53 2005

KW Plasmid. 719 AA; 81230 MW; 42746DA78359BBA7 CRC64;  
SQ SEQUENCE 99.3%; Score 3737; DB 2; Length 719;  
Query Match 99.4%; Pred. No. 4.8e-251; Indels 0; Gaps 0;  
Best Local Similarity 99.4%; 1; Mismatches 3; Indels 0; Gaps 0;  
Matches 715; Conservative

QY 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E V N E P P F V S A S T I 60  
DB 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E V N E P P F V S A S T I 60

QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L M P K G K N Q W E I F M E H V E I I N Q I S T Y A 120  
DB 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L M P K G K N Q W E I F M E H V E I I N Q I S T Y A 120

QY 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
DB 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180

QY 181 E V P L L P I Y A Q A N L H L L L D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S V H C V K W Y S 240  
DB 181 E V P L L P I Y A Q A N L H L L L D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S V H C V K W Y S 240

QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M P I K T T A Q L T R E V Y T D A I 300  
DB 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M P I K T T A Q L T R E V Y T D A I 300

QY 301 G T V H P H P S T S T T W Y N N N A P S F A S I E A A V V R N P H L L D F L E O V T T Y S L L S R W S N T Q Y M N W 360  
DB 301 G T V H P H P S T S T T W Y N N N A P S F A S I E A A V V R N P H L L D F L E O V T T Y S L L S R W S N T Q Y M N W 360

QY 361 G G H K L F R I G T L N I S T G S T N T S I N P V T L P F T S R D V R T E S L A G N L F L T Q P V N G V P R 420  
DB 361 G G H K L F R I G T L N I S T G S T N T S I N P V T L P F T S R D V R T E S L A G N L F L T Q P V N G V P R 420

QY 421 V D F H W K F V T H P I A S D N F Y P G A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
DB 421 V D F H W K F V T H P I A S D N F Y P G A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480

QY 481 A S H V K A L V S W T H R S A D R N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G D I L R T N 540  
DB 481 A S H V K A L V S W T H R S A D R N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G D I L R T N 540

QY 541 T G T F G D I R V N I N P P F A Q R Y R V R Y A S T T D L Q P H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
DB 541 T G T F G D I R V N I K P P F A Q R Y R V R Y A S T T D L Q P H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600

QY 601 T F R T V G F T P P S F L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
DB 601 T F R T V G F T P P S F L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660

QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719  
DB 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719

RESULT 5  
Q8KY61 PRELIMINARY; PRT: 719 AA.  
ID Q8KY61  
AC Q8KY61;  
DT 01-OCT-2002 (T-EMBLrel. 22, Created)  
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
DE Cry.  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Porcar M., Martinez C., Caballero P.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF278797; AA073516.1; -;  
DR PIR; B42459; B42459.

HSP; P02965; 1CIY.  
DR GO:0005102; F:receptor binding; IEA.  
DR GO:0006952; P:defense response; IEA.  
DR GO:0009405; P:pathogenesis; IEA.  
DR InterPro: IPR001178; Endotoxin.  
DR InterPro: IPR005638; endotoxin C.  
DR InterPro: IPR005639; endotoxin N.  
DR InterPro: IPR008979; Gal\_bind\_Like.  
DR Pfam: PF03944; Endotoxin C; 1.  
DR Pfam: PF03945; Endotoxin M; 1.  
DR Pfam: PF03945; Endotoxin N; 1.  
SQ SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;

Query Match 95.9%; Score 3608; DB 2; Length 719;  
Best Local Similarity 95.8%; Pred. No. 4.5e-242;  
Matches 689; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E V N E P P F V S A S T I 60  
DB 1 M L K N P D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K I S E V N E P P F V S A S T I 60

QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L M P K G K N Q W E I F M E H V E I I N Q I S T Y A 120  
DB 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L M P K G K N Q W E I F M E H V E I I N Q I S T Y A 120

QY 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
DB 121 R N K A L T D L K G L G D A L A V Y H S L E S W G N R N R K N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180

QY 181 E V P L L P I Y A Q A N L H L L L D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S V H C V K W Y S 240  
DB 181 E V P L L P I Y A Q A N L H L L L D A S I F G K E W G L S S E I S T F Y N Q V E R A G D Y S V H C V K W Y S 240

QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M P I K T T A Q L T R E V Y T D A I 300  
DB 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M P I K T T A Q L T R E V Y T D A I 300

QY 301 G T V H P H P S T S T T W Y N N N A P S F A S I E A A V V R N P H L L D F L E O V T T Y S L L S R W S N T Q Y M N W 360  
DB 301 G T V H P N A S F A S T T W Y N N N A P S F T I E S A V V R N P H L L D F L E O V T T Y S L L S R W S N T Q Y M N W 360

QY 361 G G H K L F R I G T L N I S T G S T N T S I N P V T L P F T S R D V R T E S L A G N L F L T Q P V N G V P R 420  
DB 361 G G H R L E F R I G T G M L N T S T G S T N T S I N P V T L P F T S R D V R T E S L A G N L F L T Q P V N G V P R 420

QY 421 V D F H W K F V T H P I A S D N F Y P G A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
DB 421 V D F H W K F V T H P I A S D N F Y P G A G I G T Q L O D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480

QY 481 A S H V K A L V S W T H R S A D R N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G D I L R T N 540  
DB 481 A S H V K A L V S W T H R S A D R N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G D I L R T N 540

QY 541 T G T F G D I R V N I N P P F A Q R Y R V R Y A S T T D L Q P H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
DB 541 T G T F G D I R V N I N P P F A Q R Y R V R Y A S T T D I Q P H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600

QY 601 T F R T V G F T P P S F L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
DB 601 T F R T V G F T P P S F S D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660

QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719  
DB 661 T A L F T S T N P G L K T N V E Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H T G R N M 719

RESULT 6  
Q9F0P8 PRELIMINARY; PRT: 719 AA.  
ID Q9F0P8  
AC Q9F0P8;  
DT 01-MAR-2001 (T-EMBLrel. 16, Created)  
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)  
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)

```
DE Name=cryII;
GN Bacillus thuringiensis.
OS Plasmid pBTC19.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BTC007;
RX DOI=10.1128/AEM.69.9.5207-5211.2003;
RA Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,
Hu Y., Li G., Huang D.;
RT "Identification of cryII-type genes from Bacillus thuringiensis
RL Appl. Environ. Microbiol. 69:5207-5211(2003).
DR EMBL; AF211190; AAG43526.1; -.
DR HSSP; P02965; 1CIY.
DR GO; GO:0003102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Plasmid.
SQ SEQUENCE 719 AA; 81024 MW; 7E17481922C435E6 CRC64;

Query Match 93.9%; Score 3534; DB 2; Length 719;
Best Local Similarity 93.2%; Pred. No. 6.3e-237;
Matches 670; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDTELQNHEDCLKMEYENVPFVSASTI 60
DB 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDTELQNHEDCLKMEYENVPFVSASTI 60
QY 61 QTGIGIAGKILGTLPVFPAGVASLVSFILGELWPKGQWEIFMHEVEIINOKLSTVA 120
DB 61 QTGIGIAGKILGTLPVFPAGQIASLVSFILGELWPKGQWEIFMHEVEIINOKLSTVA 120
QY 121 RNKALTDLKGDLALAVYHDSLESYVGNRNTRARSVKRSQVYIALELMFVQKLPSFVSG 180
DB 121 RNIALADLKGDLALAVYHDSLESYVGNRNTRARSVKRSQVYIALELMFVQKLPSFVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGCKWGLSSSEISFTYRQVRAGDYSYHCVKWTYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASVFGKWLSSQISTFYRQVRERTSDYSDHCVKWTYS 240
QY 241 TGLNLRGTNAESWVRYNFRDMLTLMVLDLVALPSPYDTOMYPIKTTAQLTRVYVTDAL 300
DB 241 TGLNLRGTNAESWVRYNFRDMLTLMVLDLVALPSPYDTOMYPIKTTAQLTRVYVTDAL 300
QY 301 GTVHPHFSTTTWYNNAPSSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQTMNWM 360
DB 301 GTVHPNAPSTTTWYNNAPSSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQTMNWM 360
QY 361 GGHKLEFRITGGTLNISTOGSTNTSNPVTLPPTSDDVTRTESLAGLNIFLTQPVNGVPR 420
DB 361 GGHRLFRITGGVLTNISTOGSTNTSNPVTLPPTSDDVTRTESLAGLNIFLTQPVNGVPR 420
QY 421 VDPHWFVTHPTASDNFFYPGVAGIGTQLQDSNELPPEATGPNYESYSHRLSHLGLIS 480
DB 421 VDPHWFKATPLTASDNFFYLGVAGVGTQLQDSNELPPEATGPNYESYSHRLSHLGLIS 480
QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLKAFNLSSGAAVRGPFGTGGDILRRTN 540
DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLKAFNLSSGAAVRGPFGTGGDILRRTN 540
QY 541 TGTFGDIRVNNPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSTMTNRGEDLDYK 600
DB 541 TGTFGDIRVNNPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSTMTNRGEDLDYK 600

CryII.
DB 541 TGTFGDIRVNNPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSTMTNRGEDLDYK 600
QY 601 TFRVTGFTTPFSFLDVQSTFTIGANFSSGNEVYIDRIEFVPEVVEYEAEDPEKAQEKV 660
DB 601 TFRVTGFTTPFSFLDVQSTFTIGANFSSGNEVYIDRIEFVPEVVEYEAEDPEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKQYHIDQVSNLVSLSDEFYLDKRELFEIVKVAQKIHIERNM 719
DB 661 TALFTSTNPRGLKTDVKQYHIDQVSNLVSLSDEFYLDKRELFEIVKVAQKIHIERNM 719

RESULT 7
CLIB_BACTE STANDARD; PRT; 719 AA.
ID C1IB_BACTE AC Q45709;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIB (insecticidal delta-endotoxin
DE CryII(b)) (crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIIB; Synonyms=cryII(b), cryV, cryV465;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP465;
RX MEDLINE=95314293; PubMed=7793960;
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;
RT "Distribution of cryV-type insecticidal protein genes in Bacillus
RT thuringiensis and cloning of cryV-type genes from Bacillus
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
RT entomocidus.";
RL Appl. Environ. Microbiol. 61:2402-2407(1995).
CC -!- FUNCTION: Promotes colloidsomotic lysis by binding to the midgut
CC epithelial cells of certain coleopteran and lepidopteran species.
CC Active on Plutella xylostella but not on Bombyx mori.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; U07642; AAA82114.1; -.
CC FIR; I40590; I40590.
CC HSSP; P02965; 1CIY.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC InterPro; IPR008979; Gal_bind_like.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81295 MW; E8210ABEA597688E CRC64;

Query Match 93.1%; Score 3503; DB 1; Length 719;
Best Local Similarity 92.5%; Pred. No. 9e-235;
Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDTELQNHEDCLKMEYENVPFVSASTI 60
DB 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDTELQNHEDCLKMEYENVPFVSASTI 60
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QY 61 QTGIGIAGKILGTLGVPPAGQVASYSLFGLGELWPKGKQWEIFMEHVEEIIINOKISTVA 120  
 DB 61 QTGIGIAGKILGTLGVPPAGQVASYSLFGLGELWPKGKQWEIFMEHVEEIIINOKISTVA 120  
 QY 121 RNKALTDKLGDLALAVYHDSLSWGNNRNTARSVKQSYQIALELMFVQKLPSPAVSG 180  
 DB 121 RNKALSDRLGDLALAVYHDSLSWGNNRNTARSVKQSYQIALELMFVQKLPSPAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVRAGDYSYHCVKWTYS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVRAGDYSYHCVKWTYS 240  
 QY 241 TGLNLRTGVAESWVRVYQNRDRTMLVLDLVALFSDYDQMPYPIKTTAQLTREVYTDAL 300  
 DB 241 TGLNLRTGVAESWVRVYQNRDRTMLVLDLVALFSDYDQMPYPIKTTAQLTREVYTDAL 300  
 QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
 QY 361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVTYTESLAGLNFLTQPVNGVPR 420  
 DB 361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVTYTESLAGLNFLTQPVNGVPR 420  
 QY 421 VDFHWKFTPIADSNFYGYAGIGTQLODSNELPPEATGQPNYESYSHRSLSHIGLIS 480  
 DB 421 VDFHWKFTPIADSNFYGYAGIGTQLODSNELPPEATGQPNYESYSHRSLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRPGTGGDILRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRPGTGGDILRTN 540  
 QY 541 TGTGDIIRVNINPPFAQRYRVRIBYASTDLOFHTSINGKAINQGNFSATMNGEDLDYK 600  
 DB 541 TGTGDIIRVNINPPFAQRYRVRIBYASTDLOFHTSINGKAINQGNFSATMNGEDLDYK 600  
 QY 601 TFRVGTFTPTPSFDLDVOSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAEDFEKAQEKV 660  
 DB 601 TFRVGTFTPTPSFDLDVOSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAEDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDFFYLDEKRELFEIKYANELHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDFFYLDEKRELFEIKYANELHIERNM 719

RESULT 8

CLID\_BACTU STANDARD; PRT; 719 AA.

AC Q9XDL1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryII (insecticidal delta-endotoxin)  
 DE CryII(d) (crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryII; Synonyms=cryII(d), NcrIv;  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BR30;  
 RX MEDLINE=20374042; PubMed=10919402;  
 RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;  
 RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein  
 gene.";  
 RL Curr. Microbiol. 41:65-69(2000).  
 CC -!- FUNCTION: Promotes colloidomotic lysis by binding to the midgut  
 CC epithelial cells of many lepidopteran larvae. Active on Plutella  
 CC xylostella and on Bombyx mori.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-

terminus.  
 -!- SIMILARITY: Belongs to the delta endotoxin family.  
 -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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 EMBL; AF047579; AAD44366.1; -;  
 HSSP; P02965; 1CIY.  
 DR InterPro: IPR001178; Endotoxin.  
 DR InterPro: IPR005638; Endotoxin\_C.  
 DR InterPro: IPR005639; Endotoxin\_N.  
 DR InterPro: IPR008979; Gal\_bind\_Like.  
 DR Pfam: PF03944; Endotoxin\_C; 1.  
 DR Pfam: PF00555; Endotoxin\_M; 1.  
 DR Pfam: PF03945; Endotoxin\_N; 1.  
 DR Sporulation; Toxin.  
 KW SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;  
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 Query Match 89.8%; Score 3380; DB 1; Length 719;  
 Best Local Similarity 89.4%; Pred. No. 3.2e-226; Indels 0; Gaps 0;  
 Matches 643; Conservative 36; Mismatches 40;  
 QY 1 MKLKNQDKHSPSSNAKVDKISTDSLNKNETDLELQINHEDCMKSEYENVEPVSASTI 60  
 DB 1 MMSKNQWYRFSNNATVDKSTDPLEHNTNMLQNSHEDCLMKSEYSEVFPVSSTI 60  
 QY 61 QTGIGIAGKILGTLGVPPAGQVASYSLFGLGELWPKGKQWEIFMEHVEEIIINOKISTVA 120  
 DB 61 QTGIGIAGKILGTLGVPPAGQVASYSLFGLGELWPKGKQWEIFMEHVEEIIINOKISTVA 120  
 QY 121 RNKALTDKLGDLALAVYHDSLSWGNNRNTARSVKQSYQIALELMFVQKLPSPAVSG 180  
 DB 121 RNKALADLGLGDLALAVYHDSLSWGNNRNTARSVKQSYQIALELMFVQKLPSPAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVRAGDYSYHCVKWTYS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVRAGDYSYHCVKWTYS 240  
 QY 241 TGLNLRTGVAESWVRVYQNRDRTMLVLDLVALFSDYDQMPYPIKTTAQLTREVYTDAL 300  
 DB 241 TGLNLRTGVAESWVRVYQNRDRTMLVLDLVALFSDYDQMPYPIKTTAQLTREVYTDAL 300  
 QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
 QY 361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVTYTESLAGLNFLTQPVNGVPR 420  
 DB 361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVTYTESLAGLNFLTQPVNGVPR 420  
 QY 421 VDFHWKFTPIADSNFYGYAGIGTQLODSNELPPEATGQPNYESYSHRSLSHIGLIS 480  
 DB 421 VDFHWKFTPIADSNFYGYAGIGTQLODSNELPPEATGQPNYESYSHRSLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRPGTGGDILRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRPGTGGDILRTN 540  
 QY 541 TGTGDIIRVNINPPFAQRYRVRIBYASTDLOFHTSINGKAINQGNFSATMNGEDLDYK 600  
 DB 541 TGTGDIIRVNINPPFAQRYRVRIBYASTDLOFHTSINGKAINQGNFSATMNGEDLDYK 600  
 QY 601 TFRVGTFTPTPSFDLDVOSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAEDFEKAQEKV 660  
 DB 601 TFRVGTFTPTPSFDLDVOSTFTIGAWNFSSGNEVYIDRIEFVPEVVTYEAEDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDFFYLDEKRELFEIKYANELHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDFFYLDEKRELFEIKYANELHIERNM 719



Db	661	TAMFTSTNLRUKNTVTDCHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLNTRNM	719
RESULT 9			
CLIC_BACTU STANDARD; PRT; 719 AA.			
AC	087404;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Pesticidal crystal protein cryIIc (Insecticidal delta-endotoxin		
DE	CryII(c)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).		
GN	Name=cryIIc; Synonyms=cryII(c);		
OS	Bacillus thuringiensis.		
OG	Plasmid.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1428;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C18 / Egypt;		
RA	Osman Y.A., Madkour M.A., Bulla L.A. Jr.;		
RL	Submitted (Mar-1998) to the EMBL/GenBank/DBJ databases.		
CC	-!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut		
CC	epithelial cells of insects.		
CC	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during		
CC	sporulation and is accumulated both as an inclusion and as part of		
CC	the spore coat.		
CC	-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-		
CC	terminus.		
CC	-!- SIMILARITY: Belongs to the delta endotoxin family.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
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CC	use by non-profit institutions as long as its content is in no way		
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>		
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).		
CC	-----		
DR	EMBL; AF056933; AAC62933.1; .		
DR	HSSP; P02965; 1CIV		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin.C.		
DR	InterPro; IPR005639; endotoxin.N.		
DR	InterPro; IPR008979; Gal bind like.		
DR	Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		
DR	Plasmid; Sporulation; Toxin.		
KW	SEQUENCE 719 AA; 81210 MW; 8370B3F06B905DFF CRC64;		
SQ	<p>Query Match 89.8%; Score 3379; DB 1; Length 719;</p> <p>Best Local Similarity 89.7%; Pred. No. 3.8e-226;</p> <p>Matches 645; Conservative 34; Mismatches 40; Indels 0; Gaps 0;</p>		
QY	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDTELQINHECLKMSYENVPFVSASTI	60
DB	1	MKLKNPDKHQTLSSNAKVDKIATDSLKNETDIELKMNNDYLRMSEHSIDPFVSASTI	60
QY	61	QTGIGIAGKILGTGVPPAGVASLYSFTLGEMLPKGNQWEIFMHEVVEEINQISTVA	120
DB	61	QTGIGIAGKILGTGVPPGQIASLYSFTLGEMLPKGNQWEIFMHEVVEEINQISTVA	120
QY	121	RNKALTDLKGLDALVHDSLESVGNRNNTARSVKVSOYIAELFMVQKLPSFVSG	180
DB	121	RNKALTDLKGLDALVHDSLESVGNRNNTARSVKVQNIYIAELFMVQKLPSFVSG	180
QY	181	EEVPLPIYAQAANLHLLRLDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCWKYS	240
DB	181	EEVPLPIYAQAANLHLLRLDASIFEKNGGLSASEISTFYNRQVEREDYSYHCWKNN	240
QY	241	TGLNNLRGNASWRYNQFRDMLTMLDLVALPSPYDTQMPYIKTTAQLTREVYTDAI	300
DB	241	TGLNNLRATNGQSWRYNQFRDKIDELMLDLVRFPSYDTLVYPIKTTTSQLTREVYTDI	300
QY	301	GTVHPHPGFTSTTWNNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQTMNMW	360
DB	301	GTVDNQALRSTTWNNNAPSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQTMNMW	360
QY	361	GGHKLFPRTIGGTNLISQGSTNTSINPVTLPFTSRDVTYRTESLAGNLFLTPQVNGVPR	420
DB	361	GGHRLSPRIGGALNTSQGSTNTSINPVTLOFTSRDVTYRTESWAGNLFLTPQVNGVPR	420
QY	421	VDPHKFKVTHPIASDNFYFPGVAGITQLODSENELPPEATQCPNYESVSHLSHIGLIS	480
DB	421	VDPHKFKVTHPIASDNFYFPGVAGITQLODSENELPPEATQCPNYESVSHLSHIGLIS	480
QY	481	ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
DB	481	GSVVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRYK	540
QY	541	TGTGDIRVNIWNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK	600
DB	541	SGTFGHIRVNIWNPFAQRYRVRMSYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK	600
QY	601	TPRTVGTTPPSFLDVQSTFTIGANFSSGNEVYIDRIEFVDPVEVTEYAEYDFEKAQEKV	660
DB	601	TPRTVGTTPPSFSDVQSTFTIGANFSSGNEVYIGRIEFVDPVEVTEYAEYDFEKAQEKV	660
QY	661	TALFTSTNPRGLKTDVKDHYIDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNM	719
DB	661	TALFTSTNPRGLKTDVKDHYIDQVSNLVSLSDEFYLDKRELFEIVKYAKQHIERNM	719
RESULT 10			
CLIB_BACTU STANDARD; PRT; 1229 AA.			
AC	Q45739;		
DT	30-MAY-2000 (Rel. 39, Created)		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		
DT	30-JUL-2004 (Rel. 44, Last annotation update)		
DE	Pesticidal crystal protein cryIbB (Insecticidal delta-endotoxin		
DE	CryIb(b)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).		
GN	Name=cryIbB; Synonyms=cryIb5, cryIb(b);		
OS	Bacillus thuringiensis.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1428;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=NRRL B-21110 / EG5847;		
RA	Donovan W.P., Tan Y., Jan Y.C.S., Gonzalez J.M. Jr.;		
RT	"Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins		
RT	toxic to lepidopteran insects.";		
RL	Patent number US5322687, 21-JUN-1994.		
CC	-!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut		
CC	epithelial cells of many lepidopteran larvae.		
CC	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during		
CC	sporulation and is accumulated both as an inclusion and as part of		
CC	the spore coat.		
CC	-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-		
CC	terminus.		
CC	-!- SIMILARITY: Belongs to the delta endotoxin family.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>		
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).		
CC	-----		
DR	EMBL; L32020; AAA22344.1; .		
DR	HSSP; P02965; 1CIV		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin.C.		
DR	InterPro; IPR005639; endotoxin.N.		



QY	543	TFGDIRVNINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSGATNMRGEDLDYKTF	602
DB	541	TFGDIRLNINPLVSQRYRVRIRYASTTDLQFHTSINGKAINQGNFSGATNMRGEDLDYKTF	600
QY	603	RTVGFTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYAEYDFEKAQEKVTA	662
DB	601	RTAGFSTPFNLSNAQSTFTIGAWNFSSGNEVYIDRIEFVPEVYAEYDFEKAQEKVTA	659
QY	663	LFTSTNPRGLKTDVYDHYDQVSNLVESLDFEYLDKEKELFRIKVKYANLHIERNM	719
DB	660	LFTSTNPRKLTDTVDYDHYDQVSNLVESLDFEYLDKEKELFRIKVKYANLHIERNM	716
RESULT 12			
ID	Q93T75	PRELIMINARY; PRT; 1228 AA.	
AC	Q93T75	Strain=HD-9;	
DT	01-DEC-2001	(TREMELrel. 19, Last sequence update)	
DT	01-DEC-2001	(TREMELrel. 19, Last sequence update)	
DT	01-MAR-2004	(TREMELrel. 26, Last annotation update)	
DE	Delta-endotoxin CrylBa2.		
GN	Name=CrylBa2;		
OS	Bacillus thuringiensis (subsp. entomocidus).		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1436;		
RN	[1]	SEQUENCE FROM N.A.	
RP	SEQUENCE FROM N.A.		
RC	Strain=HD-9;		
RA	Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;		
RA	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF363025; AAK51084.1; -		
DR	HSSP; P07130; 1DLC.		
DR	GO; GO:0005102; F:receptor binding; IEA.		
DR	GO; GO:0005952; P:defense response; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin_C.		
DR	InterPro; IPR005639; endotoxin_N.		
DR	InterPro; IPR008979; Gal bind like.		
DR	Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		
SQ	SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;		
Query Match			
Best Local Similarity 60.2%; Score 2263.5; DB 2; Length 1228;			
Matches 447; Conservative 79; Mismatches 165; Indels 25; Gaps 6;			
QY	23	TPSLKNETDIELQNIH-----EDCLKMEYENVPFVSASTIQTGIGIAGKI	70
DB	2	TSNRKNENELINAVSNHSAQMDLLDPARTEDSICIAEGNIDPFVSASTVQTGINIAGRI	61
QY	71	LGTGLVPPAGVASLYSFILGELWPKGNKQWEIFMEHVEEINQKISTVARNKALTDLKG	130
DB	62	LGVLPVPPAGQASLYSFILGELWPKGNKQWEIFMEHVEEINQKISTVARNKALTDLKG	121
QY	131	LGDAVAVYHDSLESWYGNENNTFARSVKSOYIALELMFVKQLPSFAVSGEEVPLPIYA	190
DB	122	LGDSFRAYQOQSLDLENDLDRDARTSVLHTQVIALELDFNAMPLFAIRNQREVPLMVA	181
QY	191	QAANLHLLLRDASIFGKWEKSSSISITFYNNQVERAGDYVHCVKWYSTGLNLRGYN	250
DB	182	QAANLHLLLRDASLFGSFGSLTSQIQRYEYQVETRDYDYCVENWTGLNSLRGYN	241
QY	251	ASWRYNQFRDMLTLMVLVDLVALPSPDYQMPYIKTTAQLREVYTDAGTVHPHPSFT	310
DB	242	ASWRYNQFRDMLTLMVLVDLVALPSPDYQMPYIKTTAQLREVYTDAGTVHPHPSFT	299
QY	311	STTWYNNAPSIAEAAVVRPHLLDFLEQVITISLLRSWNTQYNNWGGHKLFRRI	370
DB	300	SMWYNNAPSIAEAAVVRPHLLDFLEQVITISLLRSWNTQYNNWGGHKLFRRI	359
QY	371	GGTLINISTOGSTNTSINPVTLPTFTSDVYRTESLAGLNLF--LTQPVNGVPRVDFHFKFV	428
DB	360	GGGLNTSTHGATNTSINPVTLPTFTSDVYRTESLAGLNLF--LTQPVNGVPRVDFHFKFV	416
QY	429	THP-----IASNFYYPGAGIGTOLQDSENELPPEATQPNVYESYSHRLSHIGLISASH	483
DB	417	TNPQNSDRGTANYQOP-YESFGLQKQSETLPPETTERPNVYESYSHRLSHIGLILQSR	475
QY	484	VKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGQFTGGDILRRNTGT	543
DB	476	VNVFVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGQFTGGDILRRNTGT	535
QY	544	FGDIRVNINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSGATNMRGEDLDYKTF	603
DB	536	FGDIRVNINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSGATNMRGEDLDYKTF	595
QY	604	TVGFTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYAEYDFEKAQEKVTA	663
DB	596	RRRAFTTPTFTQIDRIIRTSIQGLSGNGEVYIDRIEFVPEVYAEYDFEKAQEKVTA	655
QY	664	FTSTNPRGLKTDVYDHYDQVSNLVESLDFEYLDKEKELFRIKVKYANLHIERNM	719
DB	656	FTSTNPRKLTDTVDYDHYDQVSNLVESLDFEYLDKEKELFRIKVKYANLHIERNM	711
RESULT 13			
ID	C1BA BACTK	STANDARD; PRT; 1228 AA.	
AC	P05517; Q45731;		
DT	01-NOV-1988	(Rel. 09, Created)	
DT	01-FEB-1996	(Rel. 33, Last sequence update)	
DT	05-JUL-2004	(Rel. 44, Last annotation update)	
DE	Pesticidial crystal protein crylBa (Insecticidal delta-endotoxin		
DE	CrylBa(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).		
GN	Name=CrylBa; Synonyms=cryA4, crylB(a);		
OS	Bacillus thuringiensis (subsp. kurstaki), and		
OS	Bacillus thuringiensis (subsp. entomocidus).		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=29339, 1436;		
RN	[1]	SEQUENCE FROM N.A.	
RP	SEQUENCE FROM N.A.		
RC	SPECIES=B.t.kurstaki; STRAIN=HD-2;		
RA	MEDLINE=88203216; PubMed=3362680;		
RA	Brizzard B.L., Whiteley H.R.;		
RT	"Nucleotide sequence of an additional crystal protein gene cloned from		
RT	Bacillus thuringiensis subsp. thuringiensis.";		
RL	Nucleic Acids Res. 16:2723-2723(1988).		
RN	[2]	SEQUENCE FROM N.A.	
RP	SEQUENCE FROM N.A.		
RC	SPECIES=B.t.entomocidus; STRAIN=HD-110;		
RA	Soetaert P.;		
RL	Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.		
CC	-!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut		
CC	epithelial cells of insects.		
CC	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during		
CC	sporulation and is accumulated both as an inclusion and as part of		
CC	the spore coat.		
CC	-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-		
CC	terminus.		
CC	-!- SIMILARITY: Belongs to the delta endotoxin family.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	EMBL; X06711; CAA29898.1; -		
DR	EMBL; X95704; CAA65003.1; -		
DR	PIR; S00873; S00873.		
DR	HSSP; P07130; 1DLC.		

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DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR InterPro; IPR008979; Gal bind Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Sporulation; Toxin.
DR FT VARIANT 150 150 Y -> H (in strain HD-110).
DR SEQUENCE 1228 AA; 139647 MW; C8E3A19F5D98575 CRC64;

Query Match 60.1%; Score 2262.5; DB 1; Length 1228;
Best Local Similarity 62.4%; Pred. No. 3.5e-148;
Matches 447; Conservative 79; Mismatches 165; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPVFSASTIQTGIGTAGKI 70
DB 2 TSNRKNENEIINAVNSHAQMDLLPDARIEDSLCIAEGNIDPFVSASTVQTGINIAGRI 61

QY 71 LGTLGVFPAGQVASYFLGELWPKGNQWEIFLMEHVEEIIINQISTYARNKALTDLKG 130
DB 62 LGVLGVFPAGQVASYFLGELWPKGRDQWEIFLHVQELINQIITENARNALTALRLOG 121

QY 131 LGDALAVYHDSLSWGNRNTRARSVVKSQYIALELMFVQKLPSPFVSGSEVPLPIYA 190
DB 122 LGDSFRAYQOSLEWLNDRDDATRSVLYTYQYIALELDFLNAMPLFAIRNQEVPLLMVYA 181

QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWKYSTGLNNLRGTN 250
DB 182 QAANLHLLLRDASLFGSEFGLTSQEIQRYERQVERTRDYSYCVWEYNTGLNSLRGTN 241

QY 251 AESWVRYNQRRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREVVYDAITGVHPHPSFT 310
DB 242 AASWVRYNQRRDITLGVLVLDLVALFPSYDTQMPYPIKTTAQLTREVVYDAIGAT--GVNMA 299

QY 311 STTWNNNAPSFAIAEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMMGKHLEPRTI 370
DB 300 SMWYNNNAPSFAIAEAAIRSPHLLDFLEQLTIFSSASRWSNTRHMTYWRGHTIQSRPI 359

QY 371 GGTINISTQGSTNTSINPVTLPFTSRDVRYESLAGNLF--LTQPVNGVPRVDVHKKFV 428
DB 360 GGLNTSTHGATNTSINPVTLPFTSRDVRYESLAGNLF--LTQPVNGVPRVDVHKKFV 416

QY 429 THP-----IASDNFYPGYAGIGTQLODSENELPPEATGPNYESYSHRSLSHIGLISASH 483
DB 417 TNPQNISDRGTANYSQP--YESPGIQLKDSLETLPETTERPNYESYSHRSLSHIGLILQSR 475

QY 484 VKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGT 543
DB 476 VNPVYSWTHRSADRTNTEPNSITQIPLVKASSELPGQITVVRGPGFTGGDILRRNTGG 535

QY 544 FGDIVRNINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSAATMNRGDDLYKTFR 603
DB 536 FGPVIRVTNGPLTQRYRIGFYASTVDFDFVSRGGTTVNNFRFLRMTNSGDELKYNFV 595

QY 604 TVGFTTFFSFLDVQSTFTTGAWNFSSGNEVYDRIEFVPEVTEYAEYDEKAEKVYAL 663
DB 596 RRAFTTFFTQIQDIIRTSIQGLSGNGEVYDRIEIIIPVTAPEAYDLERAQEAVAL 655

QY 664 FTSTNPRGLKTDVYKHIDQVSNLVESSLDFYLDKRELFEIVKYANELHIERNM 719
DB 656 FTNTNPRRLKTDVYDHYIDQVSNLVACLSDFCFLDEKRELLEKVKYAKRLSDERNL 711

RESULT 14
Q93NM5 PRELIMINARY; PRT; 1228 AA.
AC Q93NM5
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CrylBa.
GN Name=crylBa;
```

```
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN SEQUENCE FROM N.A.
RA Zhang J., Song F., Huang D.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368257; AAK63251.1; -.
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR InterPro; IPR008979; Gal bind Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR SEQUENCE 1228 AA; 139665 MW; E86D9842341FB439 CRC64;

Query Match 59.9%; Score 2254.5; DB 2; Length 1228;
Best Local Similarity 62.3%; Pred. No. 1.2e-147;
Matches 446; Conservative 79; Mismatches 166; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPVFSASTIQTGIGTAGKI 70
DB 2 TSNRKNENEIINAVNSHAQMDLLPDARIEDSLCIAEGNIDPFVSASTVQTGINIAGRI 61

QY 71 LGTLGVFPAGQVASYFLGELWPKGNQWEIFLMEHVEEIIINQISTYARNKALTDLKG 130
DB 62 LGVLGVFPAGQVASYFLGELWPKGRDQWEIFLHVQELINQIITENARNALTALRLOG 121

QY 131 LGDALAVYHDSLSWGNRNTRARSVVKSQYIALELMFVQKLPSPFVSGSEVPLPIYA 190
DB 122 LGDSFRAYQOSLEWLNDRDDATRSVLYTYQYIALELDFLNAMPLFAIRNQEVPLLMVYA 181

QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWKYSTGLNNLRGTN 250
DB 182 QAANLHLLLRDASLFGSEFGLTSQEIQRYERQVERTRDYSYCVWEYNTGLNSLRGTN 241

QY 251 AESWVRYNQRRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREVVYDAITGVHPHPSFT 310
DB 242 AASWVRYNQRRDITLGVLVLDLVALFPSYDTQMPYPIKTTAQLTREVVYDAIGAT--GVNMA 299

QY 311 STTWNNNAPSFAIAEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMMGKHLEPRTI 370
DB 300 SMWYNNNAPSFAIAEAAIRSPHLLDFLEQLTIFSSASRWSNTRHMTYWRGHTIQSRPI 359

QY 371 GGTINISTQGSTNTSINPVTLPFTSRDVRYESLAGNLF--LTQPVNGVPRVDVHKKFV 428
DB 360 GGLNTSTHGATNTSINPVTLPFTSRDVRYESLAGNLF--LTQPVNGVPRVDVHKKFV 416

QY 429 THP-----IASDNFYPGYAGIGTQLODSENELPPEATGPNYESYSHRSLSHIGLISASH 483
DB 417 TNPQNISDRGTANYSQP--YESPGIQLKDSLETLPETTERPNYESYSHRSLSHIGLILQSR 475

QY 484 VKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGT 543
DB 476 VNPVYSWTHRSADRTNTEPNSITQIPLVKASSELPGQITVVRGPGFTGGDILRRNTGG 535

QY 544 FGDIVRNINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSAATMNRGDDLYKTFR 603
DB 536 FGPVIRVTNGPLTQRYRIGFYASTVDFDFVSRGGTTVNNFRFLRMTNSGDELKYNFV 595

QY 604 TVGFTTFFSFLDVQSTFTTGAWNFSSGNEVYDRIEFVPEVTEYAEYDEKAEKVYAL 663
DB 596 RRAFTTFFTQIQDIIRTSIQGLSGNGEVYDRIEIIIPVTAPEAYDLERAQEAVAL 655

QY 664 FTSTNPRGLKTDVYKHIDQVSNLVESSLDFYLDKRELFEIVKYANELHIERNM 719
DB 656 FTNTNPRRLKTDVYDHYIDQVSNLVACLSDFCFLDEKRELLEKVKYAKRLSDERNL 711
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**RESULT 15**

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Q6PYW8
ID Q6PYW8 PRELIMINARY; PRT; 849 AA.
AC Q6PYW8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CrylB type crystal protein (fragment).
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=29339;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RA Li M.S., Choi J.Y., Roh J.Y., Shim H.J., Boo K.S., Je Y.H.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY570734; AAC93797.1; -.
GO: GO:0005102; F:receptor binding; IEA.
GO: GO:0006952; P:defense response; IEA.
GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR011178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C_1.
DR Pfam; PF00555; Endotoxin_M_1.
DR Pfam; PF03945; Endotoxin_N_1.
FT
SQ NON TER 849 849
SQ SEQUENCE 849 AA; 95986 MW; FCB98495787CF763 CRC64;

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Query Match 58.0%; Score 2180.5; DB 2; Length 849;  
Best Local Similarity 59.1%; Pred. No. 1e-142;  
Matches 422; Conservative 105; Mismatches 174; Indels 13; Gaps 3;

Qy	13	SSNAKVDK1STDSLKN-----FTDLELOINHEDCLKMEYENVEFPVASITQTGIG	65
Db	7	NENEIINALSIPAVNSHSAQNMNLSTDARI-----EDSLCIAEGNNIDPFPVASTVQTGIN	61
Qy	66	IAGKILGTGLVPFAGOVASLYSFILGELWPKGKNQWEIFMEHVBEIINOKLSTVARNKAL	125
Db	62	IAGRI LGVLGPFPAGQASFSYFLVGEUWPGRDPWEIFLBEHVBEOLIRQOVTENTRDTAL	121
Qy	126	TDLKGILGDALAVYHDSLSVWGNRNNTKARSVWKSQYIALELMFVOKLPSFAVSGEEVPL	185
Db	122	ARLOGLGNSFRAYQOOSLEDWLENRDADTRSVLYTQYIALELDFLNA MPLFAIRNQEVPL	181
Qy	186	LPIYAQAANLHLLLRDASIFGKEWGLSGSSBIPTYNRQVRAGDYSYCHVKWYSTGLNN	245
Db	182	LMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYEQVEKTRYESDYCARWYNTGLNN	241
Qy	246	LRGTNAESWRYNQRFRDMLTWLDLVALFPSYDTQMYPIKTTAQLTRREVYDAIGTVHP	305
Db	242	LRGTNAESWLYNQFRDRDLTLGLVDLVALFPSYDTRVYPMNTSAQLTR EYITDPIGR TNA	301
Qy	306	HPSFTSITWYNNAPSPSAIAEAAVVRNPHLLDFLEQVITYILLSWSNSTQYNNMGCHKL	365
Db	302	PSGFASTNWFNNAPSPSAIEAAVIRPPLHLLDFPEQLTIFSVLSWSNSTQYNNYVWGHRL	361
Qy	366	EFRTIGTGLNTSTOGSTNTSNPVTLPRTSRDVRYESLAGLNLFLTQVNGVPRVDFHW	425
Db	362	ESRTIRGSLSTHGNTNTSNPVTLPQRTSRDVRYESPAGINILU LTTVPNGVPPWARFNW	421
Qy	426	KFVTHPTASDNFPYGVAGIGTQLODSNELPPEATGPNTYESYSHRLSHLIGLISASHVK	485
Db	422	RNP LNSLRGSLLYITYGTGVGTQLPDSETEUPEPTTERPNYESYSHRLSNLPLISGN TLR	481
Qy	486	ALVYSWTHRSADRNTNTEBNSITQIPLVKAFNLSSGAAVVRPGPFGTGGDI LRRTNTGFG	545
Db	482	APVYSWTHRSADRNTNISDSDITQIPLVKSFN LNSGTSVVSQPGTGGDIIRTNVNGSVL	541
Qy	546	DIRVNNINPPPAQRVVRIRYASTTDLPHTSINGKAINQGNFSA TNNRGEDLDYKTFRTV	605

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:22:09 ; Search time 60.0945 Seconds  
(without alignments)  
3909.384 Million cell updates/sec

Title: US-10-019-823B-56

Perfect score: 3762

Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KRELPEIVKYANELHIERN 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pap.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pap.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pap.\*
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- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pap.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09D\_PUBCOMB.pap.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pap.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pap.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pap.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pap.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pap.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pap.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pap.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3743	99.5	719	16	US-10-782-020-10
2	3743	99.5	719	16	US-10-782-141-8
3	3459.5	92.0	710	15	US-10-428-961-42
4	2263.5	60.2	1228	16	US-10-809-953-10
5	2250.5	59.8	1207	15	US-09-988-462-7
6	2171.5	57.7	1227	15	US-10-428-961-63
7	2156.5	57.3	1186	9	US-09-826-660-23
8	2101	55.8	1228	15	US-10-428-961-38
9	2101	55.8	1228	15	US-10-614-524-2
10	1923.5	51.1	643	9	US-09-826-660-25
11	1707.5	45.4	1167	14	US-10-089-678-1
12	1678.5	44.6	653	15	US-10-428-961-6
13	1655.5	44.0	1157	16	US-10-782-141-16

14	1496	39.8	1206	13	US-10-032-717-2	Sequence 2, Appli
15	1496	39.8	1206	14	US-10-414-637-2	Sequence 2, Appli
16	1496	39.8	1206	15	US-10-606-320-2	Sequence 2, Appli
17	1480	39.3	1210	13	US-10-032-717-4	Sequence 4, Appli
18	1480	39.3	1210	14	US-10-414-637-4	Sequence 4, Appli
19	1480	39.3	1210	15	US-10-606-320-4	Sequence 4, Appli
20	1476.5	39.2	1156	14	US-10-099-285-72	Sequence 28, Appli
21	1476.5	39.2	1156	15	US-10-428-961-28	Sequence 72, Appli
22	1452	38.6	1155	9	US-09-756-643-2	Sequence 2, Appli
23	1452	38.6	1155	10	US-09-988-462-9	Sequence 9, Appli
24	1452	38.6	1155	15	US-10-136-988A-2	Sequence 2, Appli
25	1452	38.6	1177	14	US-10-035-060-6	Sequence 6, Appli
26	1452	38.6	1181	10	US-09-988-462-11	Sequence 11, Appli
27	1452	38.6	1181	10	US-09-988-462-13	Sequence 13, Appli
28	1452	38.6	1181	10	US-09-988-462-15	Sequence 15, Appli
29	1452	38.6	1181	10	US-09-988-462-17	Sequence 17, Appli
30	1452	38.6	1181	10	US-09-988-462-28	Sequence 28, Appli
31	1452	38.6	1181	15	US-10-136-988A-8	Sequence 4, Appli
32	1452	38.6	1181	15	US-10-136-988A-10	Sequence 8, Appli
33	1452	38.6	1181	15	US-10-136-988A-12	Sequence 10, Appli
34	1452	38.6	1181	15	US-10-136-988A-12	Sequence 12, Appli
35	1447	38.5	1177	14	US-10-035-060-2	Sequence 2, Appli
36	1445	38.4	1177	14	US-10-035-060-8	Sequence 8, Appli
37	1444	38.4	1177	14	US-10-102-469-24	Sequence 24, Appli
38	1428.5	38.0	1176	16	US-10-782-141-6	Sequence 6, Appli
39	1416.5	37.7	1176	11	US-09-837-961-2	Sequence 2, Appli
40	1416.5	37.7	1176	16	US-10-825-751-2	Sequence 2, Appli
41	1385	36.8	1167	15	US-10-428-961-40	Sequence 40, Appli
42	1364	36.3	1177	9	US-09-873-873-26	Sequence 26, Appli
43	1364	36.3	1177	10	US-09-918-956A-26	Sequence 26, Appli
44	1364	36.3	1177	10	US-09-997-914-26	Sequence 26, Appli
45	1364	36.3	1177	14	US-10-365-645-26	Sequence 26, Appli

ALIGNMENTS

RESULT 1

US-10-782-020-10  
; Sequence 10, Application US/10782020  
; Publication No. US20040197916A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274139  
; CURRENT APPLICATION NUMBER: US/10/782,020  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,810  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-020-10

Query Match	99.5%	Score 3743;	DB 16;	Length 719;
Best Local Similarity	99.6%	Pred. No. 1e-307;		
Matches 716;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	MKLKNQDKHQSFSSNAKVDPKISTDSLKNETDIELQNHEDCLMKSEYENVEFPVASTI	60	
Db	1	MKLKNQDKHQSFSSNAKVDPKISTDSLKNETDIELQNHEDCLMKSEYENVEFPVASTI	60	
QY	61	QTGIGTAGKILGTGLGVFPFAGQVANSLSYFSLGELWPKGKQWEIFMEHVEIINQKISTYA	120	
Db	61	QTGIGTAGKILGTGLGVFPFAGQVANSLSYFSLGELWPKGKQWEIFMEHVEIINQKISTYA	120	

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1 MCLKNDKQKQSSNAKVDKISTDLSLKNEDTIELQNHEDCLKMSYENVPFVASTI 60
61 QTGIGIAGKILGTGVPFAGQVSLYSFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120
61 QTGIGIAGKILGTGVPFAGQVSLYSFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120
121 RNKALTDLKGLGDALAVYHDSLSWGNRNNTARSVVKSQYIALELMFVQKLPFAVSG 180
121 RNKALTDLKGLGDALAVYHDSLSWGNRNNTARSVVKSQYIALELMFVQKLPFAVSG 180
181 BEVPLLPYIAQAANLHLLLRDASIIFGKEWGLSSSEISTFYNQVERAGDYSVHCVKWYS 240
181 BEVPLLPYIAQAANLHLLLRDASIIFGKEWGLSSSEISTFYNQVERAGDYSVHCVKWYS 240
241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTOMYPIKTTAQLTREVTYDAI 300
241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTOMYPIKTTAQLTREVTYDAI 300
301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNSTQYNNMW 360
301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNSTQYNNMW 360
361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTOPVNGVPR 420
361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTOPVNGVPR 420
421 VDFHMKFVTHPIASDNFYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
421 VDFHMKFVTHPIASDNFYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540
481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540
541 TGTFGDIRVNINPPFAQRVRIRVASTTDLOFHTSINGKAINQGNFSAIWMRGEDLDYK 600
541 TGTFGDIRVNINPPFAQRVRIRVASTTDLOFHTSINGKAINQGNFSAIWMRGEDLDYK 600
601 TFRVTGFTTFFSFLDVQSTFTIGANFSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
601 TFRVTGFTTFFSFLDVQSTFTIGANFSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNM 719
661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNM 719

RESULT 3
US-10-428-961-42
; Sequence 42, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; PRIOR FILING DATE: 2003-05-02
; PRIOR FILING DATE: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; FEATURE:

Query Match 99.5%; Score 3743; DB 16; Length 719;
Best Local Similarity 99.6%; Pred. No. 1e-307;
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
1 MCLKNDKQKQSSNAKVDKISTDLSLKNEDTIELQNHEDCLKMSYENVPFVASTI 60

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; NAME/KEY: misc feature
; LOCATION: (200)..(200)
; OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid
US-10-428-961-42

Query Match      92.0%; Score 3459.5; DB 15; Length 710;
Best Local Similarity 92.1%; Pred. No. 1e-283;
Matches 662; Conservative 16; Mismatches 32; Indels 9; Gaps 1;

Qy 1 MKLNQDKHQSSNAKVDKISTDSLKNETDTELQNHEDCLKMSEYENVPFVSASTI 60
Db 1 MKSKNQHQSSNNATVDKNFTGSLNNNTTELQNFH-----EGIEPFVSASTI 51

Qy 61 QTGIGIAGKILGTLGVPFAGQVASYLSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120
Db 52 QTGIGIAGKILGNLGVFPAGQVASYLSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA 111

Qy 121 RNKALTDLGLDALAVYHDSLESVGNRNNTARSVVKSYQIYALBLMFVQKLPSPAVSG 180
Db 112 RNKALADLGLDALAVYHDSLESVGNRNNTARSVVKSYQIYALBLMFVQKLPSPAVSG 171

Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSVHCVKWYS 240
Db 172 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSVHCVKWYS 231

Qy 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALPSPSYDTQMPYIKTTAQLTREVTDAI 300
Db 232 TGLNLRGMNAESWVRYNQFRDMTLMVLDLVALPSPSYDTQMPYIKTTAQLTREVTDAI 291

Qy 301 GTVHPHPSSTTTWYNNAPSPSAIEAAVVRNPHLLDLEQVTIYSLLSRWNSNTQYNNMW 360
Db 292 GTVHPHPSSTTTWYNNAPSPSTIEAAVVRNPHLLDLEQVTIYSLLSRWNSNTQYNNMW 351

Qy 361 GGHKLEFRITGTLNISTOGSTNTSINPVTLPPTSDDVYRTESLAGNLFLTPQVNGVR 420
Db 352 GGHKLEFRITGTLNISTOGSTNTSINPVTLPPTSDDVYRTESLAGNLFLTPQVNGVR 411

Qy 421 VDFHMKFVTHPIASDNFYFGYAGIGTQLQDSENELPPEATGPNVYESYSHRLSHIGLIS 480
Db 412 VDFHMKFVTHPIASDNFYFGYAGIGTQLQDSENELPPEATGPNVYESYSHRLSHIGLIS 471

Qy 481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNT 540
Db 472 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNK 531

Qy 541 TGTFGDIRVNIINPPFAQRVVRIRYASTTDLOPHTSINGKAINQGNFSAATMRGEDLDYK 600
Db 532 TGTFGDIRVNIINPPFAQRVVRIRYASTTDLOPHTSINGKAINQGNFSAATMRGEDLDYK 591

Qy 601 TFRVTGFTTFFSPDLVQSTFTIGAMNFGSGNEVYIDRIEFPVPEVTEYAEYDFEKAQEV 660
Db 592 TFRVTGFTTFFSPDLVQSTFTIGAMNFGSGNEVYIDRIEFPVPEVTEYAEYDFEKAQEV 651

Qy 661 TALFTSTNPRGLTKDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
Db 652 TALFTSTNPRGLTKDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 710

RESULT 4
US-10-809-953-10
; Sequence 10, Application US/10809953
; Publication No. US20040181825A1
; GENERAL INFORMATION:
; APPLICANT: Van Mellaert, Herman
; APPLICANT: Botterman, Johan
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Joos, Henk
; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTICIDAL PROTEINS
; FILE OF INVENTION: 021565-078
; CURRENT APPLICATION NUMBER: US/10/809,953
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/09/661,016
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; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: PCT/EP90/00905
; PRIOR FILING DATE: 1990-05-30
; PRIOR APPLICATION NUMBER: GB 89401499.2
; PRIOR FILING DATE: 1989-05-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-809-953-10

Query Match      60.2%; Score 2263.5; DB 16; Length 1228;
Best Local Similarity 62.4%; Pred. No. 4.8e-182;
Matches 447; Conservative 79; Mismatches 165; Indels 25; Gaps 6;

Qy 23 TBSLKNETDIEQLQNH-----EDCLKMSEYENVPFVSASTIQTGIGIAGKI 70
Db 2 TSNRKNENBEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61

Qy 71 LGTLGVFPAGQVASYLSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
Db 62 LGVLGVFPAGQVASYLSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 121

Qy 131 LGDALAVYHDSLESVGNRNNTARSVVKSYQIYALBLMFVQKLPSPAVSGEVPLLPIYA 190
Db 122 LGDSFRAVQOQSLDLENDRTDARTSVLHTQIYALELDELFLNAMPLFAIRNQSVPLLMVYA 181

Qy 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSVHCVKWYSTGLNLRGNT 250
Db 182 QAANLHLLLRDASIFGSEFGLTSQEIQRYSQVERQVTRDSDYCVEMVNTGLNLRGNT 241

Qy 251 AESWRYNQFRDMTLMVLDLVALPSPSYDTQMPYIKTTAQLTREVTDAIGTGVHPHPSFT 310
Db 242 AASWRYNQFRDMTLMVLDLVALPSPSYDTQMPYIKTTAQLTREVTDAIGAT--GVNMA 299

Qy 311 STTWYNNAPSPSAIEAAVVRNPHLLDLEQVTIYSLLSRWNSNTQYNNMWGGHKLFRIT 370
Db 300 SMWYNNAPSPSAIEAAVVRNPHLLDLEQVTIYSLLSRWNSNTQYNNMWGGHKLFRIT 359

Qy 371 GGTLMISTOGSTNTSINPVTLPPTSDDVYRTESLAGNLFLTPQVNGVRPVDVHMKFV 428
Db 360 GGGLTSTHGATNTSINPVTLPFASRDVYRTESYAGVLLWGIYLEPIHGVPVTRFNF--- 416

Qy 429 THP-----IASDNFYFGYAGIGTQLQDSENELPPEATGPNVYESYSHRLSHIGLISASH 483
Db 417 TNPQISDRGTANYSQP--YESPGLQKDSBELPPETTERPNVYESYSHRLSHIGLISQSR 475

Qy 484 VKALVYSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTTGT 543
Db 476 VNVVYVSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTTGT 535

Qy 544 FGDIRVNIINPPFAQRVVRIRYASTTDLOPHTSINGKAINQGNFSAATMRGEDLDYKTPR 603
Db 536 FGPVIRVNGPLTKDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 595

Qy 604 TVGFTTSPDLVQSTFTIGAMNFGSGNEVYIDRIEFPVPEVTEYAEYDFEKAQEVKVTAL 663
Db 596 RRAFTTPTFTTQIDIRTSIQGLSGNGEVYIDRIEFPVPEVTEYAEYDFEKAQEVKVTAL 655

Qy 664 FTSTNPRGLTKDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
Db 656 FTNTNPRGLTKDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLSDERNL 711

RESULT 5
US-09-988-462-7
; Sequence 7, Application US/09988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:
; APPLICANT: Kosiel, Michael G.
; APPLICANT: Desai, Nalini M.
```

Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Lauis, Karen L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Syngenta Biotechnology, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/988,462  
FILING DATE: 20-NO. US20030046726A1-2001  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 09/547,422  
FILING DATE: 11-APR-2000  
APPLICATION NUMBER: US 08/459,504  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-188051  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-988-462-7  
Query Match 59.8%; Score 2250.5; DB 10; Length 1207;  
Best Local Similarity 64.0%; Pred. No. 5.9e-181;  
Matches 440; Conservative 77; Mismatches 157; Indels 13; Gaps 5;  
Qy 40 EDCLKSEYENPVFVSASTIQIGIAGKILGTLCVPFAGOVASLYSIFILGELWPKGN 99  
Db 10 EDSLCTAEGNNIDPFVSASTIQIGIAGKILGTLCVPFAGOVASLYSIFILGELWPKGN 69  
Qy 100 QWEIFMEHVEEIIINQKISTYARNKALTDLKGDLALAVYHDSLESWGNRNTRARSVK 159  
Db 70 QWEIFMEHVEEIIINQKISTYARNKALTDLKGDLALAVYHDSLESWGNRNTRARSVK 129  
Qy 160 SQYTALELMFVKQLPSPFVSGEVEPLPIYQAANLHLLLRDASTFGKEWGLSSEIST 219  
Db 130 TQYTALELDFNAPLFAIRNQEVPLLMVYAQANLHLLLRDASTFGKEWGLSSEIST 189  
Qy 220 FYNQVERAGDYSVHCVKYKSTGLNLRGTNAESWVRYNQFRDMTLMVLDLVALPPSYD 279  
Db 190 YFEQVERTRDYSYCYVEWYNTGLNLRGTNAESWVRYNQFRDMTLMVLDLVALPPSYD 249  
Qy 280 TQMPYIKTKTAQLTREVTDAIGTVHPHPSFTSTITWYNNNAPSFAIEAAVVRNPHLLDFL 339

Db 250 TRTPINTSAQLTREVTDAIGAT--GVNMAWMYNNNAPSFSAIEAAAIRPHLLDFL 307  
Qy 340 EQVTIYLLSRWSNTQYNNMWGKLEPRIGTILNISTOGSTNTSINPVTLPFTRSDVY 399  
Db 308 EQLTIFGASSRSWNTREHMTYWRGHTIQSRPIGGGLNTHGATNTSINPVTLPFTRSDVY 367  
Qy 400 RTESLGLNLF--LTPVNGVPRVDFHWKFVTHP-----IASDNFFYPGAGIGTQLQDS 452  
Db 368 RTESVAGVLLMGIYLEPIHGVTTFVRFNF--TNPQNISDRGTANYSQP-YESPLQLKDS 423  
Qy 453 ENELPPEATGQPNYESYSHRLSHIGLISASHKALVTSWTHRSADRTNTEPNSITQIPL 512  
Db 424 ETELPPEATERPENYESYSHRLSHIGLISASHKALVTSWTHRSADRTNTEPNSITQIPL 483  
Qy 513 VKAFNLSSGAAVRGPGETGGDILRRNTGTGDIRVNNPPPAQRYKVRIRYASTTDLQ 572  
Db 484 VKASELPQGTTVVRGPGETGGDILRRNTGTGDIRVNNPPPAQRYKVRIRYASTTDLQ 543  
Qy 573 PHTSINGKAINQGNFSAATNRGEDIKYTFTVGTFTTFFSFLDVQSTFTTIGAMNPFSSGNE 632  
Db 544 FVSRGGTTVNNFRFLRTWNSGDELKYGNFVRRATFTTFTTQDIIRTSIQGLSGNGE 603  
Qy 633 VYIDRIEFVPEVTVYEAEDFEKAEKVLTALFTSTNPRGLKTDYKDHIDOVSNLVESLS 692  
Db 604 VYIDKIEIIPVATFEAEYDLERAQEAVALFTNTPRRLKTDVTDYHIDQVSNLVACL 663  
Qy 693 DSFYLDKEKELFEIVKYANLHIERNM 719  
Db 664 DFCLDEKRELEKVKYAKRLSDERNL 690

RESULT 6  
US-10-428-961-63  
; Sequence 63, Application US/10428961  
; Publication No. US20030237111A1  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Rupa, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
; FILE REFERENCE: MECO201--1  
; CURRENT APPLICATION NUMBER: US/10/428,961  
; CURRENT FILING DATE: 2003-05-02  
; PRIOR FILING DATE: 2000-09-13  
; PRIOR FILING DATE: 2000-09-13  
; PRIOR FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 63  
; LENGTH: 1227  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-428-961-63

Query Match 57.7%; Score 2171.5; DB 15; Length 1227;  
Best Local Similarity 59.0%; Pred. No. 3e-174;  
Matches 421; Conservative 104; Mismatches 176; Indels 13; Gaps 3;  
Qy 13 SSNAVKDKISTDLSKN-----ETDELQINHEDCMKSEYENVEPPFVSASTIQIGIG 65  
Db 7 NENEIINALSPVSNHSAQNNLSTDARI-----EDSLCTAEGNNIDPFVSASTIQIGIN 61  
Qy 66 IAGKILGTLCVPFAGOVASLYSIFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 125  
Db 62 IAGKILGTLCVPFAGOVASLYSIFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 121  
Qy 126 TDLKGLGDLALAVYHDSLESWGNRNTRARSVKSOYIALELMFVKQLPSPFVSGEVEPL 185



Query Match 55.8%; Score 2101; DB 15; Length 1228;  
Best Local Similarity 59.2%; Pred. No. 2.8e-168;  
Matches 422; Conservative 97; Mismatches 184; Indels 10; Gaps 7;  
QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCMKSEYENVEPVFVASTIQTGTGIGIAGKI 70  
DB 7 NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVASTVQTGTGINIAGRI 66  
QY 71 LGTLGVFPAGQVASYLFIIGELWPKGNOWEIFMEHVEEIIINOKISTYARNKALTDLKG 130  
DB 67 LGVLGVFPAGQVASYLFIIGELWPKGNOWEIFMEHVEEIIINOKISTYARNKALTDLKG 126  
QY 131 LGDALAVYHDSLSWGNRNNTARSVVKSOYIALELMFVQKLPSPFVSGSEVPLPIYA 190  
DB 127 LGDSFRAYQOOSLEDWLENRDARTSVLYTQYIALELDFLNAMPFLAIRNQEVPLLMVYA 186  
QY 191 QAAHLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSYHCVKWTSTGLNLRGTN 250  
DB 187 QAAHLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSYHCVKWTSTGLNLRGTN 246  
QY 251 AASWRYNQFRDMLVLDLVALFPSTYOTOMPIKTAAQLTREVYTDAGTGVHPHPSFT 310  
DB 247 AASWRYNQFRDMLVLDLVALFPSTYOTOMPIKTAAQLTREVYTDAGTGVHPHPSFT 304  
QY 311 STTWYNNAPSFSAIEAIVRNPPLLDLFLQVTTIYSLSRWSNTQYNNMGGHKLFPRTI 370  
DB 305 SMWYNNAPSFSAIEAIVRNPPLLDLFLQVTTIYSLSRWSNTQYNNMGGHKLFPRTI 364  
QY 371 GGTINISQTGSTNTSINPVTLPFTSRDYRTESLAGLNF--LTOPVNGVPRVDHMKFV 428  
DB 365 GGLNTSTHGSTNTSINPVLSPFSRDVYTESYAGVLLWGLIYLEPIHGVTFRFNRNP 424  
QY 429 --THPIASDNFYPGYAGIGTQLODSENELPPEATGPNYESYSHRSLSHGLISASHVKA 486  
DB 425 QNTFERGTANYSQP--YESPGLQKLDSELPETTERPNYESYSHRSLSHGLISASHVKA 483  
QY 487 LVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTGTGFGD 546  
DB 484 PVIYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTGTGFGD 543  
QY 547 IRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLYKTFRTVG 606  
DB 544 MGLNFNTSLQRYRVRVRYAASQTMVLRTVVGSTTFDQGFPTMSANESLTSQSFRFAE 603  
QY 607 FTTPFSLDVQSTFTTIGAMNFGSSGNEVYIDRIEFVPEVTEAEYDEKAEKVATLFTS 666  
DB 604 FVVGISASGSQ--TAGISISNAGROTTFHFKIEFIPITATFEAYDLEAQAENALFTN 662  
QY 667 TNPRGLKTDVVDYHIDQVSNLVESLDFYLDKRELFEIVKYANELHIERNM 719  
DB 663 TNPRGLKTDVVDYHIDQVSNLVESLDFYLDKRELFEIVKYANELHIERNM 715

RESULT 9  
US-10-614-524-2  
; Sequence 2, Application US/10614524  
; Publication No. US20040016020A1  
; GENERAL INFORMATION:  
; APPLICANT: Arnaut, Greta  
; APPLICANT: Boets, Annemie  
; APPLICANT: Damme, Nicole  
; APPLICANT: Mathieu, Eva  
; APPLICANT: Vanneste, Stijn  
; APPLICANT: Van Rie, Jeroen  
; TITLE OF INVENTION: Insecticidal proteins from *Bacillus thuringiensis*.  
; FILE REFERENCE: NEWTUS2  
; CURRENT APPLICATION NUMBER: US/10/614,524  
; CURRENT FILING DATE: 2003-07-08  
; PRIOR APPLICATION NUMBER: US/09/739,243  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/173387  
; PRIOR FILING DATE: 1999-12-28

NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1228  
; TYPE: PRT  
; ORGANISM: *Bacillus thuringiensis*  
US-10-614-524-2  
Query Match 55.8%; Score 2101; DB 15; Length 1228;  
Best Local Similarity 59.2%; Pred. No. 2.8e-168;  
Matches 422; Conservative 97; Mismatches 184; Indels 10; Gaps 7;  
QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCMKSEYENVEPVFVASTIQTGTGIGIAGKI 70  
DB 7 NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVASTVQTGTGINIAGRI 66  
QY 71 LGTLGVFPAGQVASYLFIIGELWPKGNOWEIFMEHVEEIIINOKISTYARNKALTDLKG 130  
DB 67 LGVLGVFPAGQVASYLFIIGELWPKGNOWEIFMEHVEEIIINOKISTYARNKALTDLKG 126  
QY 131 LGDALAVYHDSLSWGNRNNTARSVVKSOYIALELMFVQKLPSPFVSGSEVPLPIYA 190  
DB 127 LGDSFRAYQOOSLEDWLENRDARTSVLYTQYIALELDFLNAMPFLAIRNQEVPLLMVYA 186  
QY 191 QAAHLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSYHCVKWTSTGLNLRGTN 250  
DB 187 QAAHLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSYHCVKWTSTGLNLRGTN 246  
QY 251 AASWRYNQFRDMLVLDLVALFPSTYOTOMPIKTAAQLTREVYTDAGTGVHPHPSFT 310  
DB 247 AASWRYNQFRDMLVLDLVALFPSTYOTOMPIKTAAQLTREVYTDAGTGVHPHPSFT 304  
QY 311 STTWYNNAPSFSAIEAIVRNPPLLDLFLQVTTIYSLSRWSNTQYNNMGGHKLFPRTI 370  
DB 305 SMWYNNAPSFSAIEAIVRNPPLLDLFLQVTTIYSLSRWSNTQYNNMGGHKLFPRTI 364  
QY 371 GGTINISQTGSTNTSINPVTLPFTSRDYRTESLAGLNF--LTOPVNGVPRVDHMKFV 428  
DB 365 GGLNTSTHGSTNTSINPVLSPFSRDVYTESYAGVLLWGLIYLEPIHGVTFRFNRNP 424  
QY 429 --THPIASDNFYPGYAGIGTQLODSENELPPEATGPNYESYSHRSLSHGLISASHVKA 486  
DB 425 QNTFERGTANYSQP--YESPGLQKLDSELPETTERPNYESYSHRSLSHGLISASHVKA 483  
QY 487 LVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTGTGFGD 546  
DB 484 PVIYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTGTGFGD 543  
QY 547 IRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLYKTFRTVG 606  
DB 544 MGLNFNTSLQRYRVRVRYAASQTMVLRTVVGSTTFDQGFPTMSANESLTSQSFRFAE 603  
QY 607 FTTPFSLDVQSTFTTIGAMNFGSSGNEVYIDRIEFVPEVTEAEYDEKAEKVATLFTS 666  
DB 604 FVVGISASGSQ--TAGISISNAGROTTFHFKIEFIPITATFEAYDLEAQAENALFTN 662  
QY 667 TNPRGLKTDVVDYHIDQVSNLVESLDFYLDKRELFEIVKYANELHIERNM 719  
DB 663 TNPRGLKTDVVDYHIDQVSNLVESLDFYLDKRELFEIVKYANELHIERNM 715

RESULT 10  
US-09-826-660-25  
; Sequence 25, Application US/09826660  
; Patent No. US20010026940A1  
; GENERAL INFORMATION:  
; APPLICANT: Cardineau, Guy A.  
; APPLICANT: Stelman, Steven J.  
; APPLICANT: Narva, Kenneth E.  
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins  
; FILE REFERENCE: MA-714XC2D1  
; CURRENT APPLICATION NUMBER: US/09/826,660  
; CURRENT FILING DATE: 2001-04-05





Db 523 SKKITOIPAVKGMVLYGSSVVGPGFTGGDILKRTNPSILGTEAVTVNGSLSQRYVRRI 582  
QY 564 RVASTTDLQFHTSINGKAINQGNFSAATMRGDBLDYKTPRTVGTTPFSFLDVQSTFTIG 623  
Db 583 RVASTTDFE-TLYLGDTEIEKRNKTMGASLYEYEFKFSFIDTQFRETQDKILLS 641  
QY 624 ANPFSGNEVYIDRIEFVFPVYTYABYDEKAEKVATLFTSTNPRGLKTDVKDHYHDQ 683  
Db 642 MGFSSGQGVYIDRIEFIPVDETYEAEQLEAAKAVNALFTNTKD-GLRPGVTDYEVNQ 700  
QY 684 VSNLVESLDEFLDEKRELFEIVKANELHIERNM 719  
Db 701 AANLVECLSDLLYPNEKRLFLDAVREAKRLSGARNL 736  
  
RESULT 14  
US-10-032-717-2  
; Sequence 2, Application US/10032717  
; Publication No. US20020151709A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With  
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/032, 717  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/242, 838  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1206  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-032-717-2  
  
Query Match 39.8%; Score 1496; DB 13; Length 1206;  
Best Local Similarity 44.1%; Pred. No. 4.8e-117;  
Matches 335; Conservative 129; Mismatches 232; Indels 64; Gaps 22;  
  
QY 1 MCLKNQDKHQSFSSNAKVDKISTDS----LKNETDIELQINHEDCMKM-----SEYE-N 50  
Db 1 MSPNNQNEYEIIDATPST-SVNSDNRYPFANEPTNALQNMQDYKYLKMSAGNASPYGS 59  
  
QY 51 VEPFVSA-STIQIGIAGKILGTGVPFAGQVASYLSYFELGELWPKG-KNQEIPMEHV 108  
Db 60 PEVLVSGDAAKAAIDIVGKLLSGLGVPFVPIVSLYTLQIDLWPSGKSQWEIPMEQV 119  
  
QY 109 EEINQKISTYARNKALTDKGLGDALAVYHDSLSWGNRNTRARSVVKQYIALELM 168  
Db 120 EELINQKIAEYARNKALSELEGLNNYQLYLTALBEEENPNPGRALRDVNRFEILDSL 179  
  
QY 169 FVQKLPSFAVSGEVPPLPIYAAOANLHLLLDASIFGKEWGLSSSEISTFYNRQVERA 228  
Db 180 FTQYMPFSFRVTFNFPFLTVYAAANLHLLLDKASIFGEEGWSTTTNNYYDROMKLT 239  
  
QY 229 GDYSYHCVKWYSTGLNNLRGTAESVVRVNOFRDMLTMDVLVLPSPDYDTOMYPIKTT 288  
Db 240 AEYSDDCHVKWYETGLAKTKTSKQWVDYNOFRREMTLAVLDVVALFPYDFTYMEYTK 299  
  
QY 289 AQLTREYTDATGTHPHPSFTSTTWNNNAPSFSAEAAVVRNPHLLDFLEQVITYSL 348  
Db 300 AQLTREYTDPLGAVNV---SIGSMY-DKAPSGVIESVIRPPHVFDYITGLTYVTQS 355  
  
QY 349 SRNSNTQYMMWGHKLEFFITGTLNISTQGSTNTSINPV-TLPTSRDVTYTESLAGL 407  
Db 356 RSISARYIRHWAGHQISYHRVSRGSLNQMQYGTGNQLHSTSTFDFTNYDIYKTLSDAV 415

QY 408 NLFLTQP-----VNGVPRVDFHMKVTHPIASDN---FYPGYAGIGTQLODSENELPPE 459  
Db 416 LLDIVPGYTYIFFGMPEVEF---FMVNLNNTRKTLKYNPVSKDIIAISTRDSELEPPE 472  
QY 460 ATGQNYESYSHRLSHIGLISAS-HVKAL--VYSWTHRSADRTNTIEPNSITQIPLVKAF 516  
Db 473 TSDQNYESYSHRLCHITSIIPATGNTGLVFPVFWTHRSADLNTIYSDKITQIPAYKCM 532  
QY 517 NLSGAAVVRGPGFTGGDILR-RTNTGTFGDI---RVNINPFPFAQRYVRIRYASTTDLQ 572  
Db 533 DNLFPVPVVGPGHTGGDLLQVNRSTGSGVTLFLARYGLALEKAGKYRVLRYATDADIV 592  
QY 573 PHTSINGKAINQGNFSAATMRGDBLDYKTFR-----TVGFTTTPESFL-----DVQST 619  
Db 593 LH--VNDAGI---QMPKTMNPGEDLTSTKFKVADAITTLNLATDSSSLAKHNLGSDPNST 647  
QY 620 FTIGAWNFSSGNEVYIDRIEFVFPVETVYAEVDFEKAQOKVYATLTSTNPRGLKTDVKDY 679  
Db 648 LS-----GIVYVDRIEFIPVDETYEAEQLEAAKAVNALFTNTKD-GLRPGVTDY 697  
QY 680 HIDQVSNLVESLSDFLDEKRELFEIVKANELHIERNM 719  
Db 698 EVNQAAANLVECLSDLLYPNEKRLFLDAVREAKRLSGARNL 737  
  
RESULT 15  
US-10-414-637-2  
; Sequence 2, Application US/10414637  
; Publication No. US20030177528A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With  
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/414, 637  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: US/10/032, 717  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/242, 838  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1206  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-414-637-2  
  
Query Match 39.8%; Score 1496; DB 14; Length 1206;  
Best Local Similarity 44.1%; Pred. No. 4.8e-117;  
Matches 335; Conservative 129; Mismatches 232; Indels 64; Gaps 22;  
  
QY 1 MCLKNQDKHQSFSSNAKVDKISTDS----LKNETDIELQINHEDCMKM-----SEYE-N 50  
Db 1 MSPNNQNEYEIIDATPST-SVNSDNRYPFANEPTNALQNMQDYKYLKMSAGNASPYGS 59  
  
QY 51 VEPFVSA-STIQIGIAGKILGTGVPFAGQVASYLSYFELGELWPKG-KNQEIPMEHV 108  
Db 60 PEVLVSGDAAKAAIDIVGKLLSGLGVPFVPIVSLYTLQIDLWPSGKSQWEIPMEQV 119  
  
QY 109 EEINQKISTYARNKALTDKGLGDALAVYHDSLSWGNRNTRARSVVKQYIALELM 168  
Db 120 EELINQKIAEYARNKALSELEGLNNYQLYLTALBEEENPNPGRALRDVNRFEILDSL 179  
  
QY 169 FVQKLPSFAVSGEVPPLPIYAAOANLHLLLDASIFGKEWGLSSSEISTFYNRQVERA 228  
Db 180 FTQYMPFSFRVTFNFPFLTVYAAANLHLLLDKASIFGEEGWSTTTNNYYDROMKLT 239





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:24:54 ; Search time 22.3302 Seconds  
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Title: US-10-019-823B-56  
Perfect score: 3762  
Sequence: 1 MKLNQDQHQSFSNAKVDK.....KRELFEIVKYANELHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/prodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/PCUTUS COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3739	99.4	719	3	US-08-286-870A-8
2	3459.5	92.0	710	4	US-09-661-322A-42
3	3389	90.1	648	3	US-08-286-870A-4
4	3379	89.8	719	2	US-09-003-217-2
5	3374	89.7	719	3	US-09-218-942-2
6	2795	74.3	535	3	US-08-286-870A-6
7	2437.5	64.8	1229	1	US-08-100-709-4
8	2437.5	64.8	1229	1	US-08-176-865-4
9	2437.5	64.8	1229	1	US-08-474-038-4
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11	2437.5	64.8	1229	2	US-08-881-340-4
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17	2250.5	59.8	1207	3	US-08-459-504B-7
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20	2250.5	59.8	1207	3	US-09-547-422-7
21	2250.5	59.8	1207	4	US-09-988-462-7
22	2249.5	59.8	1227	3	US-09-053-549-2
23	2180.5	58.0	1227	1	US-08-448-170-8
24	2180.5	58.0	1227	3	US-08-961-803-9
25	2171.5	57.7	1227	4	US-09-661-322A-63
26	2156.5	57.3	1186	3	US-09-178-252-23
27	2156.5	57.3	1186	4	US-09-826-660-23

28	2101	55.8	1228	4	US-09-661-322A-38
29	1923.5	51.1	643	3	US-09-178-252-25
30	1923.5	51.1	643	4	US-09-826-660-25
31	1891	50.3	380	5	PCT-US91-02560-4
32	1678.5	44.6	653	4	US-09-661-322A-6
33	1655.5	44.0	1157	1	US-07-876-280-30
34	1655.5	44.0	1157	1	US-07-812-180A-2
35	1655.5	44.0	1157	1	US-08-315-468-2
36	1655.5	44.0	1157	3	US-07-941-650A-2
37	1492.5	39.7	1176	1	US-08-257-999-2
38	1483	39.4	1157	2	US-08-532-547-5
39	1483	39.4	1157	2	US-08-379-656B-5
40	1483	39.4	1157	3	US-08-455-838-5
41	1483	39.4	1157	3	US-09-019-809-5
42	1483	39.4	1157	4	US-09-471-177-5
43	1483	39.4	1157	4	US-09-220-806-5
44	1476.5	39.2	1156	3	US-09-002-285-72
45	1476.5	39.2	1156	4	US-09-589-477-72

ALIGNMENTS

RESULT 1  
US-08-286-870A-8  
; Sequence 8, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPEIT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PAUL N. KOKULIS  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 70608/220720  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-286-870A-8

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Query Match 99.4%; Score 3739; DB 3; Length 719;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 715; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 M K L N Q D K H Q S P S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P P V S A S T I 60
Db 1 M K L N Q D K H Q S P S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P P V S A S T I 60

Qy 61 Q T G I G I A G K I L G T L G V P P A G O V A S L Y S F I L G E L W P K G N Q W E I P M E H V E E I I N O K I S T Y A 120
Db 61 Q T G I G I A G K I L G T L G V P P A G O V A S L Y S F I L G E L W P K G N Q W E I P M E H V E E I I N O K I S T Y A 120

Qy 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V Q K L P S F A V S G 180
Db 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V Q K L P S F A V S G 180

Qy 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K W G L S S E I S T F Y N R Q V E R A G D Y S H C V K W Y S 240
Db 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K W G L S S E I S T F Y N R Q V E R A G D Y S H C V K W Y S 240

Qy 241 T G L N L R G T N A E S W V R Y N Q F R D M T L M V L D L V A L P S Y D T Q M P I K T T A Q L T R E V Y T D A I 300
Db 241 T G L N L R G T N A E S W V R Y N Q F R D M T L M V L D L V A L P S Y D T Q M P I K T T A Q L T R E V Y T D A I 300

Qy 301 G T V H P H P S F T S T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360
Db 301 G T V H P H P S F T S T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360

Qy 361 G G H K L E F T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T O P V N G V P R 420
Db 361 G G H K L E F T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T O P V N G V P R 420

Qy 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L Q S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480
Db 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L Q S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480

Qy 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G G D I L R R T N 540
Db 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G G D I L R R T N 540

Qy 541 T G T F G D I R V N I N P P P A Q R Y R V R I R Y A S T D I Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600
Db 541 T G T F G D I R V N I N P P P A Q R Y R V R I R Y A S T D I Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600

Qy 601 T F R T V G F T P P S F L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660
Db 601 T F R T V G F T P P S F L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660

Qy 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719
Db 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719

RESULT 2
US-09-661-322A-42
; Sequence 42, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Wei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rugar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compose
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRT
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ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: misc feature
LOCATION: (200)-(200)
OTHER INFORMATION: No. 6593293-Coding
US-09-661-322A-42

Query Match 92.0%; Score 3459.5; DB 4; Length 710;
Best Local Similarity 92.1%; Pred. No. 2.4e-301;
Matches 662; Conservative 16; Mismatches 32; Indels 9; Gaps 1;

Qy 1 M K L N Q D K H Q S P S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P P V S A S T I 60
Db 1 M K S Q N N H O S L S N N A T V D K N F T G S L E N N T N T E L Q N F N H -----E G I E P F V S T I 51

Qy 61 Q T G I G I A G K I L G T L G V P P A G O V A S L Y S F I L G E L W P K G N Q W E I P M E H V E E I I N O K I S T Y A 120
Db 52 Q T G I G I A G K I L G T L G V P P A G O V A S L Y S F I L G E L W P K G S Q W E I P M E H V E E I I N O K I S T Y A 111

Qy 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V Q K L P S F A V S G 180
Db 112 R N K A L A D L K G L D A L A V Y H E S L E S W I E N R N N T R S V V K S Q Y I T L E M F V Q S L P S F A V S G 171

Qy 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K W G L S S E I S T F Y N R Q V E R A G D Y S H C V K W Y S 240
Db 172 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K W G L S D S E I S T F Y N R Q S G K S K E Y S D H C V K W Y N 231

Qy 241 T G L N L R G T N A E S W V R Y N Q F R D M T L M V L D L V A L P S Y D T Q M P I K T T A Q L T R E V Y T D A I 300
Db 232 T G L N R L M G N N A E S W V R Y N Q F R D M T L M V L D L V A L P S Y D T Q M P I K T T A Q L T R E V Y T D A I 291

Qy 301 G T V H P H P S F T S T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360
Db 292 G T V H P H P S F T S T T W Y N N N A P S F S T I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 351

Qy 361 G G H K L E F T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T O P V N G V P R 420
Db 352 G G H K L E F T I G G T L N T S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T O P V N G V P R 411

Qy 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L Q S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480
Db 412 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L Q S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 471

Qy 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G G D I L R R T N 540
Db 472 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G G D I L R R K N 531

Qy 541 T G T F G D I R V N I N P P P A Q R Y R V R I R Y A S T D I Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600
Db 532 T G T F G D I R V N I N P P P A Q R Y R V R I R Y A S T D I Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 591

Qy 601 T F R T V G F T P P S F L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660
Db 592 T F R V G F T T P S F S D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E V 651

Qy 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719
Db 652 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D K F Y L D E K R E L F E I V K Y A Q L H I E R N M 710

RESULT 3
US-08-286-870A-4
; Sequence 4, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: Ely, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENN, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
```

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; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-870A-4

Query Match 90.1%; Score 3389; DB 3; Length 648;
Best Local Similarity 99.8%; Pred. No. 4.4e-295;
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCLKNQDKHQSFSNNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60
Db 1 MCLKNQDKHQSFSNNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60
Qy 61 QTGIGIAGKILGTGVPAGQVAVSLYSFILGELMPKGNQWEIFMEHVEEIIQKISTYA 120
Db 61 QTGIGIAGKILGTGVPAGQVAVSLYSFILGELMPKGNQWEIFMEHVEEIIQKISTYA 120
Qy 121 RNKALTDLKGIGDALAVYHDSLSWSVGNRNNTARSVVKSQYIALELMFVKLPSPFVSG 180
Db 121 RNKALTDLKGIGDALAVYHDSLSWSVGNRNNTARSVVKSQYIALELMFVKLPSPFVSG 180
Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLGSSEISTFYNQVERAGDYSYHCVKWS 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLGSSEISTFYNQVERAGDYSYHCVKWS 240
Qy 241 TGLNLRGTAESWVRVYNQRRDMLVLDLVALFPSYDQMPYIKTQAOTREVTYDAI 300
Db 241 TGLNLRGTAESWVRVYNQRRDMLVLDLVALFPSYDQMPYIKTQAOTREVTYDAI 300
Qy 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMW 360
Qy 361 GGHKLEPRTIGTGLNISTQSTNTSINPVLPTFSRDVYRTESLAGLNLFTQPVNGVPR 420
Db 361 GGHKLEPRTIGTGLNISTQSTNTSINPVLPTFSRDVYRTESLAGLNLFTQPVNGVPR 420
Qy 421 VDFHWKVFTHPIASDNFYCYAGIGCTQLQDSENELPPEATGQPNYESYSHRISHIGLIS 480
Db 421 VDFHWKVFTHPIASDNFYCYAGIGCTQLQDSENELPPEATGQPNYESYSHRISHIGLIS 480

; 481 ASHVKALVSWTHRSADRTNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540
; 481 ASHVKALVSWTHRSADRTNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540
; 541 TGTGFDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAIWMNGEDLDYK 600
; 541 TGTGFDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAIWMNGEDLDYK 600
; 601 TFRVTGFTTTPFSPFLDVQSTFTTIGAMNFSSGNEVYIDRIEFPVPEVYVE 648
; 601 TFRVTGFTTTPFSPFLDVQSTFTTIGAMNFSSGNEVYIDRIEFPVPEVYVE 648

RESULT 4
US-09-003-217-2
; Sequence 2, Application US/09003217
; Patent No. 5986177
; GENERAL INFORMATION:
; APPLICANT: Osman, Yehia A.
; APPLICANT: Madkour, Magdy A.
; APPLICANT: Bulla, Lee A.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
; TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
; STREET: 3605 Glenwood Ave. Suite 310
; CITY: Raleigh
; STATE: NC
; COUNTRY: US
; ZIP: 27622
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,217
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 5718-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2202
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-003-217-2

Query Match 89.8%; Score 3379; DB 2; Length 719;
Best Local Similarity 89.7%; Pred. No. 4.1e-294;
Matches 645; Conservative 34; Mismatches 40; Indels 0; Gaps 0;

Qy 1 MCLKNQDKHQSFSNNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60
Db 1 MCLKNQDKHQSFSNNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60
Qy 61 QTGIGIAGKILGTGVPAGQVAVSLYSFILGELMPKGNQWEIFMEHVEEIIQKISTYA 120
Db 61 QTGIGIAGKILGTGVPAGQVAVSLYSFILGELMPKGNQWEIFMEHVEEIIQKISTYA 120
Qy 121 RNKALTDLKGIGDALAVYHDSLSWSVGNRNNTARSVVKSQYIALELMFVKLPSPFVSG 180
Db 121 RNKALTDLKGIGDALAVYHDSLSWSVGNRNNTARSVVKSQYIALELMFVKLPSPFVSG 180
Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLGSSEISTFYNQVERAGDYSYHCVKWS 240
```

181 BEVPLLPYAAQANLHLLLRDASIFKNGGLSASEISTFYNRQVERTRDYSYHCVKWN 240  
241 TGLNLRGTNAESVRYNQFRDMTLMVLDLVALFPYSYDQMPDKTQAOLTRVYTDI 300  
241 TGLNLRGTNAESVRYNQFRDMTLMVLDLVALFPYSYDQMPDKTQAOLTRVYTDI 300  
301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW 360  
301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW 360  
361 GGHLEFRTIGTLMNISTOGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTOPVNGVR 420  
361 GGHLEFRTIGTLMNISTOGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTOPVNGVR 420  
421 VDFHWKFTVHTPIASDNFYYPGAGTQLODSENELPPEATQPNYESYSHRSLHIGLIS 480  
421 VDFHWKFTVHTPIASDNFYYPGAGTQLODSENELPPEATQPNYESYSHRSLHIGLIS 480  
481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600  
541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600  
601 TFRVGTFTPFSDVQSTFTIGANFNSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
601 TFRVGTFTPFSDVQSTFTIGANFNSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFLDEKRELFELVVKYAKQIHIERNM 719  
661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFLDEKRELFELVVKYAKQIHIERNM 719

RESULT 5  
US-09-218-942-2  
; Sequence 2, Application US/09218942  
; Patent No. 6232439  
; GENERAL INFORMATION:  
; APPLICANT: Osman, Yehia  
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum  
; TITLE OF INVENTION: Activity  
; FILE REFERENCE: CTV11  
; CURRENT APPLICATION NUMBER: US/09/218,942  
; CURRENT FILING DATE: 1998-12-22  
; EARLIER APPLICATION NUMBER: 60/035,361  
; EARLIER FILING DATE: 1997-01-10  
; EARLIER APPLICATION NUMBER: 09/003,217  
; EARLIER FILING DATE: 1998-01-06  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 719  
; TYPE: PR1  
; ORGANISM: Bacillus thuringiensis  
US-09-218-942-2

Query Match 89.7%; Score 3374; DB 3; Length 719;  
Best Local Similarity 89.7%; Pred. No. 1.2e-293;  
Matches 645; Conservative 34; Mismatches 40; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQFSSNAKVDKISTDLKNETDIELQINHEDECLKMGYENVEPVFVASTI 60  
DB 1 MCLKNPDKHQTLSSNAKVDKISTDLKNETDIELKNNNEDYLRMSEHESIDPFVASTI 60  
QY 61 QTGIGIAGKILGTGVPPAGVAGLSYFILGELPKKNQWEIFMEHVEIINQKISTYA 120  
DB 61 QTGIGIAGKILGTGVPPAGVAGLSYFILGELPKKNQWEIFMEHVEIINQKISTYA 120  
QY 121 RNKALTDLKGLDALAVHDSWVGNRNTRARSVVKQYIALELMFVQKLPSPFVAVSG 180  
DB 121 RNKALTDLKGLDALAVHDSWVGNRNTRARSVVKQYIALELMFVQKLPSPFVAVSG 180

181 BEVPLLPYAAQANLHLLLRDASIFKNGGLSASEISTFYNRQVERAGDYSYHCVKWS 240  
181 BEVPLLPYAAQANLHLLLRDASIFKNGGLSASEISTFYNRQVERTRDYSYHCVKWN 240  
241 TGLNLRGTNAESVRYNQFRDMTLMVLDLVALFPYSYDQMPDKTQAOLTRVYTDI 300  
241 TGLNLRGTNAESVRYNQFRDMTLMVLDLVALFPYSYDQMPDKTQAOLTRVYTDI 300  
301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW 360  
301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMNW 360  
361 GGHLEFRTIGTLMNISTOGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTOPVNGVR 420  
361 GGHLEFRTIGTLMNISTOGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTOPVNGVR 420  
421 VDFHWKFTVHTPIASDNFYYPGAGTQLODSENELPPEATQPNYESYSHRSLHIGLIS 480  
421 VDFHWKFTVHTPIASDNFYYPGAGTQLODSENELPPEATQPNYESYSHRSLHIGLIS 480  
481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600  
541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600  
601 TFRVGTFTPFSDVQSTFTIGANFNSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
601 TFRVGTFTPFSDVQSTFTIGANFNSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFLDEKRELFELVVKYAKQIHIERNM 719  
661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFLDEKRELFELVVKYAKQIHIERNM 719

RESULT 6  
US-08-286-870A-6  
; Sequence 6, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENN, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989

```
/ ATTORNEY/AGENT INFORMATION:
/ NAME: PAUL N. KOKULIS
/ REGISTRATION NUMBER: 16,773
/ REFERENCE/DOCKET NUMBER: 70608/220720
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 861-3000
/ TELEFAX: (202) 822-0944
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 535 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-286-870A-6

Query Match 74.3%; Score 2795; DB 3; Length 535;
Best Local Similarity 99.8%; Pred. No. 6.5e-242; Indels 0; Gaps 0;
Matches 534; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLNKNETDIELQINHEHEDCLKMSYENVEPFFVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLNKNETDIELQINHEHEDCLKMSYENVEPFFVSASTI 60
QY 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGKNQWEIFMEHVBEIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGKNQWEIFMEHVBEIINQKISTYA 120
QY 121 RNKALTDLGLGDALAVYHDSLSWGNRNNTARSVVKVSKQYIALELMFVKLPSFAVSG 180
DB 121 RNKALTDLGLGDALAVYHDSLSWGNRNNTARSVVKVSKQYIALELMFVKLPSFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISITFYNRQVERAGDYSYHCVKWTYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISITFYNRQVERAGDYSYHCVKWTYS 240
QY 241 TGLNNLRGNASWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300
DB 241 TGLNNLRGNASWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300
QY 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPPLLDLEQVTIYSLSRWSNTQYMMNMW 360
DB 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPPLLDLEQVTIYSLSRWSNTQYMMNMW 360
QY 361 GGHKLEFRITGTLNISTQSTNTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNGVPR 420
DB 361 GGHKLEFRITGTLNISTQSTNTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNGVPR 420
QY 421 VDFHWFVTHPTASDNFYYPGVAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWFVTHPTASDNFYYPGVAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535
DB 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
/ Sequence 4, Application US/08100709
/ Patent No. 5322687
/ GENERAL INFORMATION:
/ APPLICANT: Donovan, William P.
/ APPLICANT: Tan, Yeping
/ APPLICANT: Jany, Christine S.
/ APPLICANT: Gonzalez Jr., Jose M.
/ TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryETS
/ TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
/ ADDRESSEE: Nadel
/ STREET: 1601 Market Street, 36th Floor
/ CITY: Philadelphia
```

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/ STATE: Pennsylvania
/ COUNTRY: U.S.A.
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/100,709
/ FILING DATE: 19930729
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Egolf, Christopher
/ REGISTRATION NUMBER: 27633
/ REFERENCE/DOCKET NUMBER: 7205-49
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-757-1590
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1229 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-100-709-4

Query Match 64.8%; Score 2437.5; DB 1; Length 1229;
Best Local Similarity 65.4%; Pred. No. 3.1e-209;
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLNK-ETDIELQ-NINHEHEDCLKMSYENVEPFFVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPTVSNPSTQMNLSPDARIEDSLCAEVANNIDPFVSASTVQTGINIAGRI 66
QY 71 ICTLGVPPAGQVASYLSFILGELWPKGKNQWEIFMEHVBEIINQKISTYARKALTDLKG 130
DB 67 LGVLGVPPAGQVASYLSFILGELWPKGKNQWEIFMEHVBEIINQKISTYARKALTDLKG 126
QY 131 LGDALAVYHDSLSWGNRNNTARSVVKVSKQYIALELMFVKLPSFAVSGEEVPLLPYA 190
DB 127 LGRYRSYQQALETWLDNENDARSIIILERYVALELDITAIPLPRIRNEEVPLLMVYA 186
QY 191 QAANLHLLLRDASIFGKEWGLSSSEISITFYNRQVERAGDYSYHCVKWTYSTGLNNLRGN 250
DB 187 QAANLHLLLRDASIFGSEWGNMSSDVNQYQEQIRYTEYSNHCYQWNTGLNNLRGN 246
QY 251 AESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAIGTVHPHPSFT 310
DB 247 AESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAIGTVHPHPSFT 306
QY 311 STTWYNNAPSAIEAAVVRNPPLLDLEQVTIYSLSRWSNTQYMMNMWGHKLEFRIT 370
DB 307 STTWYNNAPSAIEAAVVRNPPLLDLEQVTIYSLSRWSNTQYMMNMWGHKLEFRIT 366
QY 371 GGTNLNISTQST-NTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNGVPRVDFHWFV 429
DB 367 GGTNLNISTQST-NTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNGVPRVDFHWFV 422
QY 430 HPIASDNFYYPG-----YAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 482
DB 423 --INPQNIYERGATTYSQYQGVIGIQLFDSLETLPETTERPNERNYESYSHRLSHIGLIS 480
QY 483 HVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNIG 542
DB 481 TRAPVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNIG 540
QY 543 TFGDIRVNPFPAGQVRYRIRYASTDILQFHTSINGKAINOCNFSATWNRGSDLDYKTF 602
DB 541 TFGDIRLNLNVPLSQRYRIRYASTDILQFHTSINGKAINOCNFSATWNRGSDLDYKTF 600
QY 603 RTVGFTTPPSFLDVQSTFTTIGAWNNSGNEVVIDRIEFVPEVTEYAEVDFEKAQSKVTA 662
DB 601 RTAGFSTPFNFAQSTFTTIGAWNNSGNEVVIDRIEFVPEVTEYAEVDFEKAQSKVTA 659
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663 LFTSTNPRGLKTDVYHIDQVSNVLSDEYFLDEKRELFEIVKYANLHIERM 719  
660 LFTSTNPRRLKTDVTHIDQVSNVACLSDDEFLDEKRELFEKVYAKRLSDERNL 716

Db  
Qy

RESULT 8  
US-08-176-865-4  
; Sequence 4, Application US/08176865  
; Patent No. 5616319  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yiping  
; APPLICANT: Jose M.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/176,865  
; FILING DATE: 30-DEC-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: US 08/100,709  
; FILING DATE: 29-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Egoif, Christopher  
; REGISTRATION NUMBER: 27633  
; REFERENCE/DOCKET NUMBER: 7205-49  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-757-1590  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1229 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-176-865-4

Query Match 64.8%; Score 2437.5; DB 1; Length 1229;  
Best Local Similarity 65.4%; Pred. No. 3.1e-209;  
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

Qy 13 SSNAKVDKITDSLKN-ETDIELO-NINHEDCLKMEYENVEPFVSASTIQTGIGIAGKI 70  
7 NENIILNALSIPVNSPTQNNLSPDARIEDSLCAEVANNIDPFVSASTVQGINIAGRI 66  
71 LGTLGVFPAGQVSLYSFIIGELWPKGNQWEIIFMEHVEIINQKISTYARNKALTDLAG 130  
67 LGVLGVFPAGQVSLYSFIIGELWPKGNQWEIIFMEHVEIINQKISTYARNKALTDLAG 126  
131 LGDALAVTHDSLESVGNRNTRARSVVKSYIALELMFVQKLPSPAVSGEEVPLPIYA 190  
127 LGRGVRSQQALLETWLNDRNDRSIIILERYVALELDITTAIPLFRINEEVPLLMVYA 186  
191 QAAHLHLLLRDASIFGKRWGLSSSEISTFYNQVERAGDYSVHCVKWYSTGLNLRGTN 250  
187 QAAHLHLLLRDASIFGKRWGLSSSEISTFYNQVERAGDYSVHCVKWYSTGLNLRGTN 246  
251 AESWVRYNQPRDMLVLDLVALFPSTDTQMYPIKTTAQLTREVYTDATIGTVHPHPSFT 310

Db  
Qy

1247 AESWLRYNQPRDMLVLDLVALFPSTDTQMYPIKTTAQLTREVYTDATIGTVHPHPSFT 306  
311 STTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVTVIYLLSEWNTQYMMNGHKLFRFTI 370  
307 STWYNNNAPSFAIAEAAVVRNPHLLDFLEQVTVIYLLSEWNTQYMMNGHKLFRFTI 366  
371 GGTINISTQGST-NTSINPVTLPTSDVYRTESLAGNLFLTPQVNGVPRVDFHMKFVT 429  
367 GGTINISTQGST-NTSINPVTLPTSDVYRTESLAGNLFLTPQVNGVPRVDFHMKFVT 422  
430 HPIASDNFYFPG-----YAGICTQLODSNENLPPPEATQPNYESYSHLSHIGLISAS 482  
423 --INPQNIYERGATTYQYQGVGLQFDSSETLPPETTERPNYESYSHLSHIGLISAS 480  
483 HVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVRPGPFTGDDILRRNTG 542  
481 TIRAPVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVRPGPFTGDDILRRNTG 540  
543 TEGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNGEDLDYKTF 602  
541 TEGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNGEDLDYKTF 600  
603 RTVGFTTTPSFLLDVOSTFTIGANWPFSSGNEVYIDRIEFPVVEVYEAIDPEKAQKVTA 662  
601 RTAGFSTFPFNLAQSTFTLGAQSPFN-OEVIIDRVFVPAEVIPEAYDLERAQKAVNA 659  
663 LFTSTNPRGLKTDVYHIDQVSNVLSDEYFLDEKRELFEIVKYANLHIERM 719  
660 LFTSTNPRRLKTDVTHIDQVSNVACLSDDEFLDEKRELFEKVYAKRLSDERNL 716

Db  
Qy

RESULT 9  
US-08-474-038-4  
; Sequence 4, Application US/08474038  
; Patent No. 5679343  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yiping  
; APPLICANT: Jose M.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/474,038  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION NUMBER: US 08/176,865  
; FILING DATE: 30-DEC-1993  
; APPLICATION NUMBER: US 08/100,709  
; FILING DATE: 29-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Egoif, Christopher  
; REGISTRATION NUMBER: 27633  
; REFERENCE/DOCKET NUMBER: 7205-49  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-757-1590  
; INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1229 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-474-038-4

Query Match 64.8%; Score 2437.5; DB 1; Length 1229;  
Best Local Similarity 65.4%; Pred. No. 3.1e-209;  
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

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QY 13 SSNAKVDKISTDLKLN-ETDIELQ-NINHEDCLKMSEYENVEPVFSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPVSNPSTQMNLSDPARIEDSLCAEVNNDIPFVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPAGQVASFYSLFGLWPKGKQWEIFMEHVEEIIINOKISTVARNKALDILKG 130
DB 67 LGVLGVPPAGQVASFYSLFGLWPKGKQWEIFMEHVEEIIINOKISTVARNKALDILKG 126
QY 131 LGDALAVYHDSLESVWGNRNTRARSVKQSYIALELMFVQKLPSPAVSGEEVPLPIYA 190
DB 127 LGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPFRIRNEEVPLLMVYA 186
QY 191 QAAHLHLLLRDASIFGKEWGLSSSISFTFYNRQVERAGDYSYCHVKWYSTGLNNLRGTN 250
DB 187 LGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPFRIRNEEVPLLMVYA 186
QY 251 AESSWRYNQFRDMLTLMVLVALPSPDYTPMYPIKTTAQLTREVVTDGIGTVHPHPSFT 310
DB 247 AESSWRYNQFRDMLTLMVLVALPSPDYTPMYPIKTTAQLTREVVTDGIGTVHPHPSFT 306
QY 311 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLFRFTI 370
DB 307 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLFRFTI 366
QY 371 GGTLLNSTQGST-NTSINPVTLPFTSRDVRVYRTESLAGLNLFLTQPVNGVPRVDFHKKFT 429
DB 367 GGTLLNSTQGST-NTSINPVTLPFTSRDVRVYRTESLAGLNLFLTQPVNGVPRVDFHKKFT 422
QY 430 HPIASDNFYYPG-----YAGTGTQLQDSNELPPEATGQPNYESYHRLSHIGLISAS 482
DB 423 --INPQNIYERGATTYSQPYQGVIGLFPDSELPETTERPNYESYHRLSHIGLIGN 480
QY 483 HVKALVSWTHRSADRTNTIENPSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTG 542
DB 481 TLRAPIVSWTHRSADRTNTIENPSITQIPLVKALNLSHGVTVVGGPGFTGGDILRRNTG 540
QY 543 TFGDIRVNNPPAQRYRIRYASTITDLOFHTSINGKAINQGNFATWNRGEBDLYKTF 602
DB 541 TFGDIRLNVPLSQRYRIRYASTITDLOFHTSINGKAINQGNFATWNRGEBDLYKTF 600
QY 603 RTVGFTTPSFLDVQSTFTTIGAMNFSNGEVYIDRIEFPVVEVYEAEDFEKAQEKVTA 662
DB 601 RTAGFTSPNFLNAQSTFTTIGAQFSN-QEVIYIDRVEFPAEYTFEAEYDLERAQAKVNA 659
QY 663 LFTSTNPRGLKTDVQHYHDQVNLVSESLSDEFYLDKRELPFIKVIYANELHIERNM 719
DB 660 LFTSTNPRGLKTDVQHYHDQVNLVSESLSDEFYLDKRELPFIKVIYAKRLSDERNL 716
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## RESULT 10

US-08-779-046-4

Sequence 4, Application US/08779046

Patent No. 5854053

GENERAL INFORMATION:

APPLICANT: Donovan, William P.

APPLICANT: Tan, Xuping

APPLICANT: Jany, Christine S.

APPLICANT: Gonzalez Jr., Jose M.

TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5

TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
ADDRESSEE: Nadel  
STREET: 1601 Market Street, 36th Floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19103

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/779,046  
FILING DATE: 06-JAN-1997  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/100,709  
FILING DATE: 29-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Egolf, Christopher  
REGISTRATION NUMBER: 27633  
REFERENCE/DOCKET NUMBER: 7205-49  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-757-1590  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1229 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-779-046-4

Query Match 64.8%; Score 2437.5; DB 2; Length 1229;

Best Local Similarity 65.4%; Pred. No. 3.1e-209;

Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

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QY 13 SSNAKVDKISTDLKLN-ETDIELQ-NINHEDCLKMSEYENVEPVFSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPVSNPSTQMNLSDPARIEDSLCAEVNNDIPFVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPAGQVASFYSLFGLWPKGKQWEIFMEHVEEIIINOKISTVARNKALDILKG 130
DB 67 LGVLGVPPAGQVASFYSLFGLWPKGKQWEIFMEHVEEIIINOKISTVARNKALDILKG 126
QY 131 LGDALAVYHDSLESVWGNRNTRARSVKQSYIALELMFVQKLPSPAVSGEEVPLPIYA 190
DB 127 LGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPFRIRNEEVPLLMVYA 186
QY 191 QAAHLHLLLRDASIFGKEWGLSSSISFTFYNRQVERAGDYSYCHVKWYSTGLNNLRGTN 250
DB 187 LGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPFRIRNEEVPLLMVYA 186
QY 251 AESSWRYNQFRDMLTLMVLVALPSPDYTPMYPIKTTAQLTREVVTDGIGTVHPHPSFT 310
DB 247 AESSWRYNQFRDMLTLMVLVALPSPDYTPMYPIKTTAQLTREVVTDGIGTVHPHPSFT 306
QY 311 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLFRFTI 370
DB 307 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGGHKLFRFTI 366
QY 371 GGTLLNSTQGST-NTSINPVTLPFTSRDVRVYRTESLAGLNLFLTQPVNGVPRVDFHKKFT 429
DB 367 GGTLLNSTQGST-NTSINPVTLPFTSRDVRVYRTESLAGLNLFLTQPVNGVPRVDFHKKFT 422
QY 430 HPIASDNFYYPG-----YAGTGTQLQDSNELPPEATGQPNYESYHRLSHIGLISAS 482
DB 423 --INPQNIYERGATTYSQPYQGVIGLFPDSELPETTERPNYESYHRLSHIGLIGN 480
QY 483 HVKALVSWTHRSADRTNTIENPSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTG 542
DB 481 TLRAPIVSWTHRSADRTNTIENPSITQIPLVKALNLSHGVTVVGGPGFTGGDILRRNTG 540
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Salivanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-448-170-10

Query Match 62.1%; Score 2335.5; DB 1; Length 488;
Best Local Similarity 89.5%; Pred. No. 9.6e-201;
Matches 445; Conservative 13; Mismatches 30; Indels 9; Gaps 1;

QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P F V S A S T I 60
DB 1 M K S K N Q M H Q S L S N N A T V D K N F T G S L E N N T N T E L Q N F N H -----E G I E P P F V S V S T I 51

QY 61 Q T G I G I A G K I L G T L G V P P A G Q V A S Y S F I L G E L W P K G K N Q W E I F M E H V E I I N Q K I S T Y A 120
DB 52 Q T G I G I V K I L G N I G V P P A G Q V A S Y S F I L G E L W P K G S Q W E I F M E H V E I I N Q K I S T Y A 111

QY 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A S V V K S Q Y I A L E I M F V Q L P S F A V S G 180
DB 112 R N K A L A D L K G L G D A L A V Y H S L E S W I E N R N N T R S V V K S Q Y I T L E L M F V Q S L P S F A V S G 171

QY 181 E E V P L L P I Y A Q A A N L H L L R D A S I F G K W G L S S S E I S T F Y N R Q V E R A G D Y S H C V K W Y S 240
DB 172 E E V P L L P I Y A Q A A N L H L L R D A S I F G K W G L S D S E I S T F Y N R Q S K S E Y S D H C V K W Y N 231

QY 241 T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 300
DB 232 T G L N L M G N N A E S W R Y N Q F R R D M T L M V L D L V A L P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 291

QY 301 G T V H P H P S F T S T T W Y N N N A P S F A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q T M N M W 360
DB 292 G T V H P H P S F T S T T W Y N N N A P S F T E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q T M N M W 351

; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,170
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: M/S 102DCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-961-803-10

Query Match 62.1%; Score 2335.5; DB 3; Length 488;
Best Local Similarity 89.5%; Pred. No. 9.6e-201;
Matches 445; Conservative 13; Mismatches 30; Indels 9; Gaps 1;

QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P F V S A S T I 60
DB 1 M K S K N Q M H Q S L S N N A T V D K N F T G S L E N N T N T E L Q N F N H -----E G I E P P F V S V S T I 51

QY 61 Q T G I G I A G K I L G T L G V P P A G Q V A S Y S F I L G E L W P K G K N Q W E I F M E H V E I I N Q K I S T Y A 120
DB 52 Q T G I G I V K I L G N I G V P P A G Q V A S Y S F I L G E L W P K G S Q W E I F M E H V E I I N Q K I S T Y A 111

QY 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A S V V K S Q Y I A L E I M F V Q L P S F A V S G 180
DB 112 R N K A L A D L K G L G D A L A V Y H S L E S W I E N R N N T R S V V K S Q Y I T L E L M F V Q S L P S F A V S G 171

QY 181 E E V P L L P I Y A Q A A N L H L L R D A S I F G K W G L S S S E I S T F Y N R Q V E R A G D Y S H C V K W Y S 240
DB 172 E E V P L L P I Y A Q A A N L H L L R D A S I F G K W G L S D S E I S T F Y N R Q S K S E Y S D H C V K W Y N 231

QY 241 T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 300
DB 232 T G L N L M G N N A E S W R Y N Q F R R D M T L M V L D L V A L P S Y D T O M Y P I K T T A Q L T R E V Y T D A I 291

QY 301 G T V H P H P S F T S T T W Y N N N A P S F A E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q T M N M W 360
DB 292 G T V H P H P S F T S T T W Y N N N A P S F T E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q T M N M W 351

Best Local Similarity 64.0%; Pred. No. 1.8e-192;  
Matches 440; Conservative 77; Mismatches 157; Indels 13; Gaps 5;  
QY 361 GGKLEPRTIGTINTSTQSTWTSINPVTLPFTSRDVTYRTESLAGLNLFLTPQVNGVPR 420  
Db 352 GGKLEPRTIGTINTSTQSTWTSINPVTLPFTSRDVTYRTESLAGLNLFLTPQVNGVPR 411  
QY 421 VDFHWKVTHTPIASDNFYPGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLIS 480  
Db 412 VDFHWKVTHTPIASDNFYPGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLIS 471  
QY 481 ASHKALVYSWTHRSAD 497  
Db 472 ASHKALVYSWTHRSAD 488  
RESULT 14  
US-07-951-715A-7  
; Sequence 7, Application US/07951715A  
; Patent No. 5625136  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent In Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/951,715A  
; FILING DATE: 25-SEP-1992  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8615  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1207 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-951-715A-7

QY 40 EDCKMSEYENVPFVSASTIQGTIGIAGIKILCTGVPPAGQVASYLSFILGELWPKGN 99  
Db 10 EDSICIAEGNNIDPFVSASTVQTGINIAGILGVLPAGQVASYLSFILGELWPKGRD 69  
QY 100 QWEIFMEHVEIINQKISTYARNKALTDLKLGDALAVYHDSLESVWGNRNTRASVVK 159  
Db 70 QWEIFLEHVEQLNQITENARTALRLQGLDSFRAYQQSLEDLWENRDDRARTSVLY 129  
QY 160 SQYIALELMFVKQLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEIST 219  
Db 130 TOYIALELDLFLNAPLFAIRNQEVPLMVAQAANLHLLLRDASLPGSEFGLTSQEIQR 189  
QY 220 FYNQVEAGDYSYHCVKWTSTGLNNLRGTNAESVRYNQFRDMLTMLDLVALPFSYD 279  
Db 190 YFERQVETRDYSDYCVENWTGLNSLRGTNAESVRYNQFRDMLTMLDLVALPFSYD 249  
QY 280 TOMYPIKTTAQLTREVVYDAIGTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDEL 339  
Db 250 TRTYPINTSAQLTREVVYDAIGAT--GVNMAWMWYNNAPSPSAIEAAVVRNPHLLDEL 307  
QY 340 EQVTIYILLSRWSNTQYNNMGHKLPRITIGGTILNISTQSTWTSINPVTLPFTSRD 399  
Db 308 EQLTIFSSASSRWSNTRHWTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTSRD 367  
QY 400 RTESLAGLNLFL--LTQPVNGVPRVDFHWKVTHTP-----IASDNFYPGYAGIGTQLODS 452  
Db 368 RTESYAGVLLWGIYLEPIHGVPTVRFNF--TNQNISDRGTANYSQP--YESPGLQLKDS 423  
QY 453 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIPNSITQPL 512  
Db 424 ETELPPEPTTERPNYESYSHRLSHIGLILQSRVNVVYVSWTHRSADRTNTIPNRIQIPM 483  
QY 513 VKAFNLSSGAAVVRGPGFTGGDILRRRTNTGTGDIRVNVNPPFAQRYVRIRYATTDLIQ 572  
Db 484 VKASELPQGTTVVRGPGFTGGDILRRRTNTGSGPIRVTVNGPLTQRYRIGFYASTVD 543  
QY 573 FHTSINGKAINQGNFSATNARGEDLDYKTFRTVGTTPSPFLDVOSTFTTIGAWNFSSGNE 632  
Db 544 FVSRGGTTVNPRFLRTNWSGDELKYGNGFVRRATPTTFTTQIQDIIRTSIQGLSGNCE 603  
QY 633 VIIDRIEFVPEVTEAEYDFAKQKVTALFTSTNPRGLKTDVXDYHDDQVSNLVESLUS 692  
Db 604 VIIDKIEIIPVTATFAEYDLEAEQAVNALFTNTNPRKLTVDYDHYDQVSNLVACILUS 663  
QY 693 DEFYLDKRELFEIVKYNELHIERNM 719  
Db 664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 15  
US-08-459-448A-7  
; Sequence 7, Application US/08459448A  
; Patent No. 5859336  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8582
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-448A-7

Query Match 59.8%; Score 2250.5; DB 2; Length 1207;
Best Local Similarity 64.0%; Pred. No. 1.8e-192;
Matches 440; Conservative 77; Mismatches 157; Indels 13; Gaps 5;
Qy 40 EDCLKMSEVENPFPVSASTIQTGIGIAGKILGTGVPAGQVASYSLFGLGELWPKGN 99
Db 10 EDSLCTAEGNIDPFPVSASTVQTGINIAGKILGTGVPAGQVASYSLFGLGELWPKGRD 69
Qy 100 QWEIFMEHVEEIIINQKISTYARNKALTDLKGDLALAVYHDSLESWVGNNNTARSVVK 159
Db 70 QWEIFLEHVEQLINQITENARNATALRQLGDSFRAVQQSLEDWLENRDDARTSVLY 129
Qy 160 SQVIALELMPVKLPSPFVSGSEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEIST 219
Db 130 TQVIALELDFLNAAMPLFAIRNQEVPLLMVYQAANLHLLLRDASLFGSEFGLTSQEIQR 189
Qy 220 FYNRQVERAGDYSYCHVKYSTGLNLRGTNAESWRYNQFREDMTLWLDLVALFPSYD 279
Db 190 YBERQVERTRDYSYDCEVMTNTGLNSLRGTNAESWRYNQFREDMTLWLDLVALFPSYD 249
Qy 280 TOMYPIKTTAQLTRVYVTDAGTVTHPHPSFTSTWTNNNAPSFAIEAAVVRNPHLLDFL 339
Db 250 TRYTPINTSAQLTRVYVTDAGT--GVNMASSNNWNNNAPSFAIEAAAIRSPHLLDFL 307
Qy 340 EQVTIYSLLRWNTQYMNWGGHKLFFRTIGTGLNISTOGSTNTSINPVTLPFTSRDXY 399
Db 308 EQLTIFSASSRWENRTHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTSRDXY 367
Qy 400 RTESLAGLNLF--LTQPVNCGPVKVDHFKVTHP-----IASDNFYYPGYAGIGTQLQDS 452
Db 368 RTESYAGVLLGWLYLEPIHGVPTRVFNF---TNPQNISDRGTANYSQP--YESPGLQLKDS 423

Qy 453 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIENPSITQIPL 512
Db 424 ETELPPEATTERPNYESYSHRLSHIGLILQSRVNVVPVYSWTHRSADRTNTIGPNRIQIPM 483
Qy 513 VKAFNLSSGAAVVRGPGFTGGDILARTNTGTGDIRVNVINPPFAORYRVRIRVASTDLQ 572
Db 484 VKASELPQGTTVVRGPGFTGGDILARTNTGGFGPIRVTVNGPLTQRYRIGFRYASTVDFD 543
Qy 573 FHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGTFTTTFSPFLDVQSTFTIGAWNFSSGNE 632
Db 544 FVFSRGTTVNVNFRFLRTMNSGDELKYGNFVRRATFTTFTTQIQDIIIRTSIQGLSGNGE 603
Qy 633 VYIDRIEFVPEVTEYEAAYDFEKAQEKVTALTFTSNPRGLKTDVDYHIDQVSNLVESLS 692
Db 604 VYIDKIEIIPVTATPEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLS 663
Qy 693 DEFYLDKRELEFEIVKYANELHIERNM 719
Db 664 DEFCLDKRELEKVKYAKRLSDERNL 690

Search completed: February 14, 2005, 20:59:03
Job time : 24.3302 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2005, 20:20:21 ; Search time 98.3514 Seconds  
(without alignments)  
2827.419 Million cell updates/sec

Title: US-10-019-823B-56

Perfect score: 3762

Sequence: 1 MKLKNQDKHQFSFSSNAKVCK.....KRELFEIVKYANELHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 segs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3762	100.0	719	4	AAB66909 Insectici
2	3762	100.0	719	6	AAB66909 Insectici
3	3753	99.8	719	4	AAB66909 Insectici
4	3749	99.7	719	4	AAB66911 Insectici
5	3749	99.7	719	6	AAB66911 Insectici
6	3743	99.5	719	4	AAB66908 Insectici
7	3743	99.5	719	6	AAB66908 Insectici
8	3743	99.5	719	6	AAB66912 Insectici
9	3741	99.4	719	2	AAB66912 Insectici
10	3739	99.4	719	4	AAB66910 Insectici
11	3739	99.4	719	6	AAB66910 Insectici
12	3730.5	99.2	718	6	AAB66907 Insectici
13	3724.5	99.0	718	4	AAB66907 Insectici
14	3534	93.9	719	7	ADMT4717 B. thurin
15	3503	93.1	719	4	AAB66912 Insectici
16	3503	93.1	719	6	AAB66912 Insectici
17	3459.5	92.0	710	4	AAB66910 Insectici
18	3380	89.8	719	3	ABO7073 Bacillus
19	3379	89.8	719	2	AAW49089 Bacillus
20	3295	87.6	1217	4	AAU02092 Bacillus
21	2719	72.3	1208	4	AAU02093 Bacillus
22	2439	64.8	1230	8	ADK98484 B. thurin
23	2439	64.8	1230	8	ADK98489 B. thurin
24	2439	64.8	1230	8	ADK98481 B. thurin
25	2439	64.8	1230	8	ADK98491 B. thurin

26	2439	64.8	1230	8	ADK98487 B. thuring
27	2437.5	64.8	1229	2	AAR54074 CryETs. 2
28	2437.5	64.8	1229	2	AAR54074 CryETs. 2
29	2437.5	64.8	1229	2	AAW35259 Bacillus
30	2437.5	64.8	1229	2	AAW17699 CryETs. 3
31	2437.5	64.8	1229	2	AAW87633 CryETs. pr
32	2437.5	64.8	1229	2	AAW30923 B. thurin
33	2437.5	64.8	1229	8	ADK98479 B. thuring
34	2335.5	62.1	488	2	AAW44322 Bacillus
35	2335.5	62.1	488	4	AAW19947 Bacillus
36	2258.5	60.0	1209	4	AAR50955 Bacillus
37	2249.5	59.8	1227	2	AAU02094 Chimeric
38	2180.5	58.0	1227	2	AAW44321 Bacillus
39	2180.5	58.0	1227	4	AAW19950 Bacillus
40	2171.5	57.7	1227	4	AAU02046 B. thurin
41	2156.5	57.3	1186	2	AAW16796 Amino aci
42	2141.5	56.9	1221	4	AAU00421 B. thurin
43	2127.5	56.6	1221	4	AAU00420 B. thurin
44	2101	55.8	1228	4	AAB84628 Amino aci
45	2101	55.8	1228	4	AAB84628 Amino aci

ALIGNMENTS

RESULT 1  
AAB66909  
ID AAB66909 standard; protein; 719 AA.  
AC AAB66909;  
XX XX  
DT 12-APR-2001 (first entry)  
DE Insecticidal protein cryIIa3.  
XX XX  
KW Insecticide; transgenic plant; insect-resistance.  
XX XX  
OS Paecilomyces sp.  
XX XX  
PN WO200100841-A1.  
XX XX  
PD 04-JAN-2001.  
XX XX  
PF 23-JUN-2000; 2000WO-GB002457.  
XX XX  
PR 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX XX  
PA (ZENE ) ZENECA LTD.  
XX XX  
PI Griffin J., Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX XX  
DR WPI; 2001-123015/13.  
XX XX  
PT Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
production.  
XX XX  
PS Claim 14; Page 57-59; 72pp; English.  
XX XX  
CC The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
SQ Sequence 719 AA;

Query Match 100.0%; Score 3762; DB 4; Length 719;  
Best Local Similarity 100.0%; Pred. No. 3.5e-294;  
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQININHEDCIKMSEYENVEPVSASTI 60  
DB 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQININHEDCIKMSEYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTLGVFPAGQVASYLFIKELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTLGVFPAGQVASYLFIKELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
QY 121 RNKALTDLKGDLGALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFVSG 180  
DB 121 RNKALTDLKGDLGALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFVSG 180  
QY 181 BEVPLPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNQVERAGDYSYHCVKWS 240  
DB 181 BEVPLPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNQVERAGDYSYHCVKWS 240  
QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSPYDTQMPYIKTTAQLTREVTYDAI 300  
DB 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSPYDTQMPYIKTTAQLTREVTYDAI 300  
QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDPLEQVITYSLLSRWSNTQYNNMW 360  
DB 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDPLEQVITYSLLSRWSNTQYNNMW 360  
QY 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420  
DB 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420  
QY 421 VDFHWKLVTHPSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 480  
DB 421 VDFHWKLVTHPSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 480  
QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNIINPPFAQRVVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDDLYK 600  
DB 541 TGTFGDIRVNIINPPFAQRVVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDDLYK 600  
QY 601 TPTVTGFTTPTFSDVQSTFTTGAMNFSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
DB 601 TPTVTGFTTPTFSDVQSTFTTGAMNFSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFFYLDEKRELFEIVKYANELHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFFYLDEKRELFEIVKYANELHIERNM 719

## RESULT 2

AAE36273 standard; protein; 719 AA.

AAE36273;

26-JUN-2003 (first entry)

B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.

Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

Bacillus thuringiensis.

WO200298911-A2.

12-DEC-2002.

30-MAY-2002; 2002MO-GB002666.

07-JUN-2001; 2001GB-00013900.

(SYGN) SYNGENTA LTD.

PI  
XX  
DR  
XX  
PT  
PT  
XX  
PS  
XX  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
XX  
SQ

Vincent JL, Viner R;  
WPI; 2003-175137/17.  
New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
Claim 12; Page 47-50; 67pp; English.

The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

Sequence 719 AA;

Query Match 100.0%; Score 3762; DB 6; Length 719;

Best Local Similarity 100.0%; Pred. No. 3.5e-294;

Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQININHEDCIKMSEYENVEPVSASTI 60

1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQININHEDCIKMSEYENVEPVSASTI 60

61 QTGIGIAGKILGTLGVFPAGQVASYLFIKELWPKGNQWEIFMEHVEEIIINQKISTYA 120

61 QTGIGIAGKILGTLGVFPAGQVASYLFIKELWPKGNQWEIFMEHVEEIIINQKISTYA 120

121 RNKALTDLKGDLGALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFVSG 180

121 RNKALTDLKGDLGALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFVSG 180

181 BEVPLPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNQVERAGDYSYHCVKWS 240

181 BEVPLPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNQVERAGDYSYHCVKWS 240

241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSPYDTQMPYIKTTAQLTREVTYDAI 300

241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSPYDTQMPYIKTTAQLTREVTYDAI 300

301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDPLEQVITYSLLSRWSNTQYNNMW 360

301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDPLEQVITYSLLSRWSNTQYNNMW 360

361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420

361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420

421 VDFHWKLVTHPSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 480

421 VDFHWKLVTHPSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 480

481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540

481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540

541 TGTFGDIRVNIINPPFAQRVVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDDLYK 600

541 TGTFGDIRVNIINPPFAQRVVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDDLYK 600

601 TPTVTGFTTPTFSDVQSTFTTGAMNFSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660

601 TPTVTGFTTPTFSDVQSTFTTGAMNFSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660

661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFFYLDEKRELFEIVKYANELHIERNM 719

661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFFYLDEKRELFEIVKYANELHIERNM 719

RESULT 3  
AAU02095  
ID AAU02095 standard; protein; 719 AA.  
XX  
AC AAU02095;  
XX  
DT 07-SEP-2001 (first entry)  
XX  
DE Bacillus thuringiensis partial mutant CryIIa.  
XX  
DE Crystal protein; CryIIa; CryIIa; moth; butterfly; Colorado potato beetle;  
KW mutant; mutein.  
XX  
OS Bacillus thuringiensis.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..119  
FT Protein /label= signal\_peptide  
FT Protein 20..719  
FT Protein /label= Mature\_CryIIa  
XX  
PN EP1099760-A1.  
XX  
PD 16-MAY-2001.  
XX  
PF 09-NOV-1999; 99BP-00203723.  
XX  
PR 09-NOV-1999; 99BP-00203723.  
XX  
PA (CPRO-) CPRO-DLO CENT PLANTENVERDEDELINGS REPROD.  
XX  
PI De Maagd RA, Bosch HJ;  
XX  
DR WPI: 2001-337141/36.  
DR N-PSDB; AAS04855.  
XX  
XX New hybrid Bacillus thuringiensis hybrid toxins comprising structural  
PT domains derived from at least 2 different crystal proteins, such as  
PT CryIIa and CryIIa, and having insecticidal activity, useful for combating  
PT insects.  
XX  
PS Example; Page 30-32; 43pp; English.  
XX  
CC The sequence is B. thuringiensis (8t) crystal protein CryIIa, the DNA  
CC encoding which was mutated to allow cloning of domain III or domains I  
CC and II, to make the hybrid protoxins of the invention. The hybrid toxins  
CC of the invention, having structural domains I, II and III in this order  
CC starting from the N-terminal derived from at least 2 different crystal  
CC proteins, are useful for protecting plants against pest insects, e.g.  
CC moths, butterflies and Colorado potato beetle or for combating insects  
XX  
SQ Sequence 719 AA;

Query Match 99.8%; Score 3753; DB 4; Length 719;  
Best Local Similarity 99.7%; Pred. No. 1.9e-293;  
Matches 717; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLKNQDKQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60  
DB 1 MKLKNQDKQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTLPVFPAGQVSLYSFILGELWPKQKQWEIFMEHVEEINQKISTVA 120  
DB 61 QTGIGIAGKILGTLPVFPAGQVSLYSFILGELWPKQKQWEIFMEHVEEINQKISTVA 120  
QY 121 RNKALTDLKGGLDALAVYHDSLSLSEWGNRNNTARSVVKSQYIALELMFVKQLPSFAVSG 180  
DB 121 RNKALTDLKGGLDALAVYHDSLSLSEWGNRNNTARSVVKSQYIALELMFVKQLPSFAVSG 180  
QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSISIFYNQVERAGDYSYHCWKWYS 240  
DB 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSISIFYNQVERAGDYSYHCWKWYS 240

QY 241 TGLNNLRGTNAESWVRYNQFRDMDTLMLVLDLVALPSPSYDTQMYPIKTKTQALTRVYTDAI 300  
DB 241 TGLNNLRGTNAESWVRYNQFRDMDTLMLVLDLVALPSPSYDTQMYPIKTKTQALTRVYTDAI 300  
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRPHLLDLEQVTIYSLLSRWSNTQYNNMW 360  
DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRPHLLDLEQVTIYSLLSRWSNTQYNNMW 360  
QY 361 GGHKLEFRITGTLNISTOGSTNTSINPVTLPFTSRDVYRTESLAGLNILFLTOPVNGVPR 420  
DB 361 GGHKLEFRITGTLNISTOGSTNTSINPVTLPFTSRDVYRTESLAGLNILFLTOPVNGVPR 420  
QY 421 VDFHMKFVTHPIASDNFYYPGVAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHMKFVTHPIASDNFYYPGVAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNITIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNITIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEGLDYK 600  
DB 541 TGTFGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEGLDYK 600  
QY 601 TERTVTGFTTFFSFLDVQSTFTTIGAMNFFSGNEVYIDRIEFVPEVYEAAYDPEKAQEKV 660  
DB 601 TERTVTGFTTFFSFLDVQSTFTTIGAMNFFSGNEVYIDRIEFVPEVYEAAYDPEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDHYDQVNLVESLSDEPFLDEKRELFEIVKYANELHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDHYDQVNLVESLSDEPFLDEKRELFEIVKYANELHIERNM 719

RESULT 4  
AAB66911  
ID AAB66911 standard; protein; 719 AA.  
XX  
AC AAB66911;  
XX  
DT 12-APR-2001 (first entry)  
XX  
DE Insecticidal protein cryIIa5.  
XX  
KW Insecticide; transgenic plant; insect-resistance.  
XX  
OS Paecilomyces sp.  
XX  
PN WO200100841-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-GB002457.  
XX  
PR 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX  
DR WPI: 2001-123015/13.  
XX  
PT Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PT production.  
XX  
PS Claim 14; Page 62-64; 72pp; English.  
XX  
CC The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66911 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are





QY 601 TFRVGTTPFSLDVQSTFTTCAMNFFSSGNEVYIDRIEFPVPEVTEAEYDFEKAQEKV 660  
DB 601 TFRVGTTPFSLDVQSTFTTCAMNFFSSGNEVYIDRIEFPVPEVTEAEYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNM 719

RESULT 6  
AAB66908  
ID AAB66908 standard; protein; 719 AA.  
AC AAB66908;  
XX  
DT 12-APR-2001 (first entry)  
XX  
DE Insecticidal protein cryIIa2.  
XX  
KW Insecticide; transgenic plant; insect-resistance.  
XX  
OS Paecilomyces sp.  
XX  
PN WO200100841-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-GB002457.  
XX  
PR 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX  
DR WPI; 2001-123015/13.  
XX  
PT Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PT production.  
XX  
PS Claim 14; Page 55-57; 72pp; English.  
XX  
CC The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB6699 to AAB6901 and AAB6913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX  
SQ Sequence 719 AA;

Query Match 99.5%; Score 3743; DB 4; Length 719;  
Best Local Similarity 99.6%; Pred. No. 1.2e-292;  
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSNNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEFPVSASTI 60  
DB 1 MKLKNQDKHQSFSNNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEFPVSASTI 60  
QY 61 QTGIGTAGKITLGTLPVFPAGQVSLVSPILGELWPKGNQWEIFMEHVEIINQKISTYA 120  
DB 61 QTGIGTAGKITLGTLPVFPAGQVSLVSPILGELWPKGNQWEIFMEHVEIINQKISTYA 120  
QY 121 RNKALTDLKGLDALAVYHDSLSWGNRNNTARSVVKVSYQYIALELMFVKLPSPAVSG 180  
DB 121 RNKALTDLKGLDALAVYHDSLSWGNRNNTARSVVKVSYQYIALELMFVKLPSPAVSG 180  
QY 181 EYVPLPIYAQAANLHLLLRDASIFGKEWGLSSSISITFYNQVERAGDYSYHCVKWYS 240  
DB 181 EYVPLPIYAQAANLHLLLRDASIFGKEWGLSSSISITFYNQVERAGDYSYHCVKWYS 240

QY 241 TGLNLRGTNAESWVRYNQFRDWTLMVLDLVALFPESYDTQMYPIKTTAQLTREVTDAI 300  
DB 241 TGLNLRGTNAESWVRYNQFRDWTLMVLDLVALFPESYDTQMYPIKTTAQLTREVTDAI 300  
QY 301 GTVHPHPSSTSTWYNNNAPSFAEAAVVRPHLLDLEOVYIYSLLSKWSNTQYNNMW 360  
DB 301 GTVHPHPSSTSTWYNNNAPSFAEAAVVRPHLLDLEOVYIYSLLSKWSNTQYNNMW 360  
QY 361 GGHKLEFRITGTLNISTQSTNTSINPVTLPFTSRDVTSTESLAGINLFLTOPVANGVPR 420  
DB 361 GGHKLEFRITGTLNISTQSTNTSINPVTLPFTSRDVTSTESLAGINLFLTOPVANGVPR 420  
QY 421 VDFHWKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATGQPNYESYSHRLSHGLIS 480  
DB 421 VDFHWKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATGQPNYESYSHRLSHGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
QY 541 TGTFGDIRVINPFPFAQRYRVRIRVASTTDLQFHTSINGKAINQGNFSAATMNRGEBLDYK 600  
DB 541 TGTFGDIRVINPFPFAQRYRVRIRVASTTDLQFHTSINGKAINQGNFSAATMNRGEBLDYK 600  
QY 601 TFRVGTTPFSLDVQSTFTTCAMNFFSSGNEVYIDRIEFPVPEVTEAEYDFEKAQEKV 660  
DB 601 TFRVGTTPFSLDVQSTFTTCAMNFFSSGNEVYIDRIEFPVPEVTEAEYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNM 719

RESULT 7  
AAB36272  
ID AAB36272 standard; protein; 719 AA.  
XX  
AC AAB36272;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.  
XX  
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
XX  
OS Bacillus thuringiensis.  
XX  
PN WO200298911-A2.  
XX  
PD 12-DEC-2002.  
XX  
PF 30-MAY-2002; 2002WO-GB002666.  
XX  
PR 07-JUN-2001; 2001GB-00013900.  
XX  
PA (SYGN ) SYNGENTA LTD.  
XX  
PI Vincent JL, Viner R;  
XX  
DR WPI; 2003-175137/17.  
XX  
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
XX  
PS Claim 12; Page 44-47; 67pp; English.  
XX  
CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
CC Antibodies raised to the insecticidal proteins can be used to identify

CC other proteins with insecticidal activity. The present sequence is  
CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This  
CC sequence is used in the invention  
XX  
XX  
SQ Sequence 719 AA;  
Query Match 99.5%; Score 3743; DB 6; Length 719;  
Best Local Similarity 99.6%; Pred. No. 1.2e-292;  
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MKLNQDKHQSFSNAKVDKISTSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
DB 1 MKLNQDKHQSFSNAKVDKISTSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGLVFPAGQVASYLSFILGELWPKGNQWEIPEHVEEIIINOKISTYA 120  
DB 61 QTGIGIAGKILGTGLVFPAGQVASYLSFILGELWPKGNQWEIPEHVEEIIINOKISTYA 120  
QY 121 RNKALTDLKLGLDALAVYHDSLESWVGNNRNRARSVVKQYIALELMFVKLPSPFAVSG 180  
DB 121 RNKALTDLKLGLDALAVYHDSLESWVGNNRNRARSVVKQYIALELMFVKLPSPFAVSG 180  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240  
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240  
QY 241 TGLNNLRGTNAESWRYNQFRDMLVLDLVALPPSYDTOMYDIKTAQITREYVYDAI 300  
DB 241 TGLNNLRGTNAESWRYNQFRDMLVLDLVALPPSYDTOMYDIKTAQITREYVYDAI 300  
QY 301 GTVHPHPSFTSTWYNNNAPSALSAEAAVVRNPHLLDFLEQVITYSLLSRMSNTQYNNMW 360  
DB 301 GTVHPHPSFTSTWYNNNAPSALSAEAAVVRNPHLLDFLEQVITYSLLSRMSNTQYNNMW 360  
QY 361 GGHKLEFRITGTLNISTQSTNTSINPVTLPFTSRDVRRTESLAGLNLFTQPVNGVPR 420  
DB 361 GGHKLEFRITGTLNISTQSTNTSINPVTLPFTSRDVRRTESLAGLNLFTQPVNGVPR 420  
QY 421 VDFHFWFVTHPIASDNFFYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHFWFVTHPIASDNFFYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGGAUVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGGAUVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNIINPPFAQRVRIRYASTTDLQPHTSINGKAINQGNFSTWNRGDLDYK 600  
DB 541 TGTFGDIRVNIINPPFAQRVRIRYASTTDLQPHTSINGKAINQGNFSTWNRGDLDYK 600  
QY 601 TFRVTGFTTDFSLDVQSTFTICAWNPFSSGNEVYIDRIEFPVVEVYEAEDYFEKAQEKV 660  
DB 601 TFRVTGFTTDFSLDVQSTFTICAWNPFSSGNEVYIDRIEFPVVEVYEAEDYFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVNDKHIDQVNLVSLSDYFYLDEKRELFEIVKYVANEILHIERNM 719  
DB 661 TALFTSTNPRGLKTDVNDKHIDQVNLVSLSDYFYLDEKRELFEIVKYVAKOLHIERNM 719  
RESULT 8  
ID ADR89421 standard; protein; 719 AA.  
XX ADR89421;  
AC ADR89421;  
XX 18-NOV-2004 (first entry)  
DT  
XX  
DE cryIIa.  
KW delta-endotoxin; delta-endotoxin associate polypeptide;  
KW expression cassette; transformation; transgenic; plant; bacteria;  
KW lepidoptera; coleoptera; pest; pesticide; resistance;  
KW pesticidal activity.

XX  
OS Bacillus thuringiensis.  
XX WO2004074462-A2.  
XX  
XX  
PD 02-SEP-2004.  
XX  
XX 20-FEB-2004; 2004WO-US005829.  
XX  
XX 20-FEB-2003; 2003US-0448632P.  
XX 20-FEB-2003; 2003US-0448633P.  
PR 20-FEB-2003; 2003US-0448797P.  
PR 20-FEB-2003; 2003US-0448806P.  
PR 20-FEB-2003; 2003US-0448810P.  
PR 20-FEB-2003; 2003US-0448812P.  
PR 19-FEB-2004; 2004US-00781979.  
PR 19-FEB-2004; 2004US-00782020.  
PR 19-FEB-2004; 2004US-00782096.  
PR 19-FEB-2004; 2004US-00782141.  
PR 19-FEB-2004; 2004US-00782570.  
PR 19-FEB-2004; 2004US-00783417.  
XX  
XX (ATHE-) ATHENIX CORP.  
PA Carozzi N, Hargiss T, Kozziel MG, Duck NB, Carr B;  
XX WPI; 2004-635574/61.  
XX  
XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
XX and polypeptides, useful for killing lepidopteran or coleopteran pests or  
XX for producing organisms with pesticide resistance.  
XX  
XX Example 6; SEQ ID NO 33; 178pp; English.  
XX  
XX This sequence represents a delta-endotoxin crystal protein. This protein  
XX was included in the scope of the invention as a comparison to the delta-  
XX endotoxins of the invention. Some of the delta-endotoxin coding sequences  
XX of the invention have alternative start codons, producing more than one  
XX protein from a single open reading frame. The nucleic acid sequences of  
XX the invention are useful in DNA constructs or expression cassettes for  
XX transformation and expression in plants and bacteria. The nucleic acids  
XX and corresponding polypeptides are useful for killing lepidopteran or  
XX coleopteran pests. Compositions containing the delta-endotoxins of the  
XX invention, and methods for their production, are useful for the  
XX production of organisms with pesticide resistance, specifically bacteria  
XX and plants. These organisms are useful for generating altered or improved  
XX delta-endotoxin or delta-endotoxin-associated proteins that have  
XX pesticidal activity, or for detecting the presence of delta-endotoxin or  
XX delta-endotoxin-associated proteins or nucleic acids in products or  
XX organisms.  
XX  
XX Sequence 719 AA;  
Query Match 99.5%; Score 3743; DB 8; Length 719;  
Best Local Similarity 99.6%; Pred. No. 1.2e-292;  
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MKLNQDKHQSFSNAKVDKISTSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
DB 1 MKLNQDKHQSFSNAKVDKISTSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGLVFPAGQVASYLSFILGELWPKGNQWEIPEHVEEIIINOKISTYA 120  
DB 61 QTGIGIAGKILGTGLVFPAGQVASYLSFILGELWPKGNQWEIPEHVEEIIINOKISTYA 120  
QY 121 RNKALTDLKLGLDALAVYHDSLESWVGNNRNRARSVVKQYIALELMFVKLPSPFAVSG 180  
DB 121 RNKALTDLKLGLDALAVYHDSLESWVGNNRNRARSVVKQYIALELMFVKLPSPFAVSG 180  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240  
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240

QY 241 TGLNLAGTVAESWVRYNQRRDMTLMVLVDLVALPFSYDTQMYPIKTTAQLTREVTDAI 300  
 Db 241 TGLNLAGTVAESWVRYNQRRDMTLMVLVDLVALPFSYDTQMYPIKTTAQLTREVTDAI 300  
 QY 301 GTVHPHPSFTSTWYNNAPSPSAIAEAAVVRNPHLLDLEQVITYSLSRWSNTQYNNMW 360  
 Db 301 GTVHPHPSFTSTWYNNAPSPSAIAEAAVVRNPHLLDLEQVITYSLSRWSNTQYNNMW 360  
 QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNFLTPQVNGVR 420  
 Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNFLTPQVNGVR 420  
 QY 421 VDFHWKFVTHPIASDNFYPGYAGIGTQDSENELPPEATGPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFVTHPIASDNFYPGYAGIGTQDSENELPPEATGPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 Db 481 ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTFGDIRVINPFPFAQRVRIYASTTDLPHTSINGKAINQGNFSATMNRGEDLDYK 600  
 Db 541 TGTFGDIRVINPFPFAQRVRIYASTTDLPHTSINGKAINQGNFSATMNRGEDLDYK 600  
 QY 601 TFRVTGFTTTPPSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
 Db 601 TFRVTGFTTTPPSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 719

## RESULT 9

AA08041  
 ID AAR08041 standard; protein; 719 AA.  
 AC AAR08041;  
 XX  
 XX 24-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 27-FEB-1991 (first entry)  
 XX  
 DE 81 kD endotoxin deduced from DNA carried on pJH12.  
 XX  
 XX Crystal; insecticide; toxin; delta endotoxin.  
 XX  
 XX Bacillus thuringiensis; JHCC 4353 and 4835.  
 OS WO9013651-A.  
 PN  
 XX 15-NOV-1990.  
 XX  
 XX 09-MAY-1989; 89GB-00010624.  
 XX  
 XX 09-MAY-1989; 89GB-00010624.  
 XX  
 XX (ICIL ) IMPERIAL CHEM IND PLC.  
 XX  
 XX Blenk RG, Ely S, Tailor RH, Tippet JM;  
 XX WPI; 1990-361486/48.  
 DR N-PSDB; AAQ06636.  
 XX  
 XX Bacillus thuringiensis strains - used for producing an endotoxin for  
 PT protecting plants against insects, partic. Lepidoptera and Coleoptera.  
 XX  
 XX Claim 5; Fig 5-10; 66pp; English.  
 XX  
 XX The sequence carried on pJH12 which was isolated from B. thuringiensis  
 CC strains JHCC4835 and JHCC 4353 (NCIB 40091 and 40090 resp.). The DNA can  
 CC be used to produce transformants E.coli strain MC12022/pJH12 (NCIB 40278,  
 CC or bacteriophage EMBL4 vector (NCIB 40279) or E.coli strain BL21/pJH11

CC (NCIB 40275). The delta-endo- toxin produced by the transformants can be  
 CC used in formulations for combatting Lepidoptera and Coleoptera pests.  
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 719 AA;

Query Match 99.4%; Score 3741; DB 2; Length 719;

Best Local Similarity 99.4%; Pred. No. 1.7e-292;

Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSPPSSNAKVDKISTDSLKNETDTELQNIHEDCLKSEYENPFFVSASTI 60  
 Db 1 MKLKNQDKHQSPPSSNAKVDKISTDSLKNETDTELQNIHEDCLKSEYENPFFVSASTI 60  
 QY 61 QTGIGIAGKILGTGLVPPFAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGLVPPFAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGLDALAVYHDSLESVWGNRNTRASVVKSVQYIALELMFVQKLPSPAVSG 180  
 Db 121 RNKALTDLKGLDALAVYHDSLESVWGNRNTRASVVKSVQYIALELMFVQKLPSPAVSG 180  
 QY 181 EKVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCWKYS 240  
 Db 181 EKVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCWKYS 240  
 QY 241 TGLNLRGNTNASSWRYNQFRDMLMVLVDLVALPFSYDTQMYPIKTTAQLTREVTDAI 300  
 Db 241 TGLNLRGNTNASSWRYNQFRDMLMVLVDLVALPFSYDTQMYPIKTTAQLTREVTDAI 300  
 QY 301 GTVHPHPSFTSTWYNNAPSPSAIAEAAVVRNPHLLDLEQVITYSLSRWSNTQYNNMW 360  
 Db 301 GTVHPHPSFTSTWYNNAPSPSAIAEAAVVRNPHLLDLEQVITYSLSRWSNTQYNNMW 360  
 QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNFLTPQVNGVR 420  
 Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNFLTPQVNGVR 420  
 QY 421 VDFHWKFVTHPIASDNFYPGYAGIGTQDSENELPPEATGPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFVTHPIASDNFYPGYAGIGTQDSENELPPEATGPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 Db 481 ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTFGDIRVINPFPFAQRVRIYASTTDLPHTSINGKAINQGNFSATMNRGEDLDYK 600  
 Db 541 TGTFGDIRVINPFPFAQRVRIYASTTDLPHTSINGKAINQGNFSATMNRGEDLDYK 600  
 QY 601 TFRVTGFTTTPPSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
 Db 601 TFRVTGFTTTPPSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 719

## RESULT 10

AA066910  
 ID AAB66910 standard; protein; 719 AA.  
 XX  
 XX AAB66910;  
 AC  
 XX  
 XX 12-APR-2001 (first entry)  
 DT  
 XX  
 XX Insecticidal protein cryIIa4.  
 DE  
 XX  
 XX Insecticide; transgenic plant; insect-resistance.  
 KW  
 XX  
 XX Paecilomyces sp.

XX PN W0200100841-A1.  
 XX PD 04-JAN-2001.  
 XX 23-JUN-2000; 2000WO-GB002457.  
 XX 29-JUN-1999; 99GB-00015215.  
 XX 23-DEC-1999; 99GB-00030536.  
 XX (ZENE ) ZENECA LTD.  
 XX Griffon J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 XX Vincent JL, Lee MD;  
 XX WPI; 2001-123015/13.  
 XX Novel insecticidal protein obtained from species of Paecilomyces for  
 XX controlling insects, and for insect-resistant transgenic plant  
 XX production.  
 XX Claim 14; Page 60-62; 72pp; English.  
 XX The present invention relates to novel insecticidal proteins obtained  
 XX from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
 XX insecticidal proteins can be used to produce transgenic plants, which are  
 XX insect-resistant. Also, the insecticidal proteins are useful for  
 XX controlling insects by providing them at a locus where insects feed  
 XX Sequence 719 AA;  
 SQ

Query Match 99.4%; Score 3739; DB 4; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 2.5e-292; Indels 0; Gaps 0;  
 Matches 715; Conservative 1; Mismatches 3;

QY 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60  
 DB 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60  
 QY 61 Q T G I G I A G K I L G T L G V P P A G V A S L Y S F I L G E L W P K G N O W E I F M E H V E E I I N O K I S T Y A 120  
 DB 61 Q T G I G I A G K I L G T L G V P P A G V A S L Y S F I L G E L W P K G N O W E I F M E H V E E I I N O K I S T Y A 120  
 QY 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
 DB 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
 QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q V E R A G D Y S H C V K W Y S 240  
 DB 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q V E R A G D Y S H C V K W Y S 240  
 QY 241 T G L N L R G T N A E S W R V N Q R R D M T L M V L D V A L F P S Y D T O M Y P I K T T A Q L R E V Y T D A I 300  
 DB 241 T G L N L R G T N A E S W R V N Q R R D M T L M V L D V A L F P S Y D T O M Y P I K T T A Q L R E V Y T D A I 300  
 QY 301 G T V H P H S F S T T W Y N N A P S F S A E A A V V R N P H L L D F L E Q V T I Y S L L R S W N T Q M N W 360  
 DB 301 G T V H P H S F S T T W Y N N A P S F S A E A A V V R N P H L L D F L E Q V T I Y S L L R S W N T Q M N W 360  
 QY 361 G G H K L E P T T G T L N I S T O G S T N T S I N P V T L P T S R D V V R T E S I A G L N L F L T O P V N G V P R 420  
 DB 361 G G H K L E P T T G T L N I S T O G S T N T S I N P V T L P T S R D V V R T E S I A G L N L F L T O P V N G V P R 420  
 QY 421 V D E H W K F V T H P I A S D N F Y P G Y A G I Q L O D S E N E L P P E A T G P N V E S Y S H R L S H I G L I S 480  
 DB 421 V D F H W K F V T H I A S D N F Y P G Y V G I Q L O D S E N E L P P E A T G P N V E S Y S H R L S H I G L I S 480  
 QY 481 A S H V K A L Y S W T H S A D R T N I E N S I T O I P L V K A F N L S S G A A V V R G P G T G D I L R R T N 540  
 DB 481 A S H V K A L Y S W T H S A D R T N I E N S I T O I P L V K A F N L S S G A A V V R G P G T G D I L R R T N 540  
 QY 541 T G T F G D I R V N P P F A Q R Y R V R I Y A S T T D L Q F H T S I N G K A I N O G N F S A T M N R G E D L D Y K 600

DB 541 T G T F G D I R V N P P F A Q R Y R V R I Y A S T T D L Q F H T S I N G K A I N O G N F S A T M N R G E D L D Y K 600  
 QY 601 T F R T V G F T T P F S F L D V O S T T I G A W N F S S G N E Y I I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
 DB 601 T F R T V G F T T P F S F L D V O S T T I G A W N F S S G N E Y I I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
 QY 661 T A L F T S N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719  
 DB 661 T A L F T S N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719

## RESULT 11

AAE36274

ID AAE36274 standard; protein; 719 AA.

XX AAE36274;

AC AAE36274;

DT 26-JUN-2003 (first entry)

DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.

XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

XX Bacillus thuringiensis.

XX WO200298911-A2.

XX 12-DEC-2002.

XX 30-MAY-2002; 2002WO-GB002666.

XX 07-JUN-2001; 2001GB-00013900.

XX (SYGN ) SYNGENTA LTD.

XX Vincent JL, Viner R;

XX WPI; 2003-175137/17.

XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

XX Claim 12; Page 50-53; 67pp; English.

XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.

XX Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

XX Sequence 719 AA;

Query Match 99.4%; Score 3739; DB 6; Length 719;

Best Local Similarity 99.4%; Pred. No. 2.5e-292;

Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60

DB 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60

QY 61 Q T G I G I A G K I L G T L G V P P A G V A S L Y S F I L G E L W P K G N O W E I F M E H V E E I I N O K I S T Y A 120

DB 61 Q T G I G I A G K I L G T L G V P P A G V A S L Y S F I L G E L W P K G N O W E I F M E H V E E I I N O K I S T Y A 120

QY 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180

DB 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180

QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q V E R A G D Y S H C V K W Y S 240

```
Db 181 EEPVLLPIYQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVRAGDYSCHCKWYS 240
Qy 241 TGLNLRGNTNAESWVRYNQFRDWTLMVLDFALFSDYDTQMPYPIKTTAQLTREVTDAI 300
Db 241 TGLNLRGNTNAESWVRYNQFRDWTLMVLDFALFSDYDTQMPYPIKTTAQLTREVTDAI 300
Qy 301 GTVHPHPSFTSTWYNNAPSPAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTSTWYNNAPSPAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
Qy 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVTESLAGLNFLTPQVNGVPR 420
Db 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVTESLAGLNFLTPQVNGVPR 420
Qy 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLQDSSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLQDSSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVSWTHRSADRTNTIIPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRTN 540
Db 481 ASHVKALVSWTHRSADRTNTIIPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRTN 540
Qy 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Qy 601 TFRVTGFTTTPFSLDVQSTFTIGAMNPFSSGNEVYIDRIEFPVVEVTEAEYDEFEKAQEKV 660
Db 601 TFRVTGFTTTPFSLDVQSTFTIGAMNPFSSGNEVYIDRIEFPVVEVTEAEYDEFEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 719
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## RESULT 12

```
AAE36271
ID AAE36271 standard; protein; 718 AA.
XX
AC AAE36271;
XX
DT 26-JUN-2003 (first entry)
XX
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa1.
XX
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX
OS Bacillus thuringiensis.
XX
PN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN ) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX
PS Claim 12; Page 42-44; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as
```

```
CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
XX
SQ Sequence 718 AA;
Query Match 99.2%; Score 3730.5; DB 6; Length 718;
Best Local Similarity 99.4%; Pred. No. 1.2e-291;
Matches 715; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
Qy 1 MKLKNQDKHQSSSSNAKVDKISTDSLKNETDTELQNIHEDCLKMEYENVEPFAASTI 60
Db 1 MKLKNQDKHQSSSSNAKVDKISTDSLKNETDTELQNIHEDCLKMEYENVEPFAASTI 60
Qy 61 QTGIGTAGKILGTGVPPAGQVASYLFGILGELMPKQKQWEIFMEHVEEIIQKISTYA 120
Db 61 QTGIGTAGKILGTGVPPAGQVASYLFGILGELMPKQKQWEIFMEHVEEIIQKISTYA 120
Qy 121 RNKALTDLKGLDALAVYHDSLESWGNRNNTARSVVKSQVIALELMPFQKLPSPAVSG 180
Db 121 RNKALTDLKGLDALAVYHDSLESWGNRNNTARSVVKSQVIALELMPFQKLPSPAVSG 180
Qy 181 EEPVLLPIYQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVRAGDYSCHCKWYS 240
Db 181 EEPVLLPIYQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVRAGDYSCHCKWYS 240
Qy 241 TGLNLRGNTNAESWVRYNQFRDWTLMVLDFALFSDYDTQMPYPIKTTAQLTREVTDAI 300
Db 241 TGLNLRGNTNAESWVRYNQFRDWTLMVLDFALFSDYDTQMPYPIKTTAQLTREVTDAI 300
Qy 301 GTVHPHPSFTSTWYNNAPSPAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTSTWYNNAPSPAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
Qy 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVTESLAGLNFLTPQVNGVPR 420
Db 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVTESLAGLNFLTPQVNGVPR 420
Qy 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLQDSSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLQDSSENELPPEATGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVSWTHRSADRTNTIIPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRTN 540
Db 481 ASHVKALVSWTHRSADRTNTIIPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRTN 540
Qy 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Qy 601 TFRVTGFTTTPFSLDVQSTFTIGAMNPFSSGNEVYIDRIEFPVVEVTEAEYDEFEKAQEKV 660
Db 601 TFRVTGFTTTPFSLDVQSTFTIGAMNPFSSGNEVYIDRIEFPVVEVTEAEYDEFEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 718
RESULT 13
AAE66907
ID AAE66907 standard; protein; 718 AA.
XX
AC AAE66907;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIa1.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX
```

Paecilomyces sp.	Db	540	TGTFGDIRVNI	PPFAQRVVR	IRYASTTDLQ	PHSTSI	NGKAINQ	GNFSAT	MNRGED	LDYK	599
WO200100841-A1.	Qy	601	TFRVTGFTT	PFSDVQST	FTTIGAWN	SSGNEV	YIDRIE	FPVPEV	TYEAEY	DFEKAQEKV	660
04-JAN-2001.	Db	600	TFXTVGTFT	PFSLDVQST	FTTIGAWN	SSGNEV	YIDRIE	FPVPEV	TYEAEY	DFEKAQEKV	659
23-JUN-2000; 2000WO-GB002457.	Qy	661	TALFTSTNP	RGLKTDVKD	YHIDQV	SNLVES	LSDFS	FYLDKRE	LFELFV	KYANLH	IERNM 719
29-JUN-1999; 99GB-00015215.	Db	660	TALFTSTNP	RGLKTDVKD	YHIDQV	SNLVES	LSDFS	FYLDKRE	LFELFV	KYANLH	IERNM 718
23-DEC-1999; 99GB-00030536.											
(ZENE ) ZENECA LTD.											
Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;											
Vincent JL, Lee MD;											
WPI; 2001-123015/13.											
Novel insecticidal protein obtained from species of Paecilomyces for controlling insects, and for insect-resistant transgenic plant production.											
Claim 14; Page 53-55; 72pp; English.											
The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed											
Sequence 718 AA;											
Query Match 99.0%; Score 3724.5; DB 4; Length 718;											
Best Local Similarity 99.3%; Pred. No. 3.7e-291;											
Matches 714; Conservative 1; Mismatches 3; Indels 1; Gaps 1;											
1 MKLKNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKNSEYENVEPFSASTI	Qy	60									
1 MKLKNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKNSEYENVEPFSASTI	Db	60									
61 QTGIGIAGKILGTGLGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEII	Qy	120									
61 QTGIGIAGKILGTGLGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEII	Db	120									
121 RNKALTDLKGLDALAVYHDSLESWYGNRNTRARSVVKSQYIALELMFVQKLPSFAVSG	Qy	180									
121 RNKALTDLKGLDALAVYHDSLESWYGNRNTRARSVVKSQYIALELMFVQKLPSFAVSG	Db	180									
181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCWKYS	Qy	240									
181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCWKYS	Db	240									
241 TGLNLRGTNAESWVRNQPRDMLVLDLVALFSDYDTOMYPIKTTAQLTREVYTDI	Qy	300									
241 TGLNLRGTNAESWVRNQPRDMLVLDLVALFSDYDTOMYPIKTTAQLTREVYTDI	Db	300									
301 GTVHPHPSFTTWNNAESFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQIMNMW	Qy	360									
301 GTVHPHPSFTTWNNAESFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQIMNMW	Db	360									
361 GGHKLFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNFLTOPVNGVR	Qy	420									
361 GGHKLFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNFLTOPVNGVR	Db	419									
421 VDFHWKFVTHPIADNFIYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHGLIS	Qy	480									
420 VDFHWKFVTHPIADNFIYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHGLIS	Db	479									
481 ASHKALVYSWTHRSADRTNIEPNSITQIPLVKAFLSSGAAVVRGPGFTGGDILRRTN	Qy	540									
480 ASHKALVYSWTHRSADRTNIEPNSITQIPLVKAFLSSGAAVVRGPGFTGGDILRRTN	Db	539									
541 TGTFGDIRVNI	Qy	599	PPFAQRVVR	IRYASTTDLQ	PHSTSI	NGKAINQ	GNFSAT	MNRGED	LDYK	599	

Db 121 RNIALADKGLGDAVYHESLSWTKRNNARATSVVKSQYALPELLFVQKLPSPAVSG 180  
Qy 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSYHCVKWYS 240  
Db 181 EEVPLPIYAQAANLHLLLRDASVFGKEWGLSNSQISTFYNQVERTSDYSDHCVKWYS 240  
Qy 241 TGLNLRGTVNAESWRYNQPRRDMTLMVLVDLVALPFSYDTQMPYPIKTTAQLTREVTDAI 300  
Db 241 TGLNLRGTVNAESWRYNQPRKDMTLMVLVDLIALPFSYDTLVPIKTTSLTREVTDAI 300  
Qy 301 GTVHPSPSTSTWYNNAPSFSAIAA VVRNPHLLDLEQVTIYSLSRWSNTQYMNW 360  
Db 301 GTVHPNAPSTWYNNAPSFSAIAA VVRNPHLLDLEQVTIYSLSRWSNTQYMNW 360  
Qy 361 GGHLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTPQVNGVPR 420  
Db 361 GGHLEFRTIGGLVNTSTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTPQVNGVPR 420  
Qy 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 480  
Db 421 VDFHMKFATLPIASDNFYLYGAGVGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 480  
Qy 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKA FNLSGAAVVRGPGFTGGDILRRTN 540  
Db 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKA FNLSGAAVVRGPGFTGGDILRRTN 540  
Qy 541 TGTFGDIRVNIINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSA TMNRGEDLDYK 600  
Db 541 TGTFGDIRVNIINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSA TMNRGEDLDYK 600  
Qy 601 TPTVTGFTTTPFSDVQSTFTIGAMNPFSSGNEVYIDRIEFVPVEVTEAEYDPEKAQEKV 660  
Db 601 TPTVTGFTTTPFSDVQSTFTIGAMNPFSSGNEVYIDRIEFVPVEVTEAEYDPEKAQEKV 660  
Qy 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 15

AA866912  
ID AA866912 standard; protein; 719 AA.

XX AA866912;

XX 12-APR-2001 (first entry)

XX Insecticidal protein cryIIb1.

XX Insecticide; transgenic plant; insect-resistance.

XX Paecilomyces sp.

XX WO200100841-A1.

XX 04-JAN-2001.

XX 23-JUN-2000; 2000WO-GB002457.

XX 29-JUN-1999; 99GB-00015215.

XX 23-DEC-1999; 99GB-00030536.

XX (ZENE ) ZENECA LTD.

XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;

XX Vincent J, Lee WD;

XX WPI; 2001-123015/13.

XX Novel insecticidal protein obtained from species of Paecilomyces for

PT controlling insects, and for insect-resistant transgenic plant

PT production.

XX Claim 14; Page 64-66; 72pp; English.

XX The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX Sequence 719 AA;

Query Match 93.1%; Score 3503; DB 4; Length 719;  
Best Local Similarity 92.5%; Pred. No. 2.8e-273;  
Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDLELQNHEDCLKMEYENVEPFSASTI 60  
Db 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDLELKNMNNEDYLRMSEHSDIPFVSASTI 60  
Qy 61 QTGIGIAGKILGTGVPPFAGQVAVSYFILGELMPKGKQWEIFMEHVBEIINQKISTYA 120  
Db 61 QTGIGIAGKILGTGVPPFAGQIASLYSFILGELMPKGKQWEIFMEHVBEIINQKILTVA 120  
Qy 121 RNKALTDLKGLGDALAVHDSLESWVGANRNTARSVVKSOYIALELMFKVQKLPSPAVSG 180  
Db 121 RNKALSDELKGLGDALAVHDESLEWVENRNTARSVVKQNYIALELMFKVQKLPSPAVSG 180  
Qy 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSYHCVKWYS 240  
Db 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVTRDYSDHCIKWYN 240  
Qy 241 TGLNLRGTVNAESWRYNQPRRDMTLMVLVDLVALPFSYDTQMPYPIKTTAQLTREVTDAI 300  
Db 241 TGLNLRGTVNAESWRYNQPRKDMTLMVLVDLVALPFSYDTLVPIKTTSLTREVTDAI 300  
Qy 301 GTVHPSPSTSTWYNNAPSFSAIAA VVRNPHLLDLEQVTIYSLSRWSNTQYMNW 360  
Db 301 GTVHPNAPSTWYNNAPSFSAIAA VVRNPHLLDLEQVTIYSLSRWSNTQYMNW 360  
Qy 361 GGHLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTPQVNGVPR 420  
Db 361 GGHLESPRIGALNTSTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTPQVNGVPR 420  
Qy 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 480  
Db 421 VDFHMKFPTLPIASDNFYLYGAGVGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 480  
Qy 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKA FNLSGAAVVRGPGFTGGDILRRTN 540  
Db 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKA FNLSGAAVVRGPGFTGGDILRRTN 540  
Qy 541 TGTFGDIRVNIINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSA TMNRGEDLDYK 600  
Db 541 TGTFGDIRVNIINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSA TMNRGEDLDYK 600  
Qy 601 TPTVTGFTTTPFSDVQSTFTIGAMNPFSSGNEVYIDRIEFVPVEVTEAEYDPEKAQEKV 660  
Db 601 TPTVTGFTTTPFSDVQSTFTIGAMNPFSSGNEVYIDRIEFVPVEVTEAEYDPEKAQEKV 660  
Qy 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719

Search completed: February 14, 2005, 20:50:30  
Job time : 101.351 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:11:42 ; Search time 81.1112 Seconds  
(without alignments)  
4539.261 Million cell updates/sec

Title: US-10-019-823B-57  
Perfect score: 3760  
Sequence: 1 MKLNQDKHQSFSSNAKVDK.....KRELFEIVKYAKQLHIERN 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3756	99.9	719	1 C1IA_BACTK	Q45752 bacillus th
2	3756	99.9	719	2 Q6X181	Q6x181 bacillus th
3	3751	99.8	719	2 Q93NJ5	Q93nj5 bacillus th
4	3750	99.7	719	2 Q85796	Q85796 bacillus th
5	3621	96.3	719	2 Q8XY61	Q8xy61 bacillus th
6	3547	94.3	719	2 Q9F0P8	Q9f0p8 bacillus th
7	3516	93.5	719	1 C1IB_BACTE	Q45709 bacillus th
8	3393	90.2	719	1 C1ID_BACTU	Q9xd11 bacillus th
9	3373	89.7	719	1 C1IC_BACTU	Q87404 bacillus th
10	2445.5	65.0	1239	1 C1BB_BACTU	Q45739 bacillus th
11	2445.5	65.0	1233	1 C1BC_BACTM	Q45774 bacillus th
12	2277.5	60.6	1228	2 Q93T75	Q93t75 bacillus th
13	2276.5	60.5	1228	1 C1BA_BACTX	P05517 bacillus th
14	2268.5	60.3	1228	2 Q93NM5	Q93nm5 bacillus th
15	2195.5	58.4	849	2 Q8PYW8	Q6pyw8 bacillus th
16	2195.5	58.4	1227	1 C1BE_BACTU	Q85a05 bacillus th
17	2111.5	56.2	1231	2 Q8KNY2	Q8kny2 bacillus th
18	2106.5	56.0	1231	1 C1BD_BACTZ	Q9zaz5 bacillus th
19	1984.5	52.8	1215	1 C1KA_BACTM	Q45715 bacillus th
20	1904	50.6	381	2 Q45740	Q45740 bacillus th
21	1669.5	44.4	1157	1 C8AA_BACUK	Q45704 bacillus th
22	1660	44.1	1144	2 Q8XZL7	Q8xzl7 bacillus th
23	1494	39.7	1157	1 C9CA_BACTO	Q45733 bacillus th
24	1485.5	39.5	1169	1 C8BA_BACUK	Q45705 bacillus th
25	1482.5	39.4	1166	1 C1GA_BACTU	Q45746 bacillus th
26	1482	39.4	1167	1 C1VA_BACTU	Q45738 bacillus th
27	1475	39.2	1169	1 C1FB_BACTM	Q66377 bacillus th
28	1469	39.1	1174	2 Q45749	Q45749 bacillus th
29	1465	39.0	1155	1 C1AB_BACTK	P06578 bacillus th
30	1465	39.0	1155	2 Q7BE98	Q7be98 bacillus th
31	1465	39.0	1155	2 Q9F296	Q9f296 bacillus th

32	1463	38.9	1118	2 Q9AM83	Q9am83 bacillus th
33	1460	38.8	1156	2 Q6GUA7	Q6gua7 bacillus th
34	1458.5	38.8	1180	2 Q9S5V8	Q9s5v8 bacillus th
35	1457.5	38.8	1176	2 Q7WZT9	Q7wzt9 bacillus th
36	1455	38.7	1177	2 Q8EIX3	Q8eix3 bacillus th
37	1453	38.6	1155	2 Q93T21	Q93t21 bacillus th
38	1452.5	38.6	793	2 Q6PYW7	Q6pyw7 bacillus th
39	1451.5	38.6	1176	2 Q45736	Q45736 bacillus th
40	1447.5	38.5	1176	1 C1AA_BACTK	P02965 bacillus th
41	1447.5	38.5	1176	2 Q9RC30	Q9rc30 bacillus th
42	1447.5	38.5	1181	1 C1AE_BACTL	Q03748 bacillus th
43	1437.5	38.2	1169	2 Q8GHE8	Q8gne8 bacillus th
44	1430.5	38.0	1169	1 C1GB_BACTZ	Q9zaz6 bacillus th
45	1424.5	37.9	1179	1 C1AD_BACTA	Q03744 bacillus th

ALIGNMENTS

RESULT 1  
ID C1IA\_BACTK STANDARD; PRT: 719 AA.  
AC Q45752; P71092; Q45750; Q45751; Q45756;  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DE Pesticidial crystal protein cryIIa (insecticidal delta-endotoxin)  
DE CryII(a) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
GN Name=cryIIa; Synonyms=CGCryV, cryII(a), cryV, cryVI;  
OS Bacillus thuringiensis (subsp. kurstaki).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=29339;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSIR732;  
RA MEDLINE=93298009; PubMed=8517758;  
RX Gleave A.P., Williams R., Hedges R.J.;  
RT "Screening by polymerase chain reaction of Bacillus thuringiensis  
RT serotypes for the presence of a cryV-like insecticidal protein genes and  
RT characterization of a cryV gene cloned from B. thuringiensis subsp.  
RT kurstaki".  
RL Appl. Environ. Microbiol. 59:1683-1687(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JHCC4835;  
RX MEDLINE=92269582; PubMed=1588820;  
RA Tailor R., Tippett J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;  
RT "Identification and characterization of a novel Bacillus thuringiensis  
RT delta-endotoxin entomocidal to coleopteran and lepidopteran larvae".  
RL Mol. Microbiol. 6:1211-1217(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HD-1;  
RX MEDLINE=95314293; PubMed=7793960;  
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;  
RT "Distribution of cryV-type insecticidal protein genes in Bacillus  
RT thuringiensis and cloning of cryV-type genes from Bacillus  
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.  
RT entomocidus".  
RL Appl. Environ. Microbiol. 61:2402-2407(1995).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AB88;  
RX MEDLINE=96178985; PubMed=8606196;  
RA Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,  
RA Craig J.A., Koziel M.G., Estruch J.J.;  
RT "Cloning of a cryV-type insecticidal protein gene from Bacillus  
RT thuringiensis: the cryV-encoded protein is expressed early in  
RT stationary phase".  
RL J. Bacteriol. 178:2141-2144(1996).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=61;

Db	361	GGHKLKLEFRTTGGTLLNISTQGSTNTSINPVLFTFTSRDVRVETESLAGLNLFTPTQVNGVPR	420
Qy	421	VDFFHWKVFTHPIASDNFYYPGVVIGTQLQDSENLPEATQPNYESYSHRLSHIGLIS	480
Db	421	VDFFHWKVFTHPIASDNFYYPGVVIGTQLQDSENLPEATQPNYESYSHRLSHIGLIS	480
Qy	481	ASHVKALVYSWTHRSADRTNTIPEPNSITQIPLVKAFLNSGAAVVRGPGFTGGDILRRTN	540
Db	481	ASHVKALVYSWTHRSADRTNTIPEPNSITQIPLVKAFLNSGAAVVRGPGFTGGDILRRTN	540
Qy	541	TGTFGDIRVNINPPFAQRYVRIRYASTTDLQPHSTINGKAINQGNFSAATMRGDDLDYK	600
Db	541	TGTFGDIRVNINPPFAQRYVRIRYASTTDLQPHSTINGKAINQGNFSAATMRGDDLDYK	600
Qy	601	TPRTVGTFTPPSFELDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVYIEAYEFKQAQKV	660
Db	601	TPRTVGTFTPPSFELDVQSTFTIGAWNFSSGNEVYIDRIEFVPVEVYIEAYEFKQAQKV	660
Qy	661	TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKREKLEFIVKAKQLHIERNM	719
Db	661	TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKREKLEFIVKAKQLHIERNM	719
RESULT 2			
ID	Q6X181	PRELIMINARY;	PRT; 719 AA.
AC	Q6X181;		
DT	05-JUL-2004	(TReMBLrel. 27, Created)	
DT	05-JUL-2004	(TReMBLrel. 27, Last sequence update)	
DT	05-JUL-2004	(TReMBLrel. 27, Last annotation update)	
DE	Cry11.		
GN	Names:cry11;		
OS	Bacillus thuringiensis.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OC	NCBI_FtaxID=1428;		
OC	[1]		
RP	SEQUENCE FROM N.A.		
RP	Espondola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;		
RA	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.		
RL	EMBL: AY262167; AAP86782.1; -.		
DR	GO: 0005102; F:receptor binding; IEA.		
DR	GO: 0006952; P:defense response; IEA.		
DR	GO: 0009405; P:pathogenesis; IEA.		
DR	InterPro: IPR001178; Endotoxin_C.		
DR	InterPro: IPR005638; endotoxin_N.		
DR	InterPro: IPR008979; Gal_bind like.		
DR	Pfam: PF03944; Endotoxin_C; 1.		
DR	Pfam: PF00555; Endotoxin_M; 1.		
DR	Pfam: PF03945; Endotoxin_N; 1.		
DR	SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAPF5 CRC64;		
Qy	Query Match	99.9%; Score 3756; DB 2; Length 719;	
Db	Best Local Similarity	99.9%; Pred. No. 6.1e-251; Indels 0; Gaps	
Db	Matches 718; Conservative 0; Mismatches 1;		
Qy	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYEYENVEPFSASTI	600
Db	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYEYENVEPFSASTI	600
Qy	61	QTGIGIAGKILGTVGPAGQVASYLSFIIGELWPKGKQWEIFMWHVEIINQKISTYA	120
Db	61	QTGIGIAGKILGTVGPAGQVASYLSFIIGELWPKGKQWEIFMWHVEIINQKISTYA	120
Qy	121	RNKALTDLKLGDALAVHDHLSWVGNNRNNTRARSVVKSQYIALEIMFVKQLPFAVSG	180
Db	121	RNKALTDLKLGDALAVHDHLSWVGNNRNNTRARSVVKSQYIALEIMFVKQLPFAVSG	180
Qy	181	EEVPLLPPIYAQANLHLLLRDASITFGKWCGLSSSEISTFYNQVVERAGDYSCHCVKWS	240
Db	181	EEVPLLPPIYAQANLHLLLRDASITFGKWCGLSSSEISTFYNQVVERAGDYSCHCVKWS	240

QY	241	TGLNLRGTAESWVRNQRRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI	300
Db	241	TGLNLRGTAESWVRNQRRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI	300
QY	301	GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW	360
Db	301	GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW	360
QY	361	GGHKLFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTQPVNGVPR	420
Db	361	GGHKLFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTQPVNGVPR	420
QY	421	VDFHMKFVTHPIASDNFYYPGYGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS	480
Db	421	VDFHMKFVTHPIASDNFYYPGYGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS	480
QY	481	ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
Db	481	ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
QY	541	TGTFGDIRVINPFPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK	600
Db	541	TGTFGDIRVINPFPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK	600
QY	601	TFTVGTFTTFFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFPVVEVYEAEDFEKAQEKV	660
Db	601	TFTVGTFTTFFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFPVVEVYEAEDFEKAQEKV	660
QY	661	TALFTSTNPRGLKTDVKDHYDIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM	719
Db	661	TALFTSTNPRGLKTDVKDHYDIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM	719
RESULT 3			
ID	Q93NJ5	PRELIMINARY; PRT; 719 AA.	
AC	Q93NJ5		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Crylia.		
GN	Name=crylia;		
OS	Bacillus thuringiensis.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1428;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Song F., Zhang J., Gu A., Huang D., Li G.;		
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF373207; AAK66742.1; -.		
DR	HSSP; P02965; 1CIY.		
DR	GO; GO:0005102; F:receptor binding; IEA.		
DR	GO; GO:0006952; P:defense response; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin C.		
DR	InterPro; IPR005639; endotoxin N.		
DR	InterPro; IPR008979; Gal bind Like.		
DR	Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		
SQ	SEQUENCE 719 AA; 81225 MW; C629DPF2C44827241 CRC64;		
Query Match 99.8%; Score 3751; DB 2; Length 719;			
Best Local Similarity 99.7%; Pred. No. 1.3e-250;			
Matches 717; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
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Db	1	MKLKNDQKHQSFSSNAKVDKISTDSLKNETDIELQININHDCLKMEYENVEFVSASTI	60
QY	61	QTGIGIAGKILGTLGVPPFAQVVASLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120

Db	61	QTGIGIAGKILGTLGVPPFAQVVASLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120
QY	121	RNKALTDLXGLGDALAVYHDSLESWGNRNNTARSVVKSOYIALELMFVKLPSPAVSG	180
Db	121	RNKALTDLXGLGDALAVYHDSLESWGNRNNTARSVVKSOYIALELMFVKLPSPAVSG	180
QY	181	EEVPLLPPIVAQAANLHLLLRDASIFGKEWGLSSSBISTFYNRQVERAGYSDHCWKYS	240
Db	181	EEVPLLPPIVAQAANLHLLLRDASIFGKEWGLSSSBISTFYNRQVERAGYSDHCWKYS	240
QY	241	TGLNLRGTAESWVRNQRRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI	300
Db	241	TGLNLRGTAESWVRNQRRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI	300
QY	301	GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW	360
Db	301	GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW	360
QY	361	GGHKLFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTQPVNGVPR	420
Db	361	GGHKLFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTQPVNGVPR	420
QY	421	VDFHMKFVTHPIASDNFYYPGYGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS	480
Db	421	VDFHMKFVTHPIASDNFYYPGYGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS	480
QY	481	ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
Db	481	ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
QY	541	TGTFGDIRVINPFPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK	600
Db	541	TGTFGDIRVINPFPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK	600
QY	601	TFTVGTFTTFFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFPVVEVYEAEDFEKAQEKV	660
Db	601	TFTVGTFTTFFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFPVVEVYEAEDFEKAQEKV	660
QY	661	TALFTSTNPRGLKTDVKDHYDIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM	719
Db	661	TALFTSTNPRGLKTDVKDHYDIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM	719
RESULT 4			
ID	O85796	PRELIMINARY; PRT; 719 AA.	
AC	O85796		
DT	01-NOV-1998 (TrEMBLrel. 08, Created)		
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Insecticidal protein.		
GN	Name=cryV101;		
OS	Bacillus thuringiensis (subsp. kurstaki).		
OG	Flasmid large plasmid.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=29339;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=5101;		
RA	Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;		
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF076953; AAC26910.1; -.		
DR	HSSP; P02965; 1CIY.		
DR	GO; GO:0005102; F:receptor binding; IEA.		
DR	GO; GO:0006952; P:defense response; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin C.		
DR	InterPro; IPR005639; endotoxin N.		
DR	InterPro; IPR008979; Gal bind Like.		
DR	Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		

KW Plasmid.  
SQ SEQUENCE 719 AA; 81230 MW; 42746D478359BBA7 CRC64;  
Query Match 99.78; Score 3750; DB 2; Length 719;  
Best Local Similarity 99.78; Pred. No. 1.6e-250;  
Matches 717; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 MKLNQDKHQSFSNNAKVDKISTDSLKNETDIELQINHEHEDCLKMSYENVEPVSASTI 60  
Db 1 MKLNQDKHQSFSNNAKVDKISTDSLKNETDIELQINHEHEDCLKMSYENVEPVSASTI 60  
Qy 61 QTGIGIAGKILGTLGVPPAGQVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
Db 61 QTGIGIAGKILGTLGVPPAGQVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
Qy 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVOKLPSPFAVSG 180  
Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVOKLPSPFAVSG 180  
Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSDHCVKWYS 240  
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSDHCVKWYS 240  
Qy 241 TGLNLRGTVNAESWVRYNQPRDMLVLDLVALFPSYDTQMPYIKTTAOLTREVTYDAI 300  
Db 241 TGLNLRGTVNAESWVRYNQPRDMLVLDLVALFPSYDTQMPYIKTTAOLTREVTYDAI 300  
Qy 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
Db 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
Qy 361 GGHKLEFRTTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSIESLAGLNLFITOPVNGVPR 420  
Db 361 GGHKLEFRTTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSIESLAGLNLFITOPVNGVPR 420  
Qy 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
Db 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
Qy 481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
Db 481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
Qy 541 TGTGDIRVNIINPPFAQRYRIRYASTTDIQLPHTSINGKAINQGNFSATMNRGEDLDYK 600  
Db 541 TGTGDIRVNIINPPFAQRYRIRYASTTDIQLPHTSINGKAINQGNFSATMNRGEDLDYK 600  
Qy 601 TFRVGTTPPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660  
Db 601 TFRVGTTPPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660  
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 5  
Q8KY61  
ID Q8KY61 PRELIMINARY; PRT; 719 AA.  
AC Q8KY61;  
DT 01-OCT-2002 (TremBLrel. 22, Created)  
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)  
DE Cyt.  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Porcar M., Martinez C., Caballero P.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF278797; AAM73516.1; --  
DR FIR; B42459; B42459.

DR HSP; P02965; 1CIY.  
DR GO:0005102; F:receptor binding; IEA.  
DR GO:0006952; P:defense response; IEA.  
DR GO:0009405; P:pathogenesis; IEA.  
DR InterPro: IPR001178; Endotoxin.  
DR InterPro: IPR005638; endotoxin\_C.  
DR InterPro: IPR005639; endotoxin\_N.  
DR InterPro: IPR008979; Gal\_bind\_like.  
DR Pfam: PF03944; Endotoxin\_C; 1.  
DR Pfam: PF00555; Endotoxin\_M; 1.  
DR Pfam: PF03945; Endotoxin\_N; 1.  
SQ SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;  
Query Match 96.13%; Score 3621; DB 2; Length 719;  
Best Local Similarity 96.13%; Pred. No. 1.3e-241;  
Matches 691; Conservative 12; Mismatches 16; Indels 0; Gaps 0;  
Qy 1 MKLNQDKHQSFSNNAKVDKISTDSLKNETDIELQINHEHEDCLKMSYENVEPVSASTI 60  
Db 1 MKLNQDKHQSFSNNAKVDKISTDSLKNETDIELQINHEHEDCLKSEYENVEPVSASTI 60  
Qy 61 QTGIGIAGKILGTLGVPPAGQVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
Db 61 QTGIGIAGKILGTLGVPPAGQVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
Qy 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVOKLPSPFAVSG 180  
Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVOKLPSPFAVSG 180  
Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSDHCVKWYS 240  
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSDHCVKWYS 240  
Qy 241 TGLNLRGTVNAESWVRYNQPRDMLVLDLVALFPSYDTQMPYIKTTAOLTREVTYDAI 300  
Db 241 TGLNLRGTVNAESWVRYNQPRDMLVLDLVALFPSYDTQMPYIKTTAOLTREVTYDAI 300  
Qy 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
Db 301 GTVHPNAPFASTTWYNNNAPSFTIESAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
Qy 361 GGHKLEFRTTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSIESLAGLNLFITOPVNGVPR 420  
Db 361 GGHKLEFRTTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSIESLAGLNLFITOPVNGVPR 420  
Qy 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
Db 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
Qy 481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
Db 481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
Qy 541 TGTGDIRVNIINPPFAQRYRIRYASTTDIQLPHTSINGKAINQGNFSATMNRGEDLDYK 600  
Db 541 TGTGDIRVNIINPPFAQRYRIRYASTTDIQLPHTSINGKAINQGNFSATMNRGEDLDYK 600  
Qy 601 TFRVGTTPPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660  
Db 601 TFRVGTTPPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660  
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
RESULT 6  
Q9F0P8  
ID Q9F0P8 PRELIMINARY; PRT; 719 AA.  
AC Q9F0P8;  
DT 01-MAR-2001 (TremBLrel. 16, Created)  
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)  
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)



CC 61 QTGIGTAGKILGTGVPAGVAVSIFLIGELWPKGNQWEIFMEHVVEIINOKISTYA 120  
CC 61 QTGIGTAGKILGTGVPAGVAVSIFLIGELWPKGNQWEIFMEHVVEIINOKISTYA 120  
CC 121 RNKALTDKGLDALAVYHDSLVGNNRNPARSVVKSVQVIALELMFVQKLPSPFVSG 180  
CC 121 RNKALSDRLGLDALAVYHDSLVGNNRNPARSVVKSVQVIALELMFVQKLPSPFVSG 180  
CC 181 BEVPLLIYAQAANLHLLLRDASIFGKENGWGLSSSEISFYNRQVERAGDYSDHCWKYS 240  
CC 181 BEVPLLIYAQAANLHLLLRDASIFGKENGWGLSSSEISFYNRQVERAGDYSDHCWKYS 240  
CC 241 TGLNLRGTNAESVRYNQFRDMTLMVLDLVALFSPYDTQMTPIKTTAQLTREVYTDAL 300  
CC 241 TGLNLRGTNAESVRYNQFRDMTLMVLDLVALFSPYDTQMTPIKTTAQLTREVYTDAL 300  
CC 301 GTVHPHPSFTTWNNAFSAIEAARVNRPHLLDFLEQVITYLLSRWSNTQYNNMW 360  
CC 301 GTVHPHPSFTTWNNAFSAIEAARVNRPHLLDFLEQVITYLLSRWSNTQYNNMW 360  
CC 361 GGHKLEPFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTOPVNGVPR 420  
CC 361 GGHKLEPFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTOPVNGVPR 420  
CC 421 VDFHWKFTVTHPIASDNFYPIGVIGTQLODSENELPPEATGQPNYESYSHRSLHGLIS 480  
CC 421 VDFHWKFTVTHPIASDNFYPIGVIGTQLODSENELPPEATGQPNYESYSHRSLHGLIS 480  
CC 481 ASHVKALVYSWTHRSADRTNIENPSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRTN 540  
CC 481 ASHVKALVYSWTHRSADRTNIENPSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRTN 540  
CC 541 TGTFGDIRVNIINPPFAQRVRYRIRVASTDLDQFHTSINGKAINQGNFSATWNRGEDIYK 600  
CC 541 TGTFGDIRVNIINPPFAQRVRYRIRVASTDLDQFHTSINGKAINQGNFSATWNRGEDIYK 600  
CC 601 TRFTVGFTTTPSFVLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
CC 601 TRFTVGFTTTPSFVLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
CC 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFVYKAKQLIERNM 719  
CC 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFVYKAKQLIERNM 719

RESULT 8  
C1ID BACTU STANDARD; PRT; 719 AA.  
ID C1ID BACTU  
AC Q9XDL1;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Pesticidal crystal protein cryII (Insecticidal delta-endotoxin  
DE CryII(d) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
GN Name=cryIId; Synonyms=cryII(d), Nrcryv;  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
ON NCBI\_TaxID=1428;  
RX [1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=BR30;  
RA MEDLINE=20374042; PubMed=10919402;  
RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.-M., Park S.-H.;  
RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein  
RT gene.";  
RL Curr. Microbiol. 41:65-69(2000).  
CC -!- FUNCTION: Promotes colloidal lysis by binding to the midgut  
CC epithelial cells of many lepidopteran larvae. Active on Plutella  
CC xylostella and on Bombyx mori.  
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
CC sporulation and is accumulated both as an inclusion and as part of  
CC the spore coat.  
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-

terminus.  
-!- SIMILARITY: Belongs to the delta endotoxin family.  
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or send an email to license@sib-sib.ch).  
EMBL; AF047579; AAD44366.1; -.  
HSSP; P02965; 1CIY.  
InterPro; IPR001178; Endotoxin.  
InterPro; IPR005638; Endotoxin C.  
InterPro; IPR005639; Endotoxin N.  
InterPro; IPR008979; Gal\_bind\_Like.  
Pfam; PF03944; Endotoxin\_C; 1.  
Pfam; PF00555; Endotoxin\_M; 1.  
Pfam; PF03945; Endotoxin\_N; 1.  
KW Sporulation; Toxin.  
SQ SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;  
Query Match 90.2%; Score 3393; DB 1; Length 719;  
Best Local Similarity 89.7%; Pred. No. 7,6e-236;  
Matches 645; Conservative 35; Mismatches 39; Indels 0; Gaps 0;  
1 MSLKQKQKHQSFSSNAKVDKISDLSKNETDIELONINHEDCLOKSEYENVEPVSASTI 60  
1 MSLKQKQKMYRFSFNATVDKGFDPLEHNTNMELQNSNHEDCLOKSEYEVPPFVSSTI 60  
61 QTGIGTAGKILGTGVPAGVAVSIFLIGELWPKGNQWEIFMEHVVEIINOKISTYA 120  
61 QTGIGTAGKILGTGVPAGVAVSIFLIGELWPKGNQWEIFMEHVVEIINOKISTYA 120  
121 RNKALTDKGLDALAVYHDSLVGNNRNPARSVVKSVQVIALELMFVQKLPSPFVSG 180  
121 RNKALADLKLGDALAVYHDSLVGNNRNPARSVVKSVQVIALELMFVQKLPSPFVSG 180  
181 BEVPLLIYAQAANLHLLLRDASIFGKENGWGLSSSEISFYNRQVERAGDYSDHCWKYS 240  
181 BEVPLLIYAQAANLHLLLRDASIFGKENGWGLSSSEISFYNRQVERAGDYSDHCWKYS 240  
241 TGLNLRGTNAESVRYNQFRDMTLMVLDLVALFSPYDTQMTPIKTTAQLTREVYTDAL 300  
241 TGLNLRGTNAESVRYNQFRDMTLMVLDLVALFSPYDTQMTPIKTTAQLTREVYTDAL 300  
301 GTVHPHPSFTTWNNAFSAIEAARVNRPHLLDFLEQVITYLLSRWSNTQYNNMW 360  
301 GTVHPNASPASTTWNNAFSPSTIEAARVNRPHLLDFLEQVITYLLSRWSNTQYNNMW 360  
361 GGHKLEPFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTOPVNGVPR 420  
361 GGHKLEPFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTOPVNGVPR 420  
421 VDFHWKFTVTHPIASDNFYPIGVIGTQLODSENELPPEATGQPNYESYSHRSLHGLIS 480  
421 VDFHWKFTVTHPIASDNFYPIGVIGTQLODSENELPPEATGQPNYESYSHRSLHGLIS 480  
481 ASHVKALVYSWTHRSADRTNIENPSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRTN 540  
481 ASHVKALVYSWTHRSADRTNIENPSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRTN 540  
541 TGTFGDIRVNIINPPFAQRVRYRIRVASTDLDQFHTSINGKAINQGNFSATWNRGEDIYK 600  
541 TGTFGDIRVNIINPPFAQRVRYRIRVASTDLDQFHTSINGKAINQGNFSATWNRGEDIYK 600  
601 TRFTVGFTTTPSFVLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
601 TRFTVGFTTTPSFVLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFVYKAKQLIERNM 719  
661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFVYKAKQLIERNM 719

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Db 661 TAMFTSTNLRLKNTVTDCHIDQVSNLVSLSDEFYLDKRELFELVYKAKQLNIERNM 719
RESULT 9
CLIC_BACTU STANDARD; PRT; 719 AA.
AC Q87404;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIc (Insecticidal delta-endotoxin
DE CryII(c)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Names-cryIIc; Synonyms-cryII(c);
OS Bacillus thuringiensis.
OG Plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C18 / Egypt;
RA Osman Y.A., Makour M.A., Bulla L.A. Jr.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF056933; AAC62933.1; .
DR HSP; P02965; 1CIV.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Plasmid; Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81210 MW; 8370B3F06B905DFF CRC64; .
Query Match 89.7%; Score 3373; DB 1; Length 719;
Best Local Similarity 89.7%; Pred.No. 1.8e-224;
Matches 645; Conservative 33; Mismatches 41; Indels 0; Gaps 0;
QY 1 MKLKNQDKHQSFSSNAKVDKISTDKNETDIELQNHEDCLKMGEYENVEPFVSASTI 60
DB 1 MKLKNPDKHQTLSSNAKVDKIATDSLKNETDIELKMNEDYLKMSHESIDPFVSASTI 60
QY 61 QTGIGTAGILGTLPVFPAGVASLYSFLGELMPKGNQWEIFMEHVEIINQKISTYA 120
DB 61 QTGIGTAGILGTLPVFPAGQIASLYSFLGELMPKGNQWEIFMEHVEIINRKISTYA 120
QY 121 RNKALTDLGLDALAVYHDSLSWGVRNNTARSVVKSYQYALMLFVKQLPSFAVSG 180
DB 121 RNKALTDLGLDALAVYHDSLSWGVRNNTARSVVKSYQYALMLFVKQLPSFAVSG 180
QY 181 EEPVLLPIYQAANLHLLLRDASIFEKWGLSSSISTFYNRQVRAGDYSCHVKWYS 240
DB 181 EEPVLLPIYQAANLHLLLRDASIFEKWGLSSSISTFYNRQVRAGDYSCHVKWYN 240
QY 241 TGLNNLRGNAESWRYNQFRDMTLMVLDLVALFPSTQMTYPIKTKTQALREVYTDI 300
DB 241 TGLNNLRGNAESWRYNQFRDMTLMVLDLVALFPSTQMTYPIKTKTQALREVYTDI 300
Db 241 TGLNNLRATNGOSWRYNQFRKDIELMVLDLVRVFPSTQMTYPIKTKTQALREVYTDI 300
QY 301 GTVHPHPSTTWNANNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSWSNTQYNNMW 360
DB 301 GTVDPNQLRSTTWNANNAPSFSAIEAAVVRNPHLLDFLEKVTIYSLLSWSNTQYNNMW 360
QY 361 GGHKLEFRITGGTLNISTGSGTNTSINPVTLPFTSRDVTYRTSLAGLNFLTPQVNGVPR 420
DB 361 GGHRLSRPIGGALNTSTGSGTNTSINPVTLPFTSRDVTYRTSLAGLNFLTPQVNGVPR 420
QY 421 VDFHMKFVTHPTASDNFYGVGCTGLODENELPPEATGPNYVESHSLHGLIS 480
DB 421 VDFHMKFPLPTASDNFYGVGCTGLODENELPPEATGPNYVESHSLHGLIS 480
QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGFTGDIILRTN 540
DB 481 GSHVKALVSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGFTGDIILRTN 540
QY 541 TGTFGDIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGELDYK 600
DB 541 SGTFGHIRVINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGELDYK 600
QY 601 TERTVGTFTPFSLDVOSTFTIGANNFSSGNEVYIDRIEFVPEVVEYAEYDEPKAQEKV 660
DB 601 TERTVGTFTPFSLDVOSTFTIGANNFSSGNEVYIDRIEFVPEVVEYAEYDEPKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFELVYKAKQLNIERNM 719
DB 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFELVYKAKQLNIERNM 719
RESULT 10
C1BB_BACTU STANDARD; PRT; 1229 AA.
AC Q45739;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIB (Insecticidal delta-endotoxin
DE CryIIB(b)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name-cryIIB; Synonyms-cryE5, cryIIB(b);
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL B-21110 / EG5847;
RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
RT toxic to lepidopteran insects.";
RL Patent number US5322687, 21-JUN-1994.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L32020; AAA2344.1; .
DR HSP; P02965; 1CIV.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR005638; endotoxin_N.
```



DR	InterPro: IPR008979; Gal bind like.	RP	SEQUENCE FROM N.A.
DR	Pfam: PF03944; Endotoxin_C; 1	RA	Bishop A.H., Bone E.J., Ellar D.J.;
DR	Pfam: PF00555; Endotoxin_M; 1	RT	"Cloning of novel Bacillus thuringiensis delta-endotoxin.";
DR	Pfam: PF03945; Endotoxin_N; 1	RL	Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
KW	Sporulation; Toxin.	CC	FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
SQ	SEQUENCE 1229 AA; A4C949DB675C3269 CRC64;	CC	epithelial cells of insects.
		CC	DEVELOPMENTAL STAGE: The crystal protein is produced during
		CC	sporulation and is accumulated both as an inclusion and as part of
		CC	the spore coat.
		CC	MISCELLANEOUS: Toxic segment of the protein is located in the N-
		CC	terminus.
		CC	SIMILARITY: Belongs to the delta endotoxin family.
		CC	-----
		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
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		CC	use by non-profit institutions as long as its content is in no way
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		CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
		CC	or send an email to license@isb-sib.ch).
		CC	-----
		CC	EMBL: Z46442; CA886568.1; --
DR	HSP; P02965; ICY.	DR	InterPro: IPR001178; Endotoxin.
DR	InterPro: IPR005638; endotoxin_C.	DR	InterPro: IPR005639; endotoxin_N.
DR	InterPro: IPR005639; endotoxin_N.	DR	InterPro: IPR008979; Gal bind like.
DR	Pfam: PF03944; Endotoxin_C; 1	DR	Pfam: PF00555; Endotoxin_M; 1
DR	Pfam: PF03945; Endotoxin_N; 1	DR	Pfam: PF03945; Endotoxin_N; 1
KW	Sporulation; Toxin.	KW	Sporulation; Toxin.
SQ	SEQUENCE 1233 AA; 140451 MW; 7318382413529P21 CRC64;	SQ	SEQUENCE 1233 AA; 140451 MW; 7318382413529P21 CRC64;
			Query Match 65.0%; Score 2445.5; DB 1; Length 1233;
			Best Local Similarity 65.6%; Pred. No. 5.4e-160;
			Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;
Qy	13 SSNAKVDKISTOSLKN-ETDIELQ-NINHEDCMKSEYENVEPVFVASTIQTGIGTAGKI 70	Qy	13 SSNAKVDKISTOSLKN-ETDIELQ-NINHEDCMKSEYENVEPVFVASTIQTGIGTAGKI 70
Db	7 NENEINALSIPVSNPSTQNLSPDARIEDSLCAEVNNDIPFVSASTVQTGINAGRI 66	Db	7 NENEINALSIPVSNPSTQNLSPDARIEDSLCAEVNNDIPFVSASTVQTGINAGRI 66
Qy	71 LGTGVPPAGOVASLYSFLGELWPKGNOWEIPMEHVEEIIINQKISTYARNKALDCLKG 130	Qy	71 LGTGVPPAGOVASLYSFLGELWPKGNOWEIPMEHVEEIIINQKISTYARNKALDCLKG 130
Db	67 LGVLGVPPAGQLASFYSFLVGLWPGSRDPWEIFLEHVEQLIRQOVTENTNTAIARLEG 126	Db	67 LGVLGVPPAGQLASFYSFLVGLWPGSRDPWEIFLEHVEQLIRQOVTENTNTAIARLEG 126
Qy	131 LGDALAVYHDSLSWGNRNNTARSVVKSYQYIALEIMFVQKLPSPFVSGSEVPLPIYA 190	Qy	131 LGDALAVYHDSLSWGNRNNTARSVVKSYQYIALEIMFVQKLPSPFVSGSEVPLPIYA 190
Db	127 LGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPFRIRNEEVEPLLMVYA 186	Db	127 LGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPFRIRNEEVEPLLMVYA 186
Qy	191 QAANLHLLLRDASIFGKWLGSSEISTFYNROVERAGDYSDHCVKWYSTGLNLRGTN 250	Qy	191 QAANLHLLLRDASIFGKWLGSSEISTFYNROVERAGDYSDHCVKWYSTGLNLRGTN 250
Db	187 QAANLHLLLRDASLFGSEWGMASDVNQYIQOIRYTESYHNCVQWYNTGLNLRGTN 246	Db	187 QAANLHLLLRDASLFGSEWGMASDVNQYIQOIRYTESYHNCVQWYNTGLNLRGTN 246
Qy	251 AESWVRYNQFRDRMTLMDLVALFVPSYDTQMPYIKTTAQLTREYVTDALGTVHPHSFT 310	Qy	251 AESWVRYNQFRDRMTLMDLVALFVPSYDTQMPYIKTTAQLTREYVTDALGTVHPHSFT 310
Db	247 AESWLRYNQFRDLTLGLVDLVALFVPSYDTRTPINTSAQLTREIYTDPIGRTNAPSGFA 306	Db	247 AESWLRYNQFRDLTLGLVDLVALFVPSYDTRTPINTSAQLTREIYTDPIGRTNAPSGFA 306
Qy	311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYLSLRSWNTQYNNMGHGHLEPRTI 370	Qy	311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYLSLRSWNTQYNNMGHGHLEPRTI 370
Db	307 STNWFNNAPSFSAIEAAIPRPHLLDFPQOLTIYSASSRWSSSTQHMYVWGHRLNRPFI 366	Db	307 STNWFNNAPSFSAIEAAIPRPHLLDFPQOLTIYSASSRWSSSTQHMYVWGHRLNRPFI 366
Qy	371 GGTINISTQGST-NTSINPVTLPFTSRDVRVTESLAGNLFLTOPVNGVPRVDFHWKFTV 429	Qy	371 GGTINISTQGST-NTSINPVTLPFTSRDVRVTESLAGNLFLTOPVNGVPRVDFHWKFTV 429
Db	367 GGTINTSTQGLTNTSINPVTLPFTSRDVRVTESLAGNLFLTOPVNGVPRVDFHWKFTV 422	Db	367 GGTINTSTQGLTNTSINPVTLPFTSRDVRVTESLAGNLFLTOPVNGVPRVDFHWKFTV 422
Qy	430 HPIASDNFYYPG-----YVIGITQLODSENEILPPEATGPNYESYSHRLSHGLISAS 482	Qy	430 HPIASDNFYYPG-----YVIGITQLODSENEILPPEATGPNYESYSHRLSHGLISAS 482
Db	423 --INPQNIYERGATTYSQYQGVGQLFDSFETPELPTTERPNYESYSHRLSHGLIIGN 480	Db	423 --INPQNIYERGATTYSQYQGVGQLFDSFETPELPTTERPNYESYSHRLSHGLIIGN 480
Qy	483 HVKALVYSWTHRSADRTNTEPNSITQPLVKAFLNSGAAVVRGPGTGGDILRRNTGT 542	Qy	483 HVKALVYSWTHRSADRTNTEPNSITQPLVKAFLNSGAAVVRGPGTGGDILRRNTGT 542
Db	481 TLRAPIYSWTHRSADRTNTEPNSITQPLVKAFLNSGAAVVRGPGTGGDILRRNTGT 540	Db	481 TLRAPIYSWTHRSADRTNTEPNSITQPLVKAFLNSGAAVVRGPGTGGDILRRNTGT 540
Qy	543 TFGDIRVNIPLPPAQRVRIYASTTDLQFHTSINGKAINOGNFSATNWRGEDIKYTF 602	Qy	543 TFGDIRVNIPLPPAQRVRIYASTTDLQFHTSINGKAINOGNFSATNWRGEDIKYTF 602
Db	541 TFGDIRLNIPLSQRYRRIYASTTDLQFTRINGTNTVINGNFSRTNMRGDNLEYSRF 600	Db	541 TFGDIRLNIPLSQRYRRIYASTTDLQFTRINGTNTVINGNFSRTNMRGDNLEYSRF 600
Qy	603 RTVGFTTPPSFLDVQSTFTIGAWNFGSGNEVYIDRIEFVPEVTEYAEVDPEKAQKVTA 662	Qy	603 RTVGFTTPPSFLDVQSTFTIGAWNFGSGNEVYIDRIEFVPEVTEYAEVDPEKAQKVTA 662
Db	601 RTAGFSTPFPFLNAQSTFTLGAQSFN-QEVIDRVEFPVAEVTEAEVDLERAQKAVNA 659	Db	601 RTAGFSTPFPFLNAQSTFTLGAQSFN-QEVIDRVEFPVAEVTEAEVDLERAQKAVNA 659
Qy	663 LFTSTNPRGLKTDVKYHIDQVSNLVLSDEFYLDKRELFEIVKIAKQLHIRMN 719	Qy	663 LFTSTNPRGLKTDVKYHIDQVSNLVLSDEFYLDKRELFEIVKIAKQLHIRMN 719
Db	660 LFTSTNPRRLKTDVYHIDQVSNMVAFLSDEFCLDKRELFEIVKIAKRLSDERNL 716	Db	660 LFTSTNPRRLKTDVYHIDQVSNMVAFLSDEFCLDKRELFEIVKIAKRLSDERNL 716
			RESULT 11
C1BC_BACTM	STANDARD; PRT; 1233 AA.	C1BC_BACTM	STANDARD; PRT; 1233 AA.
ID_C1BC_BACTM	Q4574;	ID_C1BC_BACTM	Q4574;
AC	30-MAY-2000 (Rel. 39, Created)	AC	30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)	DT	30-MAY-2000 (Rel. 39, Last sequence update)
DE	05-JUL-2004 (Rel. 44, Last annotation update)	DE	05-JUL-2004 (Rel. 44, Last annotation update)
DE	peptidicidal crystal protein cryIbC (insecticidal delta-endotoxin	DE	peptidicidal crystal protein cryIbC (insecticidal delta-endotoxin
DE	CryIbC) (Crystalline entomocidal protoxin) (140 kDa crystal protein).	DE	CryIbC) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN	Name=cryIbC; Synonyms=cryIb(c), cryIbC;	GN	Name=cryIbC; Synonyms=cryIb(c), cryIbC;
OS	Bacillus thuringiensis (subsp. morrisoni).	OS	Bacillus thuringiensis (subsp. morrisoni).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX	NCBI_TaxID=1441;	OX	NCBI_TaxID=1441;



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QY 543 TFGDIRVNPFPQAQRYRIRYASTTDLOFHTSINGKAINQGNFSATNNRGEDLDYKTF 602
DB 541 TFGDIRLNLNPLSQRYRIRYASTTDLOFHTSINGKAINQGNFSATNNRGEDLDYKTF 600
QY 603 RTVGFTTPTSFSDVOSTFTTIGAWNFSSGNEVYIDRIERFVPEVVEAEVDPEKAQEKVTA 662
DB 601 RTAGSTPTNFNAQSTFTLGAQSFN-QEVYIDRIERFVPEVVEAEVDPEKAQEKVTA 659
QY 663 LFTSTNPRGLKTDVVDYHIDQVSNLVESLSDFFYLDKRELFELFVYAKQLHIERNM 719
DB 660 LFTSTNPRGLKTDVVDYHIDQVSNLVESLSDFFYLDKRELFELFVYAKQLHIERNM 716

RESULT 12
Q93T75
ID Q93T75 PRELIMINARY; PRT; 1228 AA.
AC Q93T75;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Delta-endotoxin Cry1Ba2.
GN Name=cry1Ba2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAK51084.1; -.
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA24DBF59C95C3 CRC64;

Query Match 60.6%; Score 2277.5; DB 2; Length 1228;
Best Local Similarity 62.7%; Pred. No. 2.3e-148;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEFPVSASTIQTGIGIAGKI 70
DB 2 TSNRKNENEIINAVSNHSAQMDLLDPARTEDSLCIAEGNIDPFVSASTVQTGINIAGRI 61
QY 71 LGTLGVPPAGQVASYLSPFELGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
DB 62 LGVLGVPPAGQVASYLSPFELGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 121
QY 131 LGDALAVYHDSLESWSGNNRNRARSVKQSYQYALELMFVKQLPSFAVSGEEVPLPIYA 190
DB 122 LGDSFRAYQOQSLDLEWLENDDRTSRVLTQYIALELDFNAMPFAIRNQEVPLLMVTA 181
QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQRERAGDYDCHVKYKYSTGLNNLRGTN 250
DB 182 QAANLHLLLRDASLFGSEFGLTSQBIQRYERQVERTRDSDYCVETWNTGLNSLRGTN 241
QY 251 AESWRYNQFRDMTLMVLDLVALFSPYDTQMPYIKTAQLTRVYTDGATGVHPHSPST 310
DB 242 AASWRYNQFRDLTLGLVDLVALFSPYDTQMPYIKTAQLTRVYTDGATGVHPHSPST 299
QY 311 STTWYNNAPPSAIEAAVVRPHLLDLEQVITYSLLSRWNSNTQYMMNMGHGHKLEFRTI 370
DB 300 SMWYNNAPPSAIEAAVVRPHLLDLEQVITYSLLSRWNSNTQYMMNMGHGHKLEFRTI 359

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QY 371 GGTLNISTQGSTNTSINPVTLLFTSRDVRVRESLAGMLF--LTQPVNVCVPRVDHFKVF 428
DB 360 GCGLTNTHTGATNTSINPVTLLFTSRDVRVRESLAGMLF--LTQPVNVCVPRVDHFKVF 416
QY 429 THP-----IASDNFVYVGVIGTQLODSENELPPEATGQPNVYSYSHLSHIGLISASH 483
DB 417 TNPQNISDRGTANYSQP-YESFGLQDKSEVELPPTETTERPNVYSYSHLSHIGLISASH 475
QY 484 VKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRLRTNTGT 543
DB 476 VNVVYVSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRLRTNTGT 535
QY 544 FGDIRVNPFPQAQRYRIRYASTTDLOFHTSINGKAINQGNFSATNNRGEDLDYKTF 603
DB 536 FGDIRVNPFPQAQRYRIRYASTTDLOFHTSINGKAINQGNFSATNNRGEDLDYKTF 595
QY 604 TVGFTTPTSFSDVOSTFTTIGAWNFSSGNEVYIDRIERFVPEVVEAEVDPEKAQEKVTA 663
DB 596 RRAFTTPTFTTQIIDIIRTSIQGLSNGEVIYDKLEIIPVTATFAEYDLERAQEVNVAL 655
QY 664 FTSTNPRGLKTDVVDYHIDQVSNLVESLSDFFYLDKRELFELFVYAKQLHIERNM 719
DB 656 FTNTNPRKLTDDVTDYHIDQVSNLVESLSDFFYLDKRELFELFVYAKQLHIERNM 711

RESULT 13
C1BA_BACTK
ID C1BA_BACTK STANDARD; PRT; 1228 AA.
AC P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cry1Ba (insecticidal delta-endotoxin Cry1B(a)) (crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cry1Ba; Synonyms=cryA4, cry1B(a);
OS Bacillus thuringiensis (subsp. kurstaki), and
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1436;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
RX MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from Bacillus thuringiensis subsp. thuringiensis.";
RL Nucleic Acids Res. 16:2723-2723(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC
DB EMBL; X06711; CAA29898.1; -.
DB EMBL; X95704; CAA65003.1; -.
DB FIR; S00873; S00873.
DB HSSP; P07130; 1DLC.

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DR	InterPro; IPR001178; Endotoxin.	OS	Bacillus thuringiensis.
DR	InterPro; IPR005638; endotoxin.C	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
DR	InterPro; IPR005639; endotoxin.N	OX	NCBI_TaxID=1428;
DR	InterPro; IPR008979; Gal bind_Like	RN	[1]
DR	Pfam; PF03944; Endotoxin_C; 1.	RP	SEQUENCE FROM N.A.
DR	Pfam; PF00555; Endotoxin_M; 1.	RL	Zhang J., Song F., Huang D.;
DR	Pfam; PF03945; Endotoxin_N; 1.	RM	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
KW	Sporulation; Toxin.	DR	EMBL; AF368257; AAK63251.1; -
FT	VARIANT 150 150 Y -> H (in strain HD-110).	DR	HSSP; P07130; 1DLC
SQ	SEQUENCE 1228 AA; 139647 MW; C8E3A19F5D98575 CRC64;	DR	GO; GO:0005102; F:receptor binding; IEA.
		DR	GO; GO:0006952; P:defense response; IEA.
		DR	GO; GO:0009405; P:pathogenesis; IEA.
		DR	InterPro; IPR001178; Endotoxin.
		DR	InterPro; IPR005638; endotoxin.N
		DR	InterPro; IPR005639; endotoxin.C
		DR	InterPro; IPR008979; Gal bind_Like.
		DR	Pfam; PF03944; Endotoxin_C; 1.
		DR	Pfam; PF00555; Endotoxin_M; 1.
		DR	Pfam; PF03945; Endotoxin_N; 1.
		DR	SEQUENCE 1228 AA; 139665 MW; E86D9842341FB439 CRC64;
		SQ	
			Query Match 60.3%; Score 2268.5; DB 2; Length 1228;
			Best Local Similarity 62.6%; Pred. No. 9.4e-148;
			Matches 449; Conservative 80; Mismatches 163; Indels 25; Gaps 6;
QY	23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPFSASTIQTGIGIAGKI 70	QY	23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPFSASTIQTGIGIAGKI 70
DB	2 TSNRKNENIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61	DB	2 TSNRKNENIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61
QY	71 LGTLGVPPAGQVASYLFGELMPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130	QY	71 LGTLGVPPAGQVASYLFGELMPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
DB	62 LGVLGVPPAGQLASFYSFLVGLMPGRDQWEIFLEHVEQLINQOITENARNALTALRQOG 121	DB	62 LGVLGVPPAGQLASFYSFLVGLMPGRDQWEIFLEHVEQLINQOITENARNALTALRQOG 121
QY	131 LGDALAVYHDSLESWNGNRRNTRARSVVKSOYIALELMFVKQLPSFAVSGEVEPLPIYA 190	QY	131 LGDALAVYHDSLESWNGNRRNTRARSVVKSOYIALELMFVKQLPSFAVSGEVEPLPIYA 190
DB	122 LGDSFRAYQOQSLDLEWLNEDDARTSVLYTQVIALELDFLNAMPLFAIRNQEVPLLMVYA 181	DB	122 LGDSFRAYQOQSLDLEWLNEDDARTSVLYTQVIALELDFLNAMPLFAIRNQEVPLLMVYA 181
QY	191 QAAHLHLLLRDASIFGKWLGSSEISTFYNRQVERAGDYSDHCVKYSTGLNLRGTN 250	QY	191 QAAHLHLLLRDASIFGKWLGSSEISTFYNRQVERAGDYSDHCVKYSTGLNLRGTN 250
DB	182 QAAHLHLLLRDASLFGSEFGLTSQEIQRYERQVERTRDYSYCVSEWYNTGLNLRGTN 241	DB	182 QAAHLHLLLRDASLFGSEFGLTSQEIQRYERQVERTRDYSYCVSEWYNTGLNLRGTN 241
QY	251 AESWVRYNQFRDMLTMDLVALPFSYDTQMPYIKTTAQLREVYTDAGTVHPHPSFT 310	QY	251 AESWVRYNQFRDMLTMDLVALPFSYDTQMPYIKTTAQLREVYTDAGTVHPHPSFT 310
DB	242 AASWVRYNQFRDMLTMDLVALPFSYDTQMPYIKTTAQLREVYTDAGTVHPHPSFT 299	DB	242 AASWVRYNQFRDMLTMDLVALPFSYDTQMPYIKTTAQLREVYTDAGTVHPHPSFT 299
QY	311 STTWYNNAPSFSAIAAIVRNPHLLDFLEQVTIYLLSRWSTQYNNMNGHKLFRPTI 370	QY	311 STTWYNNAPSFSAIAAIVRNPHLLDFLEQVTIYLLSRWSTQYNNMNGHKLFRPTI 370
DB	300 SMWYNNAPSFSAIAAIVRNPHLLDFLEQVTIYLLSRWSTQYNNMNGHKLFRPTI 359	DB	300 SMWYNNAPSFSAIAAIVRNPHLLDFLEQVTIYLLSRWSTQYNNMNGHKLFRPTI 359
QY	371 GGTINISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNF--LTQPVNGVPRVDFHMKFV 428	QY	371 GGTINISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNF--LTQPVNGVPRVDFHMKFV 428
DB	360 GGLNTSTHGAATNTSINPVTLPFTSRDVRVRESLAGLNF--LTQPVNGVPRVDFHMKFV 416	DB	360 GGLNTSTHGAATNTSINPVTLPFTSRDVRVRESLAGLNF--LTQPVNGVPRVDFHMKFV 416
QY	429 THP-----IASDNFYPYGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISASH 483	QY	429 THP-----IASDNFYPYGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISASH 483
DB	417 TNPQNISDRGTANYSQP--YESFGLQKUSETELPEPPERPNYESYSHRLSHIGLILQSR 475	DB	417 TNPQNISDRGTANYSQP--YESFGLQKUSETELPEPPERPNYESYSHRLSHIGLILQSR 475
QY	484 VKALVYSWTHRSADRNTIENPSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTNTGT 543	QY	484 VKALVYSWTHRSADRNTIENPSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTNTGT 543
DB	476 VNVVYVSWTHRSADRNTIENPSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTNTGT 535	DB	476 VNVVYVSWTHRSADRNTIENPSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTNTGT 535
QY	544 FGDIVNINPPFAQRYVRIRYASTTDLPFTSINGKAINQGNFSAATNMRGDLDYKTFR 603	QY	544 FGDIVNINPPFAQRYVRIRYASTTDLPFTSINGKAINQGNFSAATNMRGDLDYKTFR 603
DB	536 FGPVIRVTVNGPLTQRYRIGFYASTVDFDFVSRGTTVVRGPGFTGGDILRRTNTGG 595	DB	536 FGPVIRVTVNGPLTQRYRIGFYASTVDFDFVSRGTTVVRGPGFTGGDILRRTNTGG 595
QY	604 TVGFTTPEFLDVQSTFTIGAMNPFSSGNEVYIDRIEFVEVYEAEDYFEKAQEKVTAL 663	QY	604 TVGFTTPEFLDVQSTFTIGAMNPFSSGNEVYIDRIEFVEVYEAEDYFEKAQEKVTAL 663
DB	596 RRAFTTPTFTQIQDIIRTSIQGLSGNGEVYIDKIEIIPVTATFEAYDLERAQAVNAL 655	DB	596 RRAFTTPTFTQIQDIIRTSIQGLSGNGEVYIDKIEIIPVTATFEAYDLERAQAVNAL 655
QY	664 FTSTNPRGLKTDVKYDHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719	QY	664 FTSTNPRGLKTDVKYDHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB	656 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDFECLDEKRELLEKVKYAKLSDERNL 711	DB	656 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDFECLDEKRELLEKVKYAKLSDERNL 711

RESULT 14  
Q93NM5 PRELIMINARY; PRT; 1228 AA.  
AC Q93NM5  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Cry1Ba.  
GN Name=Cry1Ba;

Q6PYW8	PRELIMINARY;	PRT;	849 AA.
AC	Q6PYW8;		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	Cry1B type crystal protein (Fragment).		
OS	Bacillus thuringiensis (subsp. kurstaki).		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=29339;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=K1;		
RA	Li M.S., Choi J.Y., Roh J.Y., Shim H.J., Boo K.S., Je Y.H.;		
RL	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY570734; AAS93797.1; --		
DR	GO; GO:0005102; P:receptor binding; IEA.		
DR	GO; GO:0006952; P:defense response; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin C.		
DR	InterPro; IPR005639; endotoxin N.		
DR	InterPro; IPR008979; Gal bind like.		
DR	Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		
FT	NON_TER 849 849		
SQ	SEQUENCE 849 AA; 95886 MW; FCB98495787CF763 CRC64;		
Query Match	58.4%;	Score 2195.5;	DB 2; Length 849;
Best Local Similarity	59.4%;	Pred. No. 6.2e-143;	
Matches 424;	Conservative 106;	Mismatches 171;	Indels 13; Gaps 3
QY	13 SSNAKVXKISTDSLKN-----ETDIELQNIHEDCLKMSYENVVBFVSASTITQTGIG 65		
DB	7 NENEIINALSIPAVNSHSAQMLSTDARI----EDSLCIAEGNNIDFPVSASTVQTGIN 61		
QY	66 TAGKITLGTGVFPAGQAVLSYFILGELWPKGNOWEIFMEHVSEIIINQKISTYARNKAL 125		
DB	62 IAGRIITLGVLPFAGQIASFYSLFGEIWLPRGRDPWEIFLEHVEQLIRQVQVTRDTAL 121		
QY	126 TDLKGLGALAVYTHPSLSEWGNRNTRARSVVKSQYIALELMFVKQLPSFAVSCEEVPL 185		
DB	122 ARLOGLSHFRAYQOSLEDWLENRDARTSRVITYQYIALELDLFLNAPLFAIRNQEVPL 181		
QY	186 LPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGYSDHCVKWYSTGLNN 245		
DB	182 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEKTRYSYDCARWYNTGLNN 241		
QY	246 LGRTNAESWRVNRQFRDWTMLVDLVALFPSYDTQMPYIKTTAQLTRVEYTDALGTVHP 305		
DB	242 LGRTNAESWLRVNRQFRDLTLGVLDLVALFPSYTRVYPMNTSAQLTRREIYTDPIGRNA 301		
QY	306 HPSFTSTWYNNNAPSFAIAEAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMGGHKL 365		
DB	302 PSGFASTWFWNNAPSFAIEAAVTRPHLLDFPEQLTIFSVLSRWSTQYNNYVWGRL 361		
QY	366 EPRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTERESLAGLNFLFTQVNGVPRVDFHW 425		
DB	362 ESRITGSLSTHGTGNTSINPVTLPFTSRDVRTERESFAGINILLTTPVNGVPPWARENW 421		
QY	426 KVTHTPIASDNFYGYVIGTQLODSENELPPEATGQPNYESYSHRLSHGLISASHVK 485		
DB	422 RNPLNSLRGSLYTTIGYTGVGQLPDSLETPEPTEPRPNYESYSHRLSNRLISGNLIR 481		
QY	486 ALVYSWTHRSADRTWNTIENSITQIPLKAFNLSSGAAVVRPGFTGGDILRRNTGTFG 545		
DB	482 APVYSWTHRSADRTWNTISSDITQIPLKSFNLNSGTSVVSQPGFTGGDILRTNVGSLV 541		
QY	546 DIRVNNPPFAQRYRVIRYASTTDLQFHTSINKAINQGNFSAATNWRGEDLDYKTPRTV 605		



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:32:21 ; Search time 16.5835 Seconds  
(without alignments)  
4171.616 Million cell updates/sec

Title: US-10-019-823B-57  
Perfect score: 3760  
Sequence: 1 MKLKNQDKHQSFSNAKVDK.....KRELFEIVKAKOLHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3756	99.9	719	2 I39815	insecticidal prote
2	3747	99.7	719	2 S25383	parasporal crystal
3	3739	99.4	719	2 I39814	insecticidal prote
4	3516	93.5	719	2 I40590	cry465 protein -
5	2276.5	60.5	1228	2 S00873	parasporal crystal
6	1900	50.5	380	2 B42459	hypothetical prote
7	1494	39.7	1157	1 S49247	parasporal crystal
8	1482.5	39.4	1166	2 S32645	parasporal crystal
9	1472	39.1	1155	2 A26513	parasporal crystal
10	1469	39.1	1174	2 S32849	parasporal crystal
11	1465	39.0	1155	2 JD0002	parasporal crystal
12	1465	39.0	1156	2 A29125	parasporal crystal
13	1458.5	38.8	934	2 A22798	parasporal crystal
14	1457.5	38.8	1176	2 JT0241	parasporal crystal
15	1451.5	38.6	1176	2 JC2219	parasporal crystal
16	1448	38.5	1155	2 S02134	parasporal crystal
17	1447.5	38.5	1176	2 A22167	parasporal crystal
18	1447.5	38.5	1176	2 S02215	parasporal crystal
19	1447.5	38.5	1181	2 A41052	parasporal crystal
20	1444	38.4	1155	2 I39838	parasporal crystal
21	1358	36.1	1174	2 A42459	parasporal crystal
22	1353	36.0	1138	2 A48944	parasporal crystal
23	1339.5	35.6	1156	2 A29838	parasporal crystal
24	1329.5	35.4	823	2 S04181	parasporal crystal
25	1320.5	35.1	1189	2 S00944	parasporal crystal
26	1310	34.8	1154	2 S39536	parasporal crystal
27	1270	33.8	1171	2 I40572	parasporal crystal
28	1270	33.8	1171	2 A37829	parasporal crystal
29	1261	33.5	1176	2 A48970	parasporal crystal

30	1238	32.9	1160	2 S32647	parasporal crystal
31	1223.5	32.5	1165	2 S11446	parasporal crystal
32	1207.5	32.1	655	2 JC7140	protoxin - Bacillu
33	1195	31.8	1172	2 S32689	parasporal crystal
34	1186	31.5	1160	2 I40589	parasporal crystal
35	1161.5	30.9	1178	1 USBSXH	parasporal crystal
36	1161	30.9	1177	2 A49785	parasporal crystal
37	1154	30.7	652	2 A27323	parasporal crystal
38	1135	30.2	659	2 S10228	parasporal crystal
39	1104.5	29.4	652	2 I39811	parasporal crystal
40	984	26.2	649	1 JH0261	parasporal crystal
41	933	24.8	618	2 S11445	parasporal crystal
42	889	23.6	1156	2 S19306	parasporal crystal
43	827	22.0	1136	1 USBS81	parasporal crystal
44	691.5	18.4	934	2 B29838	parasporal crystal
45	666	17.7	1180	2 I39870	parasporal crystal

ALIGNMENTS

RESULT 1

I39815  
insecticidal protein cryV - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I39815  
R:Gleave, A.P.; Williams, R.; Hedges, R.J.  
Appl. Environ. Microbiol. 59, 1683-1687, 1993  
A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for iensis subsp. kurstaki.  
A:Reference number: I39815; MUID:93298009; PMID:8517758  
A:Accession: I39815  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:Cross-references: UNIPROT:Q45752; GB:M98544; NID:g142767; PIDN:AAA22354.1; PID:g142768  
C:Genetic: cry  
C:Superfamily: parasporal crystal protein

Query Match 99.9%; Score 3756; DB 2; Length 719;  
Best Local Similarity 99.9%; Pred. No. 9.8e-256;  
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MKLKNQDKHQSFSNAKVDKISTDSLKNETDLELQINHEHEDCLKMSEYENVEPVSASTI	60
Db	1	MKLKNQDKHQSFSNAKVDKISTDSLKNETDLELQINHEHEDCLKMSEYENVEPVSASTI	60
Qy	61	QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA	120
Db	61	QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA	120
Qy	121	RNKALTDLKGLDALAVYHDSLESWVGNNRNNTRARSVWKSQVIALFLMFVKQLPSFAVSG	180
Db	121	RNKALTDLKGLDALAVYHDSLESWVGNNRNNTRARSVWKSQVIALFLMFVKQLPSFAVSG	180
Qy	181	EEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSSISITFYNNQVRAGDYSCHCVKWS	240
Db	181	EEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSSISITFYNNQVRAGDYSCHCVKWS	240
Qy	241	TGLNNLRGTNAESWRYNQFRDMLTMLVDLVALFPSTQMYPIKTTAQLTREVTDAI	300
Db	241	TGLNNLRGTNAESWRYNQFRDMLTMLVDLVALFPSTQMYPIKTTAQLTREVTDAI	300
Qy	301	GTVHPHPSPTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW	360
Db	301	GTVHPHPSPTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW	360
Qy	361	GGHKLFRITGIGTLNISTOGSTNTSINPVTLPSTSDVYRTESLAGNLFLTQPVNGVPR	420
Db	361	GGHKLFRITGIGTLNISTOGSTNTSINPVTLPSTSDVYRTESLAGNLFLTQPVNGVPR	420

421 VDFHWKFTVTHPIASDNFYPGYVIGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
421 VDFHWKFTVTHPIASDNFYPGYVIGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
481 ASHVKALVYSWTHRSADRTNTIEPNSITQPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
481 ASHVKALVYSWTHRSADRTNTIEPNSITQPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
541 TGTGDIRVNTNPPPAQRYRIRIYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 600  
541 TGTGDIRVNTNPPPAQRYRIRIYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 600  
601 TFRVTGFTTPSFDFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAAYDEPKAQEKV 660  
601 TFRVTGFTTPSFDFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAAYDEPKAQEKV 660  
661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFYLDKRELFVVKYAKQLHIERNM 719  
661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFYLDKRELFVVKYAKQLHIERNM 719

RESULT 2  
S25383  
parasporal crystal protein cryIIa1 - Bacillus thuringiensis  
N/Alternate names: delta-endotoxin; parasporal crystal protein cryV  
C/Species: Bacillus thuringiensis  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C/Accession: S25383  
R/Tailor, R.; Tippet, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.  
Mol. Microbiol. 6, 1211-1217, 1992  
A/Title: Identification and characterization of a novel Bacillus thuringiensis delta-end  
A/Reference number: S25383; MUID:92269582; PMID:1588820  
A/Accession: S25383  
A/Molecule type: DNA  
A/Residues: 1-719 <TAI>  
A/Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:940289; PIDN:CAA44633.1; PID:940290  
C/Genetics:  
C/Gene: cryV  
C/Superfamily: parasporal crystal protein  
C/Keywords: delta-endotoxin

Query Match 99.7%; Score 3747; DB 2; Length 719;  
Best Local Similarity 99.7%; Pred. No. 4.2e-255;  
Matches 717; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCIKMSEYENVEPVSASTI 60  
DB 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCIKMSEYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTLGVPPAGQVSLYSFILGELWPKGNQWEIFMEHVVEEIIINOKISTYA 120  
DB 61 QTGIGIAGKILGTLGVPPAGQVSLYSFILGELWPKGNQWEIFMEHVVEEIIINOKISTYA 120  
QY 121 RNKALTDLKGLGDALAVYHDSLESWGVRNNTARSVVKSYQYIALELMFVKQLPSFAVSG 180  
DB 121 RNKALTDLKGLGDALAVYHDSLESWGVRNNTARSVVKSYQYIALELMFVKQLPSFAVSG 180  
QY 181 BEVPLLPYIAQAANLHLLLRDASIFCKEWGLSSSEISTFYNQVERAGDYSDHCVKWS 240  
DB 181 BEVPLLPYIAQAANLHLLLRDASIFCKEWGLSSSEISTFYNQVERAGDYSDHCVKWS 240  
QY 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDI 300  
DB 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDI 300  
QY 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW 360  
DB 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW 360  
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRITESLAGLNLFLTQPVNGVPR 420  
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRITESLAGLNLFLTQPVNGVPR 420

421 VDFHWKFTVTHPIASDNFYPGYVIGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
421 VDFHWKFTVTHPIASDNFYPGYVIGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
481 ASHVKALVYSWTHRSADRTNTIEPNSITQPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
481 ASHVKALVYSWTHRSADRTNTIEPNSITQPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
541 TGTGDIRVNTNPPPAQRYRIRIYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 600  
541 TGTGDIRVNTNPPPAQRYRIRIYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 600  
601 TFRVTGFTTPSFDFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAAYDEPKAQEKV 660  
601 TFRVTGFTTPSFDFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAAYDEPKAQEKV 660  
661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFYLDKRELFVVKYAKQLHIERNM 719  
661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFYLDKRELFVVKYAKQLHIERNM 719

RESULT 3  
I39814  
insecticidal protein cryVI - Bacillus thuringiensis  
C/Species: Bacillus thuringiensis  
C/Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 26-Aug-1999  
C/Accession: I39814  
R/Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A/Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis  
tomocidus.  
A/Reference number: I39814; MUID:95314293; PMID:7793960  
A/Accession: I39814  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-719 <RES>  
A/Cross-references: GB:I36338; NID:9540281; PIDN:AAC36999.1; PID:9540282  
C/Genetics:  
C/Gene: cryVI  
C/Superfamily: parasporal crystal protein

Query Match 99.4%; Score 3739; DB 2; Length 719;  
Best Local Similarity 99.4%; Pred. No. 1.5e-254;  
Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCIKMSEYENVEPVSASTI 60  
DB 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCIKMSEYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTLGVPPAGQVSLYSFILGELWPKGNQWEIFMEHVVEEIIINOKISTYA 120  
DB 61 QTGIGIAGKILGTLGVPPAGQVSLYSFILGELWPKGNQWEIFMEHVVEEIIINOKISTYA 120  
QY 121 RNKALTDLKGLGDALAVYHDSLESWGVRNNTARSVVKSYQYIALELMFVKQLPSFAVSG 180  
DB 121 RNKALTDLKGLGDALAVYHDSLESWGVRNNTARSVVKSYQYIALELMFVKQLPSFAVSG 180  
QY 181 BEVPLLPYIAQAANLHLLLRDASIFCKEWGLSSSEISTFYNQVERAGDYSDHCVKWS 240  
DB 181 BEVPLLPYIAQAANLHLLLRDASIFCKEWGLSSSEISTFYNQVERAGDYSDHCVKWS 240  
QY 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDI 300  
DB 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDI 300  
QY 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW 360  
DB 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW 360  
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRITESLAGLNLFLTQPVNGVPR 420  
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRITESLAGLNLFLTQPVNGVPR 420

QY 421 VDFHWFVTHPIASDNFYFPGVIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWFVTHPIASDNFYFPGVIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAENLSSGAAVRGPFTGGDIILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAENLSSGAAVRGPFTGGDIILRRTN 540  
QY 541 TGTFGDIRVINPPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGDLKY 600  
DB 541 TGTFGDIRVINPPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGDLKY 600  
QY 601 TTRTVGFTTFFSFLDVQSTFTTGAMNFFSGNEVYIDRIEFVPEVYIEAYDFEKAQEKV 660  
DB 601 TTRTVGFTTFFSFLDVQSTFTTGAMNFFSGNEVYIDRIEFVPEVYIEAYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKOLHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKOLHIERNM 719

RESULT 4  
I40590  
CryV465 protein - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: I40590  
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A:Title: Distribution of cryv-type insecticidal protein genes in Bacillus thuringiensis  
tomocidus.  
A:Reference number: I39814; MUID:95314293; PMID:7793960  
A:Accession: I40590  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:g467234; PIDN:AAA82114.1; PID:g4672  
C:Genetics:  
A:Gene: cryV465  
C:Superfamily: paraaporal crystal protein

Query Match 93.5%; Score 3516; DB 2; Length 719;  
Best Local Similarity 92.8%; Pred. No. 7.1e-239;  
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;  
QY 1 MKLKNQDKHQSPSSNAKVDKISTDSLKNETDIELQINHEDCLKMEYENVEPVSASTI 60  
DB 1 MKLKNQDKHQSLSSNAKVDKIATDSLKNETDIELKNHEDYLRMSEHESIDPFVSASTI 60  
QY 61 QTGIGIAGKILGTVPPFAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTVPPFAGQIASLYSFILGELMPKGNQWEIFMEHVEEIIINQKILTYA 120  
QY 121 RNKALTDLGLGALAVYHDSLESVGNRNNTARSVVKSYQYIALEIMFVKQLPSPFVSG 180  
DB 121 RNKALSDLRGLGALAVYHDSLESVGNRNNTARSVVKSYQYIALEIMFVKQLPSPFVSG 180  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVRAGDYSCHCKWYS 240  
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVRAGDYSCHCKWYN 240  
QY 241 TGLNLRGNTNABSWRYNQRPRDMLMVLVDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
DB 241 TGLNLRGNTNABSWRYNQRPRDMLMVLVDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
QY 301 GTVHPHPSFTSTWYNNAPSPFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQNMW 360  
DB 301 GTVHPNQAFSTWYNNAPSPFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQNMW 360  
QY 361 GGHKLBFRITGTLNISTOGSTWNTSINPVTLPFTSRDVYRTESLAGNLPLTQPNVGNVR 420  
DB 361 GGHRLSRPITGGALNTSTOGSTWNTSINPVTLPFTSRDVYRTESLAGNLPLTQPNVGNVR 420

QY 421 VDFHWFVTHPIASDNFYFPGVIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWFVTHPIASDNFYFPGVIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAENLSSGAAVRGPFTGGDIILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAENLSSGAAVRGPFTGGDIILRRTN 540  
QY 541 TGTFGDIRVINPPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGDLKY 600  
DB 541 TGTFGDIRVINPPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGDLKY 600  
QY 601 TTRTVGFTTFFSFLDVQSTFTTGAMNFFSGNEVYIDRIEFVPEVYIEAYDFEKAQEKV 660  
DB 601 TTRTVGFTTFFSFLDVQSTFTTGAMNFFSGNEVYIDRIEFVPEVYIEAYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKOLHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKOLHIERNM 719

RESULT 5  
S00873  
paraaporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis  
N:Alternate names: paraaporal crystal protein cryA4  
C:Species: Bacillus thuringiensis subsp. thuringiensis  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C:Accession: S00873  
R:Brizard, B.L.; Whiteley, H.R.  
Nucleic Acids Res. 16, 2723-2724, 1988  
A:Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus  
A:Reference number: S00873; MUID:88203216; PMID:3362680  
A:Accession: S00873  
A:Molecule type: DNA  
A:Residues: 1-1228 <BRI>  
A:Cross-references: UNIPROT:P05517; EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PID:g58094  
C:Genetics:  
A:Gene: cryA4  
A:Start codon: TTG  
C:Superfamily: paraaporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 60.5%; Score 2276.5; DB 2; Length 1228;  
Best Local Similarity 62.7%; Pred. No. 2e-151;  
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;  
QY 23 TDSLKNETDIELQINH-----EDCLKMEYENVEPVSASTIQTGIGTAGKI 70  
DB 2 TSNRKNENIINAVSNHSAQMDLLPDARIEDSLCTAEGNNIDPFVSASTVQTGINTAGRI 61  
QY 71 LGTLGVPPFAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130  
DB 62 LGVLGVPPFAGQASLYSFVLGELMPGRDQWEIFLEHVEQLINQOITENARNALALQOG 121  
QY 131 LGDALAVYHDSLESVGNRNNTARSVVKSYQYIALEIMFVKQLPSPFVSGEEVPLPIYA 190  
DB 122 LGDSFRAYQQSLEDMLNRRDARTRSVLYTQVIALELDFLNAMPLFAIRNQEVPLLMVYA 181  
QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVRAGDYSCHCKWYSSTGLNLRGNTN 250  
DB 182 QAANLHLLLRDASIFGSEFGLTSOIQRYSRQVRERTRDYSYCVQVWNTGLNLRGNTN 241  
QY 251 AESWRYNQRPRDMLMVLVDLVALFPSYDTQMPYIKTTAQLTREYVTDALGTVHPHPSFT 310  
DB 242 AASWRYNQRPRDMLMVLVDLVALFPSYDTQMPYIKTTAQLTREYVTDALGTAT--GVNMA 299  
QY 311 STTWYNNAPSPFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQNMWGGHKLFRPTI 370  
DB 300 SMWYNNAPSPFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQNMWGGHKLFRPTI 359  
QY 371 GGTINISTOGSTWNTSINPVTLPFTSRDVYRTESLAGNLPLTQPNVGNVRDHWKVF 428  
DB 360 GGLANTSTHGANTSTOGSTWNTSINPVTLPFTSRDVYRTESLAGNLPLTQPNVGNVRDHWKVF 416





Db 709 YGHDKQMLLEAVRAAKRLSRNL 732

RESULT 8  
S32645  
parasporeal crystal protein crylGal - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S32645  
R:Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A:Reference number: S32645  
A:Accession: S32645  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1166 <LAW>  
A:Cross-references: UNIPROT:Q45746; EMBL:Z22510; NID:g295861; PIDN:CAA80233.1; PID:g2958  
C:Superfamily: parasporeal crystal protein  
C:Keywords: delta-endotoxin

Query Match 39.4%; Score 1482.5; DB 2; Length 1166;  
Best Local Similarity 46.2%; Pred. No. 1.1e-95;  
Matches 326; Conservative 97; Mismatches 207; Indels 75; Gaps 16;

Qy 41 DCLKMEYE----NVEPFVASTIQGIGIAGKILGTGLVPPAGQVASYSLFELGELWPK 96  
Db 13 NCLNPESEIFNARNSEFGLVQVSSGL---TRFLLEAAVPEAGFALGFLDIWGAL--- 66

Qy 97 GKNOWEIFMEHVEEIIINQISTYARNKALTDLKGDLALAVYHDSLESWGNTRARS 156  
Db 67 GVDQSLFLRQEQILRQIRITELERNRATILTLGSSSYNLYVEALREWENPNPNPASQE 126

Qy 157 VVKSOYIALELMPVQKLPSPFVSGEVEPLPIYAQAANLHLLLRDASFFGKRWGLSSSE 216  
Db 127 RVTRFRLTDDALVTGLPLATRNLEVNLSVYTAQANLHLSLRDADVFGRWGLTQAN 186

Qy 217 ISTFYNRQVERAGDSDHCKVYKYSTGLNLRGTAESWRYNQFRDMTLMVLVALPP 276  
Db 187 IEDLYRLTNSIQEYSDHCKARWQGLNEIGGISR---RYLDFQRLDILSVLDIVALPP 242

Qy 277 SYDTQMPYIKTTAQLTRVYTDAL--GTVHPHPSFTSTWYNNNAPSFAIAEAVVRNPH 334  
Db 243 NYDIRTYPIQTSQQLREIYTSVWAGNI-----NFGLSANVLRLAPH 285

Qy 335 LLDLFLEQVITYSLRSWSTQYNNMGHKLFRITIG-GTLN-----ISTQGSTNTS 385  
Db 286 LMDFIDRIYVYNSVR--STPY---WAGHEVISRRTGQGGNEIRFPLVGAANAEPVYT 340

Qy 386 INPVTLPFTSRDVRYES-----LAGNLFLTPQVNGVPRVDFHKKFVTHPIASDNFY 439  
Db 341 IRPTGFTDEQORWYRARSRVSPSSGQDFSLVDAVG-----FLT--IFSASVSY 388

Qy 440 PGVVGIGTQLODSENELPPEATQCPNYESYSHRLSHIGLISAS-----HVKALVSWTHR 494  
Db 389 RNGFGFNT--DTIDRPIEGTDP--FTGYSHRLCHVGFGLASSPFTISQARAPIFSWTHR 443

Qy 495 SADRTWTIBPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTFGDIRVNNPP 554  
Db 444 SATLTWTIAPDVITQIPLVKAFNLHSGATVKGPGFTGGDILRRNTGVSFGDMRVNITAP 503

Qy 555 FAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYKPTFTVGTFTPPSFL 614  
Db 504 LSQRVVRIRYASTTDLQFVTNINGTTINGNFSTMSGDDLLQYGRFRVAGFTTPTFTS 563

Qy 615 DVQSTTTICAWNFSSGNEVYIDRIEFVPEVYEAEDPEKAQEKVLTALFTSTNPEGLKT 674  
Db 564 DANSTFTTGAFGSPNNEVYIDRIEFVPAEVTFAEYDLEKAQKAYNALFTSSNQTLGKT 623

Qy 675 DVKDYHIDQVSNLVESLDEFLDEKRELFEIVKYAKQLHIERNM 719  
Db 624 DVTDYHIDKVSNLVLECLSDFLDEKRELSEKVKHAKRLSDERNL 668

RESULT 9  
A26513  
parasporeal crystal protein - Bacillus thuringiensis (strain aizawai)  
C:Species: Bacillus thuringiensis  
C:Date: 11-Mar-1988 #sequence\_revision 11-Mar-1988 #text\_change 09-Jul-2004  
C:Accession: A26513  
R:Oeda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H.  
Gene 53, 113-119, 1987  
A:Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis  
A:Reference number: A26513; MUID:87248103; PMID:3297927  
A:Accession: A26513  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1155 <OED>  
A:Cross-references: UNIPROT:P06578; GB:M16463; NID:g143098; PIDN:AAA22551.1; PID:g143099  
C:Superfamily: parasporeal crystal protein  
C:Keywords: delta-endotoxin

Query Match 39.1%; Score 1472; DB 2; Length 1155;  
Best Local Similarity 44.4%; Pred. No. 6e-95;  
Matches 315; Conservative 113; Mismatches 227; Indels 54; Gaps 12;

Qy 36 NINHEDCLKMSEYENVE--PFVSASTIQG-----IGIAGKILGTGLVPPAGQVASYLS 87  
Db 4 NPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSTQTLSEF-VPGAGFVLGLVD 62

Qy 88 FTGLGELWPKGNQWEIFMEHVEEIIINQISTYARNKALTDLKGDLALAVYHDSLESWVG 147  
Db 63 IHWGIF--GPSQDAFLVQIQEQLNQRIEERARQAISRLGSLNLYQIYAESFREWEA 119

Qy 148 NNNNTRASVVKSVQIALELMPVQKLPSPFVSGEVEPLPIYAQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREEMRIQNDMNSALTATPLFAVQNYQVPLLSVYVQAANLHLSLRDVSVEG 179

Qy 208 KEMGLSSSEISFTFYNRQVERAGDSDHCKVYKYSTGLNLRGTAESWRYNQFRDMTLM 267  
Db 180 QRMGDAATINSYNDLTRLIGNYTDHARVNTGLERVMGDPDSRDMIRYNQFRRLTUT 239

Qy 268 VLDELVALPSPDYTMQYPIKTTAQLTRVYTDALGTVHPHPSFTSTWYNNNAPSFAIBA 327  
Db 240 VLDIVSLFPNYSRYTPRTVSQTLREIYTNPV-----LENFPGSPALAAQ 285

Qy 328 AV---VRPHLLDFLEQVITYSLRS---WSNTQYMM---WGHKLEFRITIGTLNIS 377  
Db 286 GTEGSIRSPHLMIDILNSITITVDAHGEVYWSGHQIMASPVGFGSGPEFTFPLYGTMGNA 345

Qy 378 TQGSTNTSINPVTLPFTSRDVRYESLGLNLFLTPQVNGVPRVDFHKKFVTHPIASDNF 437  
Db 346 POORIVAQGGQVYRTSLTLYRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSNL 396

Qy 438 YYPGVVGIGTQLODSENELPPEATQCPNYESYSHRLSHIGLI-----SASHKALVYS 490  
Db 397 PSAVYRKSGT--VDSLDEIPQNNVPPRQGSRLSHVSMFSGFSNSVSIIRAPMS 454

Qy 491 WTHRSADRTWTIBPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTFGDIRVN 550  
Db 455 WTHRSAEFNFIIPSSQITQIPLTKSNLGSSTVVKPGFTGGDILRRTPSQQISTLRVN 514

Qy 551 INPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYKPTFTVGTFTTP 610  
Db 515 ITAPUSQRYVRIRYASTTDLQFHTSIDGRPNQGNFSAATMNRGDLDYKPTFTVGTFTTP 574

Qy 611 FSFLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVYEAEDPEKAQEKVLTALFTSTNPR 670  
Db 575 FNFSNGSSVFTLSAHVFNSENEVYIDRIEFVPAEVTFAEYDLEKAQKAVNELFTSSNQI 634

Qy 671 GLKTDVYHIDQVSNLVESLDEFLDEKRELFEIVKYAKQLHIERNM 719  
Db 635 GLKTDVTDYHIDQVSNLVLECLSDFLDEKRELSEKVKHAKRLSDERNL 683

RESULT 10  
S32649

parasporal crystal protein cry1Pa3 - Bacillus thuringiensis  
C;Species: Bacillus thuringiensis  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: S32649  
R;Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A;Reference number: S32645  
A;Accession: S32649  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1174 <LAM>  
A;Cross-references: UNIPROT:Q45749; EMBL:Z22512; NID:Z293865; PIDN:CAA80235.1; PID:g2958  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 39.1%; Score 1469; DB 2; Length 1174;  
Best Local Similarity 44.8%; Pred. No. 9.9e-95;  
Matches 325; Conservative 103; Mismatches 202; Indels 96; Gaps 17;

36 NINHE-----DCLKMEYENVEPFVASTIQTGIGIA-GKILGTGLGVFPAGOVASLYSFIL 90  
4 NIQNCQFYNCLSNPEVILSEERSTGRPLDIDISLSTRFLLSFVPGVGVAFLFLIWL 63  
91 GELPFGKGNQWEIPEHVEEIIINOKISTYARNKALTDLKGIGDALAYVHDSLSWGNRN 150  
64 GFITP---SEWSFLQIEQLQRIETLERNRAITTLRLGLADSYEVVLEALREWEENPN 120  
151 NTRARSVKSOYIAELMFVQKLPFAVSGEEVPLPIYAQAANHLHLLRDASIFGKEW 210  
121 NAQLREDVRIRFANTDDALIAINFTLTSFEIPLLSVYQAANHLHLLRDASVFGOG 180  
211 GLSSEISTFYNRQVERAGDYSCHCKWYSLGNLRGTNAESVVRVNRQFDRMTLMVLD 270  
181 GDIAIVANNHNLNLHRTHECLDYNQGLNLRGTNTQWRSRNFQFRELTLVLVD 240  
271 LVALPFSYDTOMYPIKTTAQLTREYVYDAITGVPHPSFTTWTNNNAPS-PSAIAAV 329  
241 IVALFPYDARAYPIOTSSQLTREYTSV--IEDSP-----VSANIPNGFNRAEFG- 290  
330 VERNPHLLPLEQVITYSLRSKSNQYNNMGHKLERTTGTLNISTQGSTNTSINPV 389  
291 VAPPHLDMFN-----SLFVTAETVRSQTVMGHLLV-----SSRTAGNPI 331  
390 TLFP-----TGRDVTYRTSLAGNLFLTPQVNGVPRVDFHWKVFYTHPIAS 434  
332 NFPIYGFNPGGAIWIADEDPFVRT-----LSDPV-----FVRGGFGN 371  
435 DNFFYGVYVIGTQLQ-----DSENLPEATGQPNYESYSHLSHI----- 476  
372 PH-YVLGLRGVAFQQTGNTHTTFRNSGTTDSLDEIPPDNSGAPMWDYSHVLAHVTFR 430  
477 --GLISASHV-KALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGG 533  
431 WPEGELAGSOWRPMFSWTHRSADRTNINFNIIQIPAVKANHLSGSTVVRGPGFTGG 490  
534 DILRLTNTGTGDIRVINPFPQRYRVRIRVASTTDLOFTHSINGKAINQGNFSAWNR 593  
491 DILRLTNTGTADIRVINITGPLSQRYRVRIRVASTTDLOFFTRINGTSVNOGNFOTNR 550  
594 GEDLDYKTRTGVFTTPPSFLDVQSTFTIGANNFSGNEVYIDRIEFPVPEVYAEYDF 653  
551 GGNLESGNFRTAGFSFPFSNAQSTFTLTGTQAFSN-QEYVIDRIEFPVPAETFAESDL 609  
654 ERAQEKVTLFTSTNPRGLKTDVKYHIDQVNLVLSDESDFYLDKRELFELVIAKQL 713  
610 ERAQKAVNALFTSTSQLGLKTNVTGVHIDQVNLVACLSDSECLDKRELSKVKHAKRL 669  
714 HERNM 719  
670 SDRKNL 675

JD0002  
paraesporal crystal protein cry1Ab3 - Bacillus thuringiensis  
N;Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal prot  
C;Species: Bacillus thuringiensis  
C;Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 09-Jul-2004  
C;Accession: A90025; A91560; A90955; S14555; A24172; A29043; JD0002  
R;Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.  
Agric. Biol. Chem. 51, 455-463, 1987  
A;Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from  
A;Reference number: A90025  
A;Accession: A90025  
A;Molecule type: mRNA  
A;Residues: 1-1155 <KON>  
A;Cross-references: UNIPROT:P06578  
A;Experimental source: subsp. kurstaki  
R;Geisler, M.; Schweitzer, S.; Grimm, C.  
Gene 48, 109-118, 1986  
A;Title: The hypervariable region in the genes coding for entomopathogenic crystal prote.  
A;Reference number: A91560; MUID:87163505; PMID:3557124  
A;Accession: A91560  
A;Molecule type: DNA  
A;Residues: 1-1155 <GET>  
A;Cross-references: GB:M15271; NID:g143123; PIDN:AAA22561.1; PID:g143124  
R;Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.  
DNA 5, 305-314, 1986  
A;Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product anal.  
A;Reference number: A90955; MUID:86300092; PMID:3743328  
A;Accession: A90955  
A;Molecule type: DNA  
A;Residues: 1-1155 <WAB>  
A;Cross-references: GB:M13898; NID:g142719; PIDN:AAA22330.1; PID:g142720  
A;Experimental source: subsp. berliner  
R;Chak, K.F.; Jen, J.C.  
submitted to the EMBL Data Library, October 1990  
A;Description: Complete nucleotide sequence and expression in Escherichia coli of a cry  
A;Reference number: S14555  
A;Accession: S14555  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1155 <CHA>  
A;Cross-references: EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273  
R;Hoft, H.; de Greve, H.; Seuring, J.; Janssens, S.; Mahillon, J.; Ampe, C.; Vandekerck  
Eur. J. Biochem. 161, 273-280, 1986  
A;Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thur  
A;Reference number: A26461; MUID:87054026; PMID:3023091  
A;Accession: A26461  
A;Molecule type: DNA  
A;Residues: 1-730, 'L', 732-784, 'R', 786-1155 <HOF>  
A;Cross-references: GB:X04698; NID:g40254; PIDN:CAA28405.1; PID:g40255  
A;Experimental source: strain berliner 1715  
C;Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.  
C;Genetics:  
A;Gene: cry-1-2; bt2  
A;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin  
F;82-586/Product: toxic peptide #status predicted <TXP>  
F;82-300/Region: toxic #status predicted  
F;300-586/Region: insecticidal #status predicted

Query Match 39.0%; Score 1465; DB 2; Length 1155;  
Best Local Similarity 44.5%; Pred. No. 1.8e-94;  
Matches 316; Conservative 112; Mismatches 226; Indels 56; Gaps 13;

36 NINHECLKMEYENVE-PFVASTIQTG-----IGIAGKILGTGLGVFPAGOVASLYS 87  
4 NPINIECIPYNCLSNPEVFLGGERIETGTPIDISLSLTFQLLSEF-VPGAGFVLGLVD 62  
88 FILGELWPKGNQWEIPEHVEEIIINOKISTYARNKALTDLKGIGDALAYVHDSLSWVG 147  
63 IINGIF--GPSQWDAFLVQIEQLINQRIEFARNQAIISLEGLSNLYQIVAESFREWEA 119  
148 NRNTRARSVKSOYIAELMFVQKLPFAVSGEEVPLPIYAQAANHLHLLRDASIFG 207

Qy	208	KEWGLSSSEISTFYNRQVERAGDYSDHCWKWYSTGLNNLRGNASWVRYNOFRDMTLM	267
Db	180	QRWGFDAAINSRYNDILRLIGNYTHDAVRWYNTGLERWGPDSRDWIRYNQFRELTLT	239
Qy	268	VLDLVALPPSDYQWPIKTTAQLTRVYTDAGTVHPHPSFTSTWYNNAPSF----	323
Db	240	VLDIVLFPFNDSRYPIRYSQLTREIYITNP-----LENFGSFRGSAQ	285
Qy	324	AIEAAVRNPHLLDFLEQVITYSLLSR-----WSNTQYNNM---WGCHKLEFETIGTGLNI	376
Db	286	GIEGS-IRSPHMLDILNSITIVTDAHRGEYVWSGHOIMASPVGFSGPBETFPFLYGTWGNA	344
Qy	377	STQSGTNTSINPVTLPFTSRDVRYESLAGLNLFLTQPNVGVRVDFHWKFVTHPIASDN	436
Db	345	APOQRIVAQLGGQGYRTLSSTLYRRFPNIGIN---NQOLSVLDDGTFEAYG-----TSSN	395
Qy	437	FYPYCYVGIGTQLODSENELPEATGQPNYESYSHRLSHIGLI-----SASHVKALVY	489
Db	396	LPSAVYRKSGT--VDSDLDEIIPPQNNVPPROGFSHRLSHVMSFRSGFNSSVSIIRAPNF	453
Qy	490	SWTHRSADRTWTIBPNSITQIPLVKAFNLSSGAAVVRGFGTGGDILRNTNGTFGDIRV	549
Db	454	SWIHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVGPGFTGGDILRRTSPQISTLAV	513
Qy	550	NINPPFAQRYVRIRYASTTDLOPHTSINGKAINQGNFSATNWRGEDLDYKTRFTVGFTT	609
Db	514	NITAPLSQRYVRIRYASTTNLQPHTSIDGRPINOQGNFSATNWSGNSLQSGSFRVTGFTT	573
Qy	610	PFSLDVQSTETIGAWNPFSSGNEVYIDRIEFVPVEVTVEABEDPFAQKVTALFTSTNP	669
Db	574	PFNFSNGSVFTLSAHVPNSGNEVYIDRIEFVPAEVTFEAEVLDLRAQKAVNELFTSSNQ	633
Qy	670	RGLKTDVKDYHIDQVSNLJVESLSEFYLDKRELFEIVKYAKQLHIERNM	719
Db	634	IGLKTVDVTDYHIDQVSNLVECLSDSEFCJDEKKESEKVKHAKRLSDERNL	683

A22798  
parasporal crystal protein - *Bacillus thuringiensis*  
C:Species: *Bacillus thuringiensis*  
C:Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 09-Jul-2004  
C:Accession: A22798  
R:Shibano, Y.; Yamagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, Gene 34, 243-251, 1985  
A:Title: Nucleotide sequence coding for the insecticidal fragment of the Bacil  
A:Reference number: A22798; MUID:85232070; PMID:2989108  
A:Accession: A22798  
A:Molecule type: DNA  
A:Residues: 1-934 <SH1>  
A:Cross-references: UNIPROT:Q985V8; GB:M10917; NID:q143100; PIDN:AAA22552.1; P  
C:Comment: The authors translated the codon ACA for residue 264 as Ser.  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 38.8%; Score 1458.5; DB 2; Length 934;  
Best Local Similarity 43.7%; Pred.No. 3.8e-94;  
Matches 311; Conservative 119; Mismatches 221; Indels 61; Gaps 12  
Ov 36 NINHEDCLKNSEYENVE-PFVSASTIQTG-----IGIAGKILGTGVPPAGQVASLYS 87

Db	4	NNPINECIPYNCLNPENPEVIVGGRIETGYTPIDISLSTQFLLSEF-VFGAGFVLGLVD	62
Qy	88	FILGELMPKGNQWEIEMFHEVEEIIINQIKSTVARNKALTDLGLGDALAVYHDSLSWSVG	147
Db	63	IINGIF---GPSQWDAFLVQIEQLINQRIEFARNQASRLBGLSNLQIYAESSFEWEA	119
Qy	148	NRNNTARSVVYKSYALALELMFVKLPSPFAYSGSEVPLLPIYQAANLHLLLLRDASIEG	207
Db	120	DPTPALREEWRIQENDMNSALTTAIPFAVQNYQVPLPSVYQAANLHLSVLDRDVSVEG	179
Qy	208	KEWGLSSEISTFYNRQVERAGDYSDDHCKWYSTGLNNLRGTNAESWSWRYNOFRDMTLM	267

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Db 180 QRMGDAATNSRNDLTRIGNYTDYAVRWYNTGLERVWGPDSRDWVRNQFRRELTLT 239
Qy 268 VLDLVALPSPYDTOMYPIKTTAQLTRREYVTDAGTVHPHPSFTSTTWYNNAPSPSAIEA 327
Db 240 VLDLVALFNSYDSRRYPIRTVSQLTREIYTNPV-----LENFDGSGFRGMAQ 285
Qy 328 AV---VRNPHLLDFLEQVTVIYSLLSRWSNTQYMMWGGHKLFRPTIGGT---LNISQGS 381
Db 286 RIEQNIQPHLMDILNRIITYDVHVG-----FNWSGHQITASPVGSPGPEFAFPLFGN 340
Qy 382 TNSINPVTLPFTSRDVRVYTESL-----AGNLFLTPQVNGVPRVDFHMKFVTHPI 432
Db 341 AGNAAPPVLVSLTGLGIFRTLSPLRYRIILGSGPN---NQELFVLDTGTEFSASLTNL 397
Qy 433 ASDNFYYPGVGIGTQLQDSENELPPEATQPNYESYSHLSHIGLISAS-----HVKAL 487
Db 398 PSTIYRQGRGV-----DSLVDVIPPQDNSVPPRAGFSHRLSHVTVLMSQAAGAVYTLRAP 450
Qy 488 VYSWTHRSADRTNTIEPNSITQIPLKAFNLSSGAAVVRGPGFTGGDILRRNTGTGFGDI 547
Db 451 TFSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVGKPGFTGGDILRRTPSGQISTL 510
Qy 548 RVNINPPPAQRVRIRYASTTDLQHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGF 607
Db 511 RVNITAPLSQRVRIRYASTTDLQHTSIDGRPINQGNFSATMSSGSLNLSQSGSFRVGF 570
Qy 608 TTPSFVLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDYFEKAQEKYTAFTST 667
Db 571 TTPFNFGSSVFTLSAHVFNFGNEVYIDRIEFVPAEVTFEAYDLERAQKAVNELFTSS 630
Qy 668 NPRGLKTDVDYHIDQVSNLVESLDEFYLDKRELFEIVKAKQLHIERNM 719
Db 631 NOIGLKTVDYHIDQVSNLVESLDEFYLDKRELFEIVKAKQLHIERNM 682
```

## RESULT 14

parasporal crystal protein - *Bacillus thuringiensis* (strain aizawai IPL7)  
N: Alternate names: 135K insecticidal protein  
C: Species: *Bacillus thuringiensis*  
C: Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C: Accession: J02041  
R: Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.  
A: Title: Cloning and expression in *Escherichia coli* of the 135-kDa insecticidal protein  
A: Reference number: J02041  
A: Accession: J02041  
A: Molecule type: DNA  
A: Residues: 1-1176 <SHI>  
A: Cross-references: UNIPROT: P02965  
A: Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal proteins  
C: Comment: The 135K protein has insecticidal activity against *Plutella xylostella* larvae  
C: Superfamily: parasporal crystal protein  
C: Keywords: delta-endotoxin

Query Match 38.8%; Score 1457.5; DB 2; Length 1176;  
Best Local Similarity 43.7%; Pred. No. 6.4e-94;  
Matches 311; Conservative 118; Mismatches 222; Indels 61; Gaps 12;  
Qy 36 NINHEDCLKMEYENVE-PFVSASTIQTG-----IGIAGKILGTIGVVPAGQVASIYS 87  
Db 4 NPNINECIPYNCLSNPEVEVLGGERIETGTPIDISLSTQFLLSEF-VPGAGFVLGLVD 62  
Qy 88 FILGELWPKGNOWEIFMEHVEEIIQKISTYARNKALTDLKGDLALAVYHDSLESVVG 147  
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFARNQAIISRLGSLNLYQIYVAESFREWEA 119  
Qy 148 NRNNTRARSVKQYIALELMFVQKLPSFAVSGEEVPLPIYQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMNSALTTPALPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVG 179  
Qy 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNLRGTNAESWVRYNQFRDRTLM 267

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Db 180 QRMGDAATNSRNDLTRIGNYTDYAVRWYNTGLERVWGPDSRDWVRNQFRRELTLT 239
Qy 268 VLDLVALPSPYDTOMYPIKTTAQLTRREYVTDAGTVHPHPSFTSTTWYNNAPSPSAIEA 327
Db 240 VLDLVALFNSYDSRRYPIRTVSQLTREIYTNPV-----LENFDGSGFRGMAQ 285
Qy 328 AV---VRNPHLLDFLEQVTVIYSLLSRWSNTQYMMWGGHKLFRPTIGGT---LNISQGS 381
Db 286 RIEQNIQPHLMDILNRIITYDVHVG-----FNWSGHQITASPVGSPGPEFAFPLFGN 340
Qy 382 TNSINPVTLPFTSRDVRVYTESL-----AGNLFLTPQVNGVPRVDFHMKFVTHPI 432
Db 341 AGNAAPPVLVSLTGLGIFRTLSPLRYRIILGSGPN---NQELFVLDTGTEFSASLTNL 397
Qy 433 ASDNFYYPGVGIGTQLQDSENELPPEATQPNYESYSHLSHIGLISAS-----HVKAL 487
Db 398 PSTIYRQGRGV-----DSLVDVIPPQDNSVPPRAGFSHRLSHVTVLMSQAAGAVYTLRAP 450
Qy 488 VYSWTHRSADRTNTIEPNSITQIPLKAFNLSSGAAVVRGPGFTGGDILRRNTGTGFGDI 547
Db 451 TFSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVGKPGFTGGDILRRTPSGQISTL 510
Qy 548 RVNINPPPAQRVRIRYASTTDLQHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGF 607
Db 511 RVNITAPLSQRVRIRYASTTDLQHTSIDGRPINQGNFSATMSSGSLNLSQSGSFRVGF 570
Qy 608 TTPSFVLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAEDYFEKAQEKYTAFTST 667
Db 571 TTPFNFGSSVFTLSAHVFNFGNEVYIDRIEFVPAEVTFEAYDLERAQKAVNELFTSS 630
Qy 668 NPRGLKTDVDYHIDQVSNLVESLDEFYLDKRELFEIVKAKQLHIERNM 719
Db 631 NOIGLKTVDYHIDQVSNLVESLDEFYLDKRELFEIVKAKQLHIERNM 682
```

## RESULT 15

parasporal crystal protein cryIAa - *Bacillus thuringiensis*  
C: Species: *Bacillus thuringiensis*  
C: Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004  
C: Accession: J02219  
R: Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.  
Biosci. Biotechnol. Biochem. 58, 830-835, 1994  
A: Title: Cloning of a new cryIA(a) gene from *Bacillus thuringiensis* strain FU-2-7 and analysis of its function  
A: Reference number: J02219; MUID: 94289859; PMID: 7764972  
A: Accession: J02219  
A: Molecule type: DNA  
A: Residues: 1-1176 <UDA>  
A: Cross-references: UNIPROT: Q45736; DBJ: D17518; MID: g506190; PIDN: BAA04468.1; PID: g53578  
C: Geneticks:  
C: Gene: cryIA(a)  
C: Superfamily: parasporal crystal protein  
C: Keywords: delta-endotoxin

Query Match 38.6%; Score 1451.5; DB 2; Length 1176;  
Best Local Similarity 43.5%; Pred. No. 1.7e-93;  
Matches 310; Conservative 118; Mismatches 223; Indels 61; Gaps 12;  
Qy 36 NINHEDCLKMEYENVE-PFVSASTIQTG-----IGIAGKILGTIGVVPAGQVASIYS 87  
Db 4 NPNINECIPYNCLSNPEVEVLGGERIETGTPIDISLSTQFLLSEF-VPGAGFVLGLVD 62  
Qy 88 FILGELWPKGNOWEIFMEHVEEIIQKISTYARNKALTDLKGDLALAVYHDSLESVVG 147  
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFARNQAIISRLGSLNLYQIYVAESFREWEA 119  
Qy 148 NRNNTRARSVKQYIALELMFVQKLPSFAVSGEEVPLPIYQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMNSALTTPALPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVG 179  
Qy 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNLRGTNAESWVRYNQFRDRTLM 267

Db 180 QRWGFDAAATNSRYNDLTLIGNYTDYAVRWYNTGLERVWGPDSRDWRYNQFRRELTLT 239  
QY 268 VLDLVALFPSTQMYPIKTTAQLTREVTDAIGTVHHPSEFTSTTWYNNAPSFSAIEA 327  
Db 240 VLDLVALFNSYDSRRYPITVSQLTEIYTNPV-----LENFDGSRGMAQ 285  
QY 328 AV---VRNPHLLDFLEQVTIYSLLSRWSNTQYNNMGHGKLEFRTIGGT---LNISTQGS 381  
Db 286 RIEQNIHQPHLMDILNSITITVDVHRG-----FNYWSGHQITASPVGFSGPEFAFLFCN 340  
QY 382 TWTSPNPVTLPTSRDQVYTESL-----AGLNLFLTQPVNGVPRVDEHMKFVTHEI 432  
Db 341 AGNAAPPVLVSLTGLGIFRTLSPYRRILSGGPN---NQELFVLDGTEFSASLTNLD 397  
QY 433 ASDNFYYPGVVGIGTQLQDSENELPPEATCQPNYESYSHRLSHIGLISAS-----HVKAL 487  
Db 398 PSTIYFQRTV-----DSLVIPODNSVPRAGFSHRLSHVYMLSOAAGAVYTLRAP 450  
QY 488 VYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGGDI 547  
Db 451 TFSWQHRSAAEFNNIIPSSQITQIPLTKSTNLGSGTSVWKGPGFTGGDILRRTPGQISTL 510  
QY 548 RVNINPPFAQRYVRIRYASTTDLQFHTSINGKAINOGNESATMNRGEDIKYTFRTVGF 507  
Db 511 RVNITAPLSQRYVRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGF 570  
QY 608 TTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTVYAEYDPEKAQEKVLTALFTST 667  
Db 571 TTPFNFSNGSSVFTLSAHVFNSENEVYIDRIEFVPAEVTFEAEYDLERAKAVNELFTSS 630  
QY 668 NPGRLKTDVYHIDQVSNLVECLSDYFVLDKRELFEIVKYAKQLHIERNM 719  
Db 631 NQIGLKTVDYHIDQVSNLVECLSDYFVLDKRELFEIVKYAKQLHIERNL 682

Search completed: February 14, 2005, 21:00:52  
Job time : 18.5835 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:22:09 ; Search time 60.0945 Seconds  
(without alignments)  
3909.384 Million cell updates/sec

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Perfect score: 3760  
Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KRELFEIVKAKQLHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*  
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20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3756	99.9	719	16	US-10-782-020-10
2	3756	99.9	719	16	Sequence 10, Appl
3	3472.5	92.4	710	15	US-10-782-141-8
4	3472.5	92.4	710	15	Sequence 8, Appl
5	2264.5	60.2	1227	16	US-10-809-953-10
6	2264.5	60.2	1227	16	Sequence 10, Appl
7	2186.5	58.2	1227	15	US-09-988-462-7
8	2186.5	58.2	1227	15	Sequence 7, Appl
9	2115	57.8	1186	9	US-10-428-961-63
10	2115	57.8	1186	9	Sequence 63, Appl
11	1932.5	51.4	643	9	US-09-826-660-25
12	1932.5	51.4	643	9	Sequence 25, Appl
13	1724.5	45.9	1167	14	US-10-089-678-1
14	1724.5	45.9	1167	14	Sequence 1, Appl
15	1680.5	44.7	653	15	US-10-428-961-6
16	1680.5	44.7	653	15	Sequence 6, Appl
17	1669.5	44.4	1157	16	US-10-782-141-16
18	1669.5	44.4	1157	16	Sequence 16, Appl

14	1510	40.2	1206	13	US-10-032-717-2	Sequence 2, Appl
15	1510	40.2	1206	14	US-10-414-637-2	Sequence 2, Appl
16	1510	40.2	1206	15	US-10-606-320-2	Sequence 2, Appl
17	1494	39.7	1210	13	US-10-032-717-4	Sequence 4, Appl
18	1494	39.7	1210	14	US-10-414-637-4	Sequence 4, Appl
19	1494	39.7	1210	15	US-10-606-320-4	Sequence 4, Appl
20	1487.5	39.6	1156	14	US-10-039-285-72	Sequence 72, Appl
21	1487.5	39.6	1156	15	US-10-428-961-28	Sequence 28, Appl
22	1465	39.0	1155	9	US-09-756-643-2	Sequence 2, Appl
23	1465	39.0	1155	10	US-09-988-462-9	Sequence 9, Appl
24	1465	39.0	1155	15	US-10-136-998A-2	Sequence 2, Appl
25	1465	39.0	1177	14	US-10-035-060-6	Sequence 6, Appl
26	1465	39.0	1181	10	US-09-988-462-11	Sequence 11, Appl
27	1465	39.0	1181	10	US-09-988-462-13	Sequence 13, Appl
28	1465	39.0	1181	10	US-09-988-462-15	Sequence 15, Appl
29	1465	39.0	1181	10	US-09-988-462-17	Sequence 17, Appl
30	1465	39.0	1181	10	US-09-988-462-28	Sequence 28, Appl
31	1465	39.0	1181	15	US-10-136-998A-4	Sequence 4, Appl
32	1465	39.0	1181	15	US-10-136-998A-8	Sequence 8, Appl
33	1465	39.0	1181	15	US-10-136-998A-10	Sequence 10, Appl
34	1465	39.0	1181	15	US-10-136-998A-12	Sequence 12, Appl
35	1460	38.8	1177	14	US-10-035-060-2	Sequence 2, Appl
36	1458	38.8	1177	14	US-10-035-060-8	Sequence 8, Appl
37	1457	38.8	1177	14	US-10-102-459-24	Sequence 24, Appl
38	1447.5	38.5	1176	16	US-10-782-141-6	Sequence 6, Appl
39	1424.5	37.9	1176	11	US-09-837-961-2	Sequence 2, Appl
40	1424.5	37.9	1176	11	US-10-825-751-2	Sequence 2, Appl
41	1398	37.2	1167	9	US-10-428-961-40	Sequence 40, Appl
42	1377	36.6	1177	9	US-09-873-873-26	Sequence 26, Appl
43	1377	36.6	1177	10	US-09-916-956A-26	Sequence 26, Appl
44	1377	36.6	1177	10	US-09-997-914-26	Sequence 26, Appl
45	1377	36.6	1177	14	US-10-365-645-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1  
US-10-782-020-10  
; Sequence 10, Application US/10782020  
; Publication No. US20040197916A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for its Use  
; FILE REFERENCE: 045600/274139  
; CURRENT APPLICATION NUMBER: US/10/782,020  
; PRIOR FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,810  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-020-10

Query Match 99.9%; Score 3756; DB 16; Length 719;  
Best Local Similarity 99.9%; Pred. No. 1.5e-308;  
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB	1	MLKNQDKHQSFSSNAKVDKISTDSLNKNTDIELQNHEDCLKMSEYENVEPFVASTI	60
QY	61	QTGIGTAGKILGTGLGVPFAGQVASYLSFTILGELWPKGNQWEIFMEHVEEINQKISTYA	120
DB	61	QTGIGTAGKILGTGLGVPFAGQVASYLSFTILGELWPKGNQWEIFMEHVEEINQKISTYA	120

QY	121	RNKALTDLKGIGDALAVYHDSLSWGNRNNTARSVVKSQYIALELMFVQKLPFAVSG	180
DB	121		
QY	181	EEVPLLPYAAQANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSDHCVKWS	240
DB	181		
QY	241	TGLNLRGTNAESWVRVYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI	300
DB	241		
QY	301	GTVPHPSPFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW	360
DB	301		
QY	361	GGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR	420
DB	361		
QY	421	VDFHWKFVTHPIASDNFYPGYVIGIGIQDSENELPPEATGQPNYESYSHRLSHIGLIS	480
DB	421		
QY	481	ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGDILRTN	540
DB	481		
QY	541	TCTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK	600
DB	541		
QY	601	TPTVTGFTTFFSFLDVQSTFTTGAWNFSNGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV	660
DB	601		
QY	661	TALFTSTNPRGLKTDVKDQVHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM	719
DB	661		
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US-10-782-141-8			
; Sequence 8, Application US/10782141			
; Publication No. US20040197917A1			
; GENERAL INFORMATION:			
; APPLICANT: Carozzi, Nadine			
; APPLICANT: Hargiss, Tracy			
; APPLICANT: Koziel, Michael G.			
; APPLICANT: Duck, Nicholas B.			
; APPLICANT: Carr, Brian			
; TITLE OF INVENTION: AXMT-014, A Delta-Endotoxin Gene and			
; FILE REFERENCE: 045600/274143			
; CURRENT APPLICATION NUMBER: US/10782,141			
; CURRENT FILING DATE: 2004-02-20			
; PRIOR APPLICATION NUMBER: 60/448,632			
; PRIOR FILING DATE: 2003-02-20			
; NUMBER OF SEQ ID NOS: 23			
; SOFTWARE: Fast-Seq for Windows Version 4.0			
; SEQ ID NO 8			
; LENGTH: 719			
; TYPE: PRT			
; ORGANISM: Bacillus thuringiensis			
US-10-782-141-8			
Query Match 99.9%; Score 3756; DB 16; Length 719;			
Best Local Similarity 99.9%; Pred. No. 1.5e-308;			
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVFVSASTI	60



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; NAME/KEY: misc feature
; LOCATION: (200)..(200)
; OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid
US-10-428-961-42

Query Match      92.4%; Score 3472.5; DB 15; Length 710;
Best Local Similarity 92.4%; Pred. No. 1.4e-284;
Matches 664; Conservative 15; Mismatches 31; Indels 9; Gaps 1;

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DB 1 MGSKNQWQSLSNATVDKNTGSLERNNTTELQNFH-----EGIEPFPVSSTI 51

QY 61 QTGIGIAGKILGTLGVPFAGQVASYLFGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 52 QTGIGIAGKILGNLGVPPAGQVASYLFGELWPKGNQWEIFMEHVEEIIINQKISTYA 111

QY 121 RNKALTDLKGLDALAVYHDSLESWGNRNNTARSVVKQVIALELMFVQKLPSPFVSG 180
DB 112 RNKALADLKGLDALAVYHDSLESWGNRNNTARSVVKQVIALELMFVQKLPSPFVSG 171

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKQWGLSSSEISTFYNRQVRAGDYDHCWKVYS 240
DB 172 BEVPLLPPIYAQAANLHLLLRDASIFGKQWGLSSSEISTFYNRQVRSKSEYDHCWKVYN 231

QY 241 TGLNLRGTNAESWRYNQFRDMLTLMVLDLVALFPSYDTQMPYIKTTAQLTREVVYTDI 300
DB 232 TGLNLRGMNAESWRYNQFRDMLTLMVLDLVALFPSYDTQMPYIKTTAQLTREVVYTDI 291

QY 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVITYSLSRWNTQYMMNMW 360
DB 292 GTVHPHPSFTSTWYNNAPSPSTIEAAVVRNPHLLDFLEQVITYSLSRWNTQYMMNMW 351

QY 361 GGHKLEFRITGTLNISTGNTNTSINPVTLPSTRDVRVTTESLAGNLFLTPQVNGVPR 420
DB 352 GGHKLEFRITGTLNISTGNTNTSINPVTLPSTRDVRVTTESLAGNLFLTPQVNGVPR 411

QY 421 VDFHWFVTHPIASDNFYPGYVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 412 VDFHWFVTHPIASDNFYPGYVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 471

QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGDIILRRNT 540
DB 472 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGDIILRRN 531

QY 541 TGTGFGDIRVNINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGDLDYK 600
DB 532 TGTGFGDIRVNINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGDLDYK 591

QY 601 TFRTVGFTTTPFSDVQSTFTIGAMNFSNGEYVIDRIEFPVPEVTEYAEYDPEKAQEV 660
DB 592 TFRTVGFTTTPFSDVQSTFTIGAMNFSNGEYVIDRIEFPVPEVTEYAEYDPEKAQEV 651

QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEPYLDEKRELFELIVKYAKQLHIERNM 719
DB 652 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEPYLDEKRELFELIVKYAKQLHIERNM 710

RESULT 4
US-10-809-953-10
; Sequence 10, Application US/10809953
; Publication No. US20040181825A1
; GENERAL INFORMATION:
; APPLICANT: Van Mellaert, Herman
; APPLICANT: Botterman, Johan
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Joos, Henk
; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTICIDAL PROTEINS
; FILE REFERENCE: 021565-078
; CURRENT APPLICATION NUMBER: US/10/809,953
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/09/661,016
```

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; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: PCT/EP90/00905
; PRIOR FILING DATE: 1990-05-30
; PRIOR APPLICATION NUMBER: GB 89401499.2
; PRIOR FILING DATE: 1989-05-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-809-953-10

Query Match      60.6%; Score 2277.5; DB 16; Length 1228;
Best Local Similarity 62.7%; Pred. No. 4.5e-183;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQNH-----EDCLKSEYENVEPFPVSASTIQTGIGIAGKI 70
DB 2 TSNRKNENEIINAVNSHSAQMDLLDPARIEDSLCAEGNNIDFPVSASTVQTGINIAGRI 61

QY 71 LCTLGVPPAGQVASYLFGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLAG 130
DB 62 LGLVGVPPAGQVASYLFGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLAG 121

QY 131 LGDALAVYHDSLESWGNRNNTARSVVKQVIALELMFVQKLPSPFVSGBEVPLLPPIYA 190
DB 122 LGDSFRAVQOQSLDLENRDARTSVLHTQVIALELDPLNAMPFLAIRNQSVPLLMVYA 181

QY 191 QAAANLHLLLRDASIFGKQWGLSSSEISTFYNRQVRAGDYDHCWKVYSTGLNLRGTN 250
DB 182 QAAANLHLLLRDASIFGSEFGLTSQEIQRVQVRERTRDSDYCVWEYNTGLNLRGTN 241

QY 251 AFSWRYNQFRDMLTLMVLDLVALFPSYDTQMPYIKTTAQLTREVVYTDIAGTVHPHPSFT 310
DB 242 AASWRYNQFRDMLTLMVLDLVALFPSYDTQMPYIKTTAQLTREVVYTDIAGTVHPHPSFT 299

QY 311 STTWYNNAPSPSAIEAAVVRNPHLLDFLEQVITYSLSRWNTQYMMNMWGGHKLFRIT 370
DB 300 SMWYNNAPSPSAIEAAVVRNPHLLDFLEQVITYSLSRWNTQYMMNMWGGHKLFRIT 359

QY 371 GGTINISTGNTNTSINPVTLPSTRDVRVTTESLAGNLFLTPQVNGVPRDHHKVF 428
DB 360 GGLTSTHTGATNTSINPVTLPSTRDVRVTTESLAGNLFLTPQVNGVPRDHHKVF 416

QY 429 THP-----IASDNFYPGYVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISASH 483
DB 417 TNPQISDRGTANYSQP-YESPGLQKDESETLPPETTERPNYESYSHRLSHIGLISASH 475

QY 484 VKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGDIILRRNTGT 543
DB 476 VNPVYVSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGDIILRRNTGT 535

QY 544 FGDIRVNINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGDLDYKTR 603
DB 536 FGPRTVNGPLTQYRIGFRYASTVDFDFVSRGTTVNNFRFLRTMTMNGDELKYGNFV 595

QY 604 TVGFTTPSPFLDVQSTFTIGAMNFSNGEYVIDRIEFPVPEVTEYAEYDPEKAQEV 663
DB 596 RRAFTTPTFTTQIDIIIRTSIOGLSNGEYVIDRIEFPVPEVTEYAEYDPEKAQEV 655

QY 664 FTSTNPRGLKTDVKDYHIDQVSNLVSLSDEPYLDEKRELFELIVKYAKQLHIERNM 719
DB 656 FTNTNPRKTDVTDYHIDQVSNLVSLSDEPYLDEKRELFELIVKYAKQLHIERNM 711

RESULT 5
US-09-988-462-7
; Sequence 7, Application US/09988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
```

Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Launis, Karen L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Syngenta Biotechnology, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 09/988,462  
FILING DATE: 20-NO. US20030046726A1-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/547,422  
FILING DATE: 11-APR-2000  
APPLICATION NUMBER: US 08/459,504  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-188051  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-988-462-7

Query Match 60.2%; Score 2264.5; DB 10; Length 1207;  
Best Local Similarity 64.3%; Pred. No. 5.5e-182; Indels 13; Gaps 5;  
Matches 442; Conservative 78; Mismatches 154;  
QY 40 EDCLMSEYENVEPVFSASTIQTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGKN 99  
Db 10 EDSLCAIEGNNIDFVSASTVQTGINTAGRIAGLIGLVGVPFAGQVASYLSFILGELWPKGRD 69  
QY 100 QWEIFMEHVEEIIINQKISTYARNKALDLDKGLDALAVYHDSLESVWGNRNNTARSVK 159  
Db 70 QWEIFLHVEQLINQKITENARNALARLOGLGDSFRAYQOGLDMLNDRDARTSRVLY 129  
QY 160 SQYALELMFVQKLPSPAVSGEEVPLPIVAQAANLHLLLRDASIFGKSWGLSSSIST 219  
Db 130 TOYALELDFUNAPLFAIRNQEVPLLMVTAQAANLHLLLRDASLFGSEFGLTSQBIQR 189  
QY 220 FYNRQVRAGDYSCHVKVYSTGLNNLRGTNAESWRYNQFRDMTLMVLDLVALFPESYD 279  
Db 190 YERQVRTERDYSYDCEVWYNTGLNSLRGTNAESWRYNQFRDRLTLGLVLDLVALFPESYD 249  
QY 280 TOMYPIKTAQLREVYTDALGTGTHPHSPSTSTWYNNAPSAIEAAVVRPHLLDLFL 339

Db 250 TRTYPINTSAQLTREVYTDALGT--GVNMAWYNNYNNAPSPSAIEAAAIRSPHLLDLFL 307  
QY 340 EQVTIYSLLSRWNTQYMNWGWGHKLEFRITGGTILNISTOGSTNTSINPVTLPTSDVY 399  
Db 308 EQLTIFSSASSRWNTHTMYRGTIIQSRPIGGGLANTSTHGATNTSINPVTLRFASRDVY 367  
QY 400 RTESLAGLNLFF--LTQPVNGVPRVDHFKVTHP----IASDNFYVPGVVGIGTQLQDS 452  
Db 368 RTESYAGVLLWGLYLEPIHGVPTVRNF---TNPQNISDRGTANYSQP--YESPGLQKDS 423  
QY 453 ENELPPEATQOPNYESYSHLSHIGLSASHVYKALVYSWTHRSADRTNTIEPNSITQPL 512  
Db 424 ETELPPETTERPNVYESYSHLSHIGLILQSRVNVVYSWTHRSADRTNTIGPNRITQIPM 483  
QY 513 VKAFNLSSGAUVVRGPGTGGDILRLRTNTGDIRVIRNPPFAQORVIRVIRASTYDLQ 572  
Db 484 VKASELPQGTTVVRGPGTGGDILRLRTNTGFGPIRVTVNGPLTQYRIGFYASTYDFF 543  
QY 573 FHTSINGKAINOCNFSATMNRGDLDTKFTRTVGTTPFPFSLDVQSTFTIGAMNFFSGNE 632  
Db 544 FVSRGCTTVNFRFLRTMNSGDELKXGNFVRAFTTFTTQIOLIRTSIQGLSNGE 603  
QY 633 VYIDRIEFVPEVYEAEDYFEKAQEKVATLFTSTNPRGLTKDVKDHYHDQVSNLVBLS 692  
Db 604 VYIDKIEIIPVTATFEAEYDLERAQEAVALFTNTNPRLKTDTVYHIDQVSNLVACLS 663  
QY 693 DEYVLDKRELFEIVKAKOLHIERNM 719  
Db 664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

## RESULT 6

US-10-428-961-63  
; Sequence 63, Application US/10428961  
; Publication No. US20030237111A1  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Ruper, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)  
; FILE REFERENCE: MECO201--1  
; CURRENT APPLICATION NUMBER: US/10/428,961  
; CURRENT FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: 09/661,322  
; PRIOR FILING DATE: 2000-09-13  
; PRIOR APPLICATION NUMBER: 60/153,995  
; PRIOR FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 63  
; LENGTH: 1227  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-428-961-63

Query Match 58.2%; Score 2186.5; DB 15; Length 1227;  
Best Local Similarity 59.2%; Pred. No. 2.2e-175;  
Matches 423; Conservative 105; Mismatches 173; Indels 13; Gaps 3;  
QY 13 SSNAKVDKSTDSLKN-----ETDIELQININHCLKMKSEVENVEPVFSASTIQTGIG 65  
Db 7 NENEINALISIPAVNSHSAQMNLSIDARI-----EBSLCIAEGNIDPFPVFASTVQTGIN 61  
QY 66 IAGKILGTLPVFPAGQVASYLSFILGELWPKGKNQWEIFMEHVEEIIINQKISTYARNKAL 125  
Db 62 IAGRIILGVLPVFPAGQVASYLSFILGELWPKGRDPWEIFLHVEHLIRQOVNTDRTAL 121  
QY 126 TDLKGLGDALAVYHDSLESVWGNRNNTARSVKVSYIALELMFVQKLPSPAVSGEVL 185



Query Match 56.2%; Score 2115; DB 15; Length 1228;  
Best Local Similarity 59.5%; Pred. No. 2.5e-169;  
Matches 424; Conservative 98; Mismatches 181; Indels 10; Gaps 7;  
13 SSNAKVKDSTLKN-ETDIEIQ-NINHEDCLKMEYENVEPFVSASTIQTGIGIAGKI 70  
7 NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66  
71 LGTLGVPPAGQVASLYFLIGELWPKGNQWEI FMEHVEEII NOKISTYARNKALTDLKG 130  
67 LGVLGVPPAGQVASFYFLVGLWPRGRDQWEI FLEHVEQLINQQTENARNALTALOG 126  
131 LGDALAVYHDSLESWGNRNTRARSVVKQYIALELMFVQKLPSPAVSGEEVPLPIYA 190  
127 LGDSFRAYQOQSLDLEWLNDRDARTRSVLYTQYIALELDFLNAFLPAIRNQEVPLLMVYA 186  
191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTN 250  
187 QAANLHLLLRDASLFGSEFGLTSQEIORYYERQVETRDYSDYCVEMVYNTGLNSLRGTN 246  
251 AESWRYNQFRDMLVLDLVALFPSPDYDTQMPDIKTAAQLTRVYTDATGTVHPHSFT 310  
247 AASWRYNQFRDMLVLDLVALFPSPDYDTQMPDIKTAAQLTRVYTDATGTVHPHSFT 310  
311 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMGGHKLERTI 370  
305 SMWYNNNAPSFAIETAVIRSPHLLDFLEQVTIYSLSRWSNTQYNNMGGHKLERTI 370  
371 GGTINISQGSTNTSINPVLTPFTSRDYRTESLAGLNF--LTQPVGVPRVDHFKFV 428  
365 GGGLNTSTHGSTNTSINPVLTPFTSRDYRTESLAGLNF--LTQPVGVPRVDHFKFV 428  
429 --THPIASDNFYGVGIGTQLODSENELPPEATGPNYESYSHRLSHGLISASHVKA 486  
425 QNTFERGTANTSQP--YESPGLQKLDSELTPEPTTERPNYESYSHRLSHGLISASHVKA 483  
487 LVYSWTHRSADRTNTIENSTIQLPKAFNLSSGAAVVRGPGTGGDIILRRNTGTGFGD 546  
484 PVSWSHRSADRTNTIENSTIQLPKAFNLSSGAAVVRGPGTGGDIILRRNTGTGFGD 543  
547 IRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGELDLYKTFTVG 606  
544 MGLNFNTSLQRYRVRVRYAAQTMLRVTVGGSTTFDQGFPTMSANESLTSQSFRFAE 603  
607 FTTPFSLDQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEKAEKVTALFTS 666  
604 FVVGISASGSQ--TAGISISNAGRTQFHFDFKIEFIPITATFEAYDLERAQEAVALFTN 662  
667 TNPRGLKTDVYHIDQVSNLVSLSDEFYLDKRELFELVYKAKQLHIERNM 719  
663 TNPRGLKTDVYHIDQVSNLVSLSDEFYLDKRELFELVYKAKQLHIERNM 715

RESULT 9  
US-10-614-524-2  
Sequence 2, Application US/10614524  
Publication No. US20040016020A1  
GENERAL INFORMATION:  
APPLICANT: Arnaut, Greta  
APPLICANT: Boets, Annemie  
APPLICANT: Damme, Nicole  
APPLICANT: Mathieu, Eva  
APPLICANT: Vanneste, Stijn  
APPLICANT: Van Rie, Jeroen  
TITLE OF INVENTION: Insecticidal proteins from *Bacillus thuringiensis*.  
FILE REFERENCE: NEWBTSUS2  
CURRENT APPLICATION NUMBER: US/10/614,524  
CURRENT FILING DATE: 2003-07-08  
PRIOR APPLICATION NUMBER: US/09/739,243  
PRIOR FILING DATE: 2000-12-19  
PRIOR APPLICATION NUMBER: 60/173387  
PRIOR FILING DATE: 1999-12-28

NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 1228  
TYPE: PRT  
ORGANISM: *Bacillus thuringiensis*  
US-10-614-524-2

Query Match 56.2%; Score 2115; DB 15; Length 1228;  
Best Local Similarity 59.5%; Pred. No. 2.5e-169;  
Matches 424; Conservative 98; Mismatches 181; Indels 10; Gaps 7;  
13 SSNAKVKDSTLKN-ETDIEIQ-NINHEDCLKMEYENVEPFVSASTIQTGIGIAGKI 70  
7 NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66  
71 LGTLGVPPAGQVASLYFLIGELWPKGNQWEI FMEHVEEII NOKISTYARNKALTDLKG 130  
67 LGVLGVPPAGQVASFYFLVGLWPRGRDQWEI FLEHVEQLINQQTENARNALTALOG 126  
131 LGDALAVYHDSLESWGNRNTRARSVVKQYIALELMFVQKLPSPAVSGEEVPLPIYA 190  
127 LGDSFRAYQOQSLDLEWLNDRDARTRSVLYTQYIALELDFLNAFLPAIRNQEVPLLMVYA 186  
191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTN 250  
187 QAANLHLLLRDASLFGSEFGLTSQEIORYYERQVETRDYSDYCVEMVYNTGLNSLRGTN 246  
251 AESWRYNQFRDMLVLDLVALFPSPDYDTQMPDIKTAAQLTRVYTDATGTVHPHSFT 310  
247 AASWRYNQFRDMLVLDLVALFPSPDYDTQMPDIKTAAQLTRVYTDATGTVHPHSFT 310  
311 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMGGHKLERTI 370  
305 SMWYNNNAPSFAIETAVIRSPHLLDFLEQVTIYSLSRWSNTQYNNMGGHKLERTI 370  
371 GGTINISQGSTNTSINPVLTPFTSRDYRTESLAGLNF--LTQPVGVPRVDHFKFV 428  
365 GGGLNTSTHGSTNTSINPVLTPFTSRDYRTESLAGLNF--LTQPVGVPRVDHFKFV 424  
429 --THPIASDNFYGVGIGTQLODSENELPPEATGPNYESYSHRLSHGLISASHVKA 486  
425 QNTFERGTANTSQP--YESPGLQKLDSELTPEPTTERPNYESYSHRLSHGLISASHVKA 483  
487 LVYSWTHRSADRTNTIENSTIQLPKAFNLSSGAAVVRGPGTGGDIILRRNTGTGFGD 546  
484 PVSWSHRSADRTNTIENSTIQLPKAFNLSSGAAVVRGPGTGGDIILRRNTGTGFGD 543  
547 IRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGELDLYKTFTVG 606  
544 MGLNFNTSLQRYRVRVRYAAQTMLRVTVGGSTTFDQGFPTMSANESLTSQSFRFAE 603  
607 FTTPFSLDQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEKAEKVTALFTS 666  
604 FVVGISASGSQ--TAGISISNAGRTQFHFDFKIEFIPITATFEAYDLERAQEAVALFTN 662  
667 TNPRGLKTDVYHIDQVSNLVSLSDEFYLDKRELFELVYKAKQLHIERNM 719  
663 TNPRGLKTDVYHIDQVSNLVSLSDEFYLDKRELFELVYKAKQLHIERNM 715

RESULT 10  
US-09-826-660-25  
Sequence 25, Application US/09826660  
Patent No. US20010026940A1  
GENERAL INFORMATION:  
APPLICANT: Cardineau, Guy A.  
APPLICANT: Steiman, Steven J.  
APPLICANT: Narva, Kenneth E.  
TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins  
FILE REFERENCE: MA-714XC2D1  
CURRENT APPLICATION NUMBER: US/09/826,660  
CURRENT FILING DATE: 2001-04-05

```

; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
; US-09-826-660-25

Query Match      51.4%; Score 1932.5; DB 9; Length 643;
Best Local Similarity 57.7%; Pred. No. 2.6e-154;
Matches 371; Conservative 100; Mismatches 199; Indels 13; Gaps 3;

Qy      13  SSNAKVDKISTSLKN-----ETDIELQNHINHDCLKMSEYENVPFVSASTIQTGIG 65
Db      7  NENEIINALSIPAVNSHSAQNLSTDARI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61

Qy      66  IAGKILGTGVPPAGQAVASLYSPFILGELPKGKQWEIPEHVEHVEIINOKLISTVARKAL 125
Db      62  IAGRILVLGVPPAGQIASFYSLFVLGELWPRGRDPWEIFLEHVQLRIQQVETRTOTAL 121

Qy      126  TDLKGLGDALAVYHDSLESVGNRNNTRRASVVKSOYIALSLMFVKLPSFAVSGEEVPL 185
Db      122  ARLOGLGNSFPAYOOOSLEDWLENRDDARTREVLTYQYIALDELDFNAMPLFAIRNQEVPL 181

Qy      186  LPIYAQAANLHLLLRRDASIFGKEWGLSSSSISITFYNRQVRAGDYSCHCKWYSTGLNN 245
Db      182  LMWYAQAANLHLLLRRDASLFGSEFGLTSQRIQRYERQVEKTRREYSDYCARWYNTGLNN 241

Qy      246  LRGTNASSWRYNQFRDRMTLMVLDLVALPFSYDTOMYPIKTTAQLTREVTDAIGTVHP 305
Db      242  LRGTNASSWLRYNQFRDRDLTLGVLDLVALPFSYDTRVYPMNTSAQLTREIYTDPIGRNA 301

Qy      306  HPSFTSTWYNNNAPSASIAEAAVVRPHLLDLFLEOVITYLSLRWSNTQYMMWGGHKL 365
Db      302  PSGFASNTWFNNNAPSASIAEAAVIRPHLLDFPEQLTIFSVLSRWSNTQYMWYVGHRL 361

Qy      366  EFRITGTLNISTOGSTNTSINPVTLPSTRSDVRVTESLAGINLFLTQPVNGVRVDVPHW 425
Db      362  ESRTIRGSLSTSTHGNTNTSINPVTLOFTSRDVRVTESFAGINILLTTPVNGVPAWENW 421

Qy      426  KFTVTHPIASDNFYYPGVIGTQLQDGENELPPEATQGNPYESYSHRLSHGLISASHVK 485
Db      422  RNPLNSLRGSLLYTIGYTGVTGQLFDSLETLPPTTERPNYESYSHRLSNIRLISGNTLR 481

Qy      486  ALVYSWTHRSADRNTTIEPNSITQIPLVKAFLNSGAANVVGPGFTGSDIILRRNTYTFG 545
Db      482  APVYSWTHRSADRNTTSSSDITQIPLVKSFLNLSGTSVWSGPGFTGSDIILRTNVNGSVL 541

Qy      546  DIRVINPPPAQRVVRIRYASTTDLQPHTEHSKAINQGNFSAATMNRGEDLDVYKTFRTV 605
Db      542  SMGLNFNNTSLQRRVVRVRYAASQTMVLRVTVGSGSTTFDQGFPTSMNASLESITSGSFPA 601

Qy      606  GFTTFFSFLDVQSTFTTIGAMNFFSGNEVYIDRIEFPVPEVTYE 648
Db      602  EFPVGISASGSGQ-TAGISISNNAGRQTDFHKIEFIPITATLE 643

RESULT 11
US-10-089-678-1
; Sequence 1, Application US/10089678
; Publication No. US20030017967A1
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shinichiro
; TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
; TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD

```

RESIT.T 11

RESULTS II  
US-10-089-678-1

03-10-069-078-1  
: Sequence 1. Application US/10089678

; sequence 1; application US/1008  
; Publication No. US20030017967A1

: GENERAL INFORMATION:

APPLICANT: ASANO, shinichiro

; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN,

**TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD**

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; FILE REFERENCE: Q69821
; CURRENT APPLICATION NUMBER: US/10/089,678
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: JP 2000-236140
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/JPO1/06660
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1167
; TYPE: prt
; ORGANISM: Bacillus thuringiensis
; US-10-089-678-1

```

Query Match	45.9%	Score 1724.5	DB 14	Length 1167
Best Local Similarity	48.1%	Pred. No. 2.6e-136		
Matches	362	Conservative 125	Mismatches 220	Indels 45
Gaps	11			
QY	1	MLKKNQDKHO---	SFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYE-----	NV 51
DB	1	MSPNQNEVEILDASSTSVSDNSVRYPLANDQTTILQNNYKDYLFKMSGEENPELFGNP	60	
QY	52	EPFVSASTIQTGIGIAGKILGTIGVPPAGQVASLYSFIGELGMPKKG-KNOWEIPMEHVEE	110	
DB	61	ETFISSSTVQTGIGIVGVQLGALGVFPAGQIASFYSPFVIGQLMPSSTSVSVWEMIMKQVED	120	
QY	111	IINOKISTYARNKALTDLKGLDGALAVYHDSLSASWGNRNTARSVVVKSOYTALELMFEV	170	
DB	121	LIDDKITDSVRKLTALAGLQGLGDGVYQSKLNKLENRNDTARSVVVTQYIALELDVF	180	
QY	171	QKLPSFAVSAGEEYVLLPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGD	230	
DB	181	AKIPSAISGOEYVLLSVYAQAANLHLLLRDASIFGAEWGFTPEGEISTFYDQVTRTAQ	240	
QY	231	YSHCVKWTSTGLNNLRGTNAESWRYNQPRRDMTLVLDLVALFPDYDTQMPIKTTAQ	290	
DB	241	YSYCYKWTNTGLDKLGTNAASWLKYHQPRRMTLLVLDLVALFPNYDRTYPIETTAQ	300	
QY	291	LTRVVYTDALGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDPLEOVITYSLLS-	349	
DB	301	LTRVYTDPIVFNRETSGGFCRRWSLNSDISFSEVASIVRSRPHLPILISEIFYTTRAG	360	
QY	350	-RWSNTQYMMWGGHKLFEPTIGTLNISTQGSTNTSINPVTLPFTSRDVTYRTESL-AGL	407	
DB	361	LPLNTEYLEYVWGHISIKYKNTWASSALERNYGTITSNKIYDLANKDKFQVRESLGLADL	420	
QY	408	NLFELTPQVNGPRVDVFWKKEVTHPIASDNFYFGYVG-----	455	
DB	421	ANYTAQ-VYGVPYASF-----	471	
QY	456	LPPEATGQPNYESYSHRLSHIGLIS-----	507	
DB	472	IPPE--NEPLSRGYSHRLSHITSYSPSKNASSPARYGNLPVFAWTHRSADVNTVYSDKI	529	
QY	508	TOIPLVKAFNLSSCAA-VVRPGFTGGDILRRTWNTGTFGDIRVININPFPQAQRYRIRIYAS	567	
DB	530	TOIPVVKHTLVSGTTVIKGPFGTGGNLLKRTSSGPLAYTSVSVKSPLSQRYRARIYAS	589	
QY	568	TTDLQFHTSINGKAINQGNFSATWNRGEDLDYKTFRTVGGFTTPPSFLDVQSTFTTIGAWNF	627	
DB	590	TTNLRLPVTISGTRIYSINVKNTWKNGDDTLFTNTFDLATGTACTFSNYSDSLTVGADSF	649	
QY	628	SSGNEVYIDRIEFVPVEVTYEAEDYDEKAQEKVYALTFTSTNPRGLKTDVKDYHDQVSNL	687	
DB	650	ASGGEVYVDFELIPVNAATEAEEDLDVAKAVNGLFTSKKD-ALQTSVTDYQVNAANL	708	
QY	688	VESLSDEFYLDKRELFVEIVKYAKQLHIERNM	719	
DB	709	VECLSDLEYENKRMMLWDVAKEAKRLVQARNL	740	

## RESULT 12

US-10-428-961-6  
; Sequence 6, Application US/10428961  
; Publication No. US20030237111A1  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Ruper, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
; FILE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)  
; CURRENT APPLICATION NUMBER: US/10428.961  
; CURRENT FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: 09/661,322  
; PRIOR FILING DATE: 2000-09-13  
; PRIOR APPLICATION NUMBER: 60/153,995  
; PRIOR FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 653  
; TYPE: PRP  
; ORGANISM: Bacillus thuringiensis  
US-10-428-961-6

Query Match 44.7%; Score 1680.5; DB 15; Length 653;  
Best Local Similarity 51.5%; Pred. No. 5.6e-133; Mismatches 173; Indels 47; Gaps 14;  
Matches 346; Conservative 106; Mismatches 173; Indels 47; Gaps 14;

QY 13 SSNAKVDKISTDSUKN---ETDIELQINIHEDCLKMSYENVEPVFSASTIQTGTGIGAGK 69  
DB 2 NENEIINALSIPAVSNHSAQMDLSI-DARIEDSLCIAEGNNINPLVSASTVQTGINAGR 60  
QY 70 ILGLGVFPAGQALSYFLIGELWPKGNQWEIFMEHVEIINQKISTVARNKALTDLK 129  
DB 61 ILGLGVFPAGQALSYFLIGELWPKGNQWEIFMEHVEIINQKISTVARNKALTDLK 120  
QY 130 GLGDALAVYHDSLESWGNRNNTARSVVKQYIALELMFVKLPSPAVSGEEVPLPIY 189  
DB 121 GLGRYRYQQALETWLNDRNDARSILERYVALELDITAIPLFRINEEVPLLMVY 180  
QY 190 AQAANLHLLLRDASIFGKWLGSSEISTFYNRQVERAGYSDHCVKWSYGTGLNNLRGT 249  
DB 181 AQAANLHLLLRDASIFGKWLGSSEISTFYNRQVERAGYSDHCVKWSYGTGLNNLRGT 240  
QY 250 NAESWRYNQRRDMLVLDLVALFPSYDTQMPYIKTAQITREYVTDAGTGVHPHSP 309  
DB 241 NAESWRYNQRRDMLVLDLVALFPSYDTQMPYIKTAQITREYVTDAGTGVHPHSP 300  
QY 310 TSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSWSNTQYNNMGGHKLFRIT 369  
DB 301 ASTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSWSNTQYNNMGGHKLFRIT 360  
QY 370 IGGTLNISTQGST-NTSINPVTLFP-TSRDVRVRESLAGLNFELTQPVNGVPRVDFHWKF 427  
DB 361 IGGTLNISTQGST-NTSINPVTLFP-TSRDVRVRESLAGLNFELTQPVNGVPRVDFHWKF 418  
QY 428 VTHPIASDNFYPP-----GYVIGTQLODSENELPEATGPNYESYSHRLSHIG-- 477  
DB 419 ITRIFRMEAPLTVNRIRLGFNFVLIQKLNHQK-----QONDQIMHIVIDISYR 470  
QY 478 LISASHVKALVYSWTHRSADRNTNTPNSITQIPLVKAFNLSSGAAVVRGFGTGGDILR 537  
DB 471 LIIGNTLAPVYVSWTHRSADRNTNTPNSITQIPLVKAFNLSSGAAVVRGFGTGGDILR 529  
QY 538 -RTWTGTP---GDIVRNIN-PPFAQRYRVRYASTTDLOFHTSINGKAINQGFSAATMN 592  
DB 530 LNRNNGNIQNRGIEVPIQFTSTRYRVRYASTTDLOFHTSINGKAINQGFSAATMN 589  
QY 593 RGEDLDYKTRFTVGTFTTFFSLDVOSTFT-----IGAWNFSSGNEVVIDRIEFVPEVT 646  
DB 590 SLDNLQ-----SGDFGYVEINNAFTSATGNIVGARNFSANREVIDRIEFIPVTAT 640

QY 647 YEAEDYFEKAQOE 658  
DB 641 FEVEYDLERAQK 652

RESULT 13  
US-10-782-141-16  
; Sequence 16, Application US/10782141  
; Publication No. US20040197917A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
; FILE OF INVENTION: Methods for its Use  
; FILE REFERENCE: 045600/274143  
; CURRENT APPLICATION NUMBER: US/10782.141  
; CURRENT FILING DATE: 2004-02-20  
; PRIOR APPLICATION NUMBER: 60/448,632  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 1157  
; TYPE: PRP  
; ORGANISM: Bacillus thuringiensis  
US-10-782-141-16

Query Match 44.4%; Score 1669.5; DB 16; Length 1157;  
Best Local Similarity 49.1%; Pred. No. 1.2e-131;  
Matches 371; Conservative 98; Mismatches 230; Indels 57; Gaps 18;

QY 1 MKLNQDKQKQSPSSNAKVDKISTDS-----LKNETDIELQINIHEDCLKMSYE-----N 50  
DB 1 MSPNNQNEYBIIDATPST-SVSSDSNRYPPANEPTDALQNNMYKYDKLKMSSGGENBELFGN 59  
QY 51 VEPFVSASTIQTGTGIGAGKILGTGVPFAGQVAVSLYSFILGELWPK-KGKNQWEIFMEHVE 109  
DB 60 PETFISSTIQTGTGIGAGKILGTGVPFAGQVAVSLYSFIVGQWPKSVSDIWEIMEHVE 119  
QY 110 EIINQKISTVARNKALTDLKGLDGLAVYHDSLESWGNRNNTARSVVKQVIALELMF 169  
DB 120 ELVDQKIEKYVKDKALAEKGLGNALDVKQSLLEDLENRNDARTSRVSNQFIALDLNF 179  
QY 170 VQKLPSPAVSGEEVPLPIYQAANLHLLLRDASIFGKWLGSSEISTFYNRQVERAG 229  
DB 180 VSSIPSPAVSGEEVPLPIYQAANLHLLLRDASIFGKWLGSSEISTFYNRQVERAG 239  
QY 230 DYSDHCVKWSYGTGLNNLRGTNAESWRYNQRRDMLVLDLVALFPSYDTQMPYIKTTA 289  
DB 240 EYSDYCVKWKYKIGLQKLTGTSKSLNLYHQFRREMTLLVLDLVALFPNYDTHMYPETTA 299  
QY 290 QLTREYVTDAGTGVHPHSPSTST-----TWNNNAPSFAIEAAVVRNPHLLDFLEQVITY 345  
DB 300 QLTREYVTDAGTGVHPHSPSTST-----TWNNNAPSFAIEAAVVRNPHLLDFLEQVITY 355  
QY 346 SLISR-----WSNTQYNNMGGHKLFR-----TIGGTLNISTQGSTNTSINPVTLPTSR 396  
DB 356 T-SRGGITUNDAYINWGSHTLKRRTADSTVITYTANYGRITSEKNS-----FALED 408  
QY 397 DVYRTESLAGLNFELTQPVNGVPRVDFHWKFVTHPIASDNFY-----YPOVYVIGTQLOD 451  
DB 409 DIFEINSTVANLANYQKAYGVFGSNFH--WVKRGTSSTTAYLYSKTHTALQGC-TQVYE 465  
QY 452 SENELPEATGPNYESYSHRLSHI-----GLISASHVKALVYSWTHRSADRNTNIE 503  
DB 466 SSDEIPLDRT-VPVAESYSHRLSHITSHSPKNG--SAYYGSFPVFWVTHTSADLNNTIY 522  
QY 504 PNSTIQTPLVKAFNLSSGAAVVRGFGTGGDILRRNTGTGDIRVNNINPPFAQRYRVRI 563  
DB 504 PNSTIQTPLVKAFNLSSGAAVVRGFGTGGDILRRNTGTGDIRVNNINPPFAQRYRVRI 563

Db 523 SOKITQIPAVGMDLVLGSGVVGPGFTGGDILKRNTPSILGTFVAVTVNGSLSQRRVRI 582  
QY 564 RYASTTDLOPHTSINGKAINQGNFSAATMRGDLKYKTRTVGFTTPFPFLDVQSTFTIG 623  
Db 583 RYASTTDFP-TLYLGDITIEKRNFKMTMGASLTVEFKFASFTDFQFRETQDKILLS 641  
QY 624 AMNFFSGNEWYIDRIEFPVVEVTEYAEYDEPEKAQEKVTAFTSTNPRGLKTDVKDHIQO 683  
Db 642 MGFDFSSQGEVYIDRIEFPVDEYAEQLEAKKAVNALFTNTKD-GLRPGVTDVENVQ 700  
QY 684 VSNLVESLDEFLYDEKRELFEIVKYAKOLHIERNM 719  
Db 701 AANLVECLSDLLYPNEKRLLFDAVREAKRLSGARNL 736  
RESULT 14  
US-10-032-717-2  
; Sequence 2, Application US/10032717  
; Publication No. US20020151709A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With  
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/032,717  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/242,838  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1206  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-032-717-2  
Query Match 40.2%; Score 1510; DB 13; Length 1206;  
Best Local Similarity 44.3%; Pred. No. 3.9e-118;  
Matches 337; Conservative 130; Mismatches 229; Indels 64; Gaps 22;  
QY 1 MCLKNODKHQSFSNAKVDKISTDS----LKNETDIELQININHEDCMKM-----SEVE-N 50  
Db 1 MSPNNQNEVEIIDATPST-SVNSDSNRYPPANEPTNALQNM DYKYLKMSAGNASIYPGS 59  
QY 51 VEPFVSA-STIQTGIGIAGKILGTGVPFAGQVASYLSYFILGELWPKG-KNQEWEIFMEHV 108  
Db 60 PEVLVSGDAAKAAIDIVGKLLSGLGVPFVGPVIVSLYTLQIDILMPSGKSQWEIFMEQV 119  
QY 109 EEIINOKISTYARNKALTDLKGIGDALAVYHDSLSWGNRNTRARSVVKQYIALELM 168  
Db 120 EEIINOKIAEYARNKALSLEGLGNKYLYLTALBEEENPNNGSRALRDVNRFEILDSL 179  
QY 169 FVQKLPSFAVSGEVPILPIYAAANLHLLLDASIFGKEMGLSSSEISTFYNNROVERA 228  
Db 180 FTQYMPSPRVNTEVFPFLTVYAAANLHLLLDKASIFGEEGWSTTTNNIYDROMKLT 239  
QY 229 GDYSDHCVKMYSTGLNLRGNTAESWVRVYQFRDMLVLDLVALFPSTDTQMYPIKTT 288  
Db 240 AEVSDHCVKMYETGLAKTGTSKQWVDYQFREMFLAVLDVVALFPNVDRTYPMETK 299  
QY 289 AOLTRVYTDATGVPHSPFTTWTYNNNAPSFAIEAAVRNPHLLDFLEQVITYSL 348  
Db 300 AOLTRVYTDPLGAVNVS---SIGSWY-DKAPSGVIESVIRPPHVFYITGLTYVTQS 355  
QY 349 SRWSNTQYNNMWGKHLKLEFRTIGTGLNISTQGSTNTSINPV-TLPSTSRDVTETSLAGL 407  
Db 356 RSISSARYIRHWHAGHOISYHRVSRGSLNLOQMYGTGNQLHSTSTFDTNVDIYKLSKDAV 415

QY 408 NULFLTOP-----VNGVPRVDHFHWKFTVTHPIASDN---FYYPGVVIGTQLODSENELPPE 459  
Db 416 LLDIVVPGYTYIFFGMPEVEF---FMVNLNNTRKTLKYNPVSKOIIASTRDESELELPPE 472  
QY 460 ATGQPNYESYSHRLSHIGLISAS-HVKAL--VYSWTHRSADRNTTIEPNSITQIPLVAKAF 516  
Db 473 TSDQPNYESYSHRLCHITSIPATGNTGLVPVFWSTHRSADLNNITYSDKIQTQIPAVKCM 532  
QY 517 NLSSGAAVVRGPGFTGGDILR-RTNTGTGFDI---RVNINPPFAQRYRVRIRYASTTDLQ 572  
Db 533 DNLFPVVPVVGFGHTGGDILQYNRSTGSGVGLFLARYGLALEKAGKYRVRLAYATDADIV 592  
QY 573 PHTSINGKAINQGNFSAATMRGDLKYKTR-----TVGFTTPPSFL-----DVQST 619  
Db 593 LH--VNDAQI---QMPKTMNPGEDLTSKTFKVADAITTLNLTATDSSLALKHNLGDPNST 647  
QY 620 FTIGAWNFSSGNEVYIDRIEFPVVEVTEYAEYDEPEKAQEKVTAFTSTNPRGLKTDVKDY 679  
Db 648 LS-----GIVYVDRIEFPVDEYAEQLEAKKAVNALFTNTKD-GLRPGVTDY 697  
QY 680 HIDQVSNLVESLSDEFLYDEKRELFEIVKYAKOLHIERNM 719  
Db 698 EVNQAANLVECLSDLLYPNEKRLLFDAVREAKRLSGARNL 737  
RESULT 15  
US-10-414-637-2  
; Sequence 2, Application US/10414637  
; Publication No. US20030177528A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With  
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/414,637  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: US/10/032,717  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/242,838  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1206  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-414-637-2  
Query Match 40.2%; Score 1510; DB 14; Length 1206;  
Best Local Similarity 44.3%; Pred. No. 3.9e-118;  
Matches 337; Conservative 130; Mismatches 229; Indels 64; Gaps 22;  
QY 1 MCLKNODKHQSFSNAKVDKISTDS----LKNETDIELQININHEDCMKM-----SEVE-N 50  
Db 1 MSPNNQNEVEIIDATPST-SVNSDSNRYPPANEPTNALQNM DYKYLKMSAGNASIYPGS 59  
QY 51 VEPFVSA-STIQTGIGIAGKILGTGVPFAGQVASYLSYFILGELWPKG-KNQEWEIFMEHV 108  
Db 60 PEVLVSGDAAKAAIDIVGKLLSGLGVPFVGPVIVSLYTLQIDILMPSGKSQWEIFMEQV 119  
QY 109 EEIINOKISTYARNKALTDLKGIGDALAVYHDSLSWGNRNTRARSVVKQYIALELM 168  
Db 120 EEIINOKIAEYARNKALSLEGLGNKYLYLTALBEEENPNNGSRALRDVNRFEILDSL 179  
QY 169 FVQKLPSFAVSGEVPILPIYAAANLHLLLDASIFGKEMGLSSSEISTFYNNROVERA 228  
Db 180 FTQYMPSPRVNTEVFPFLTVYAAANLHLLLDKASIFGEEGWSTTTNNIYDROMKLT 239





Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	3752	99.8	719	3	US-08-286-870A-8	Sequence 8, Appli
2	3472.5	92.4	710	4	US-09-661-322A-42	Sequence 42, Appli
3	3394	90.3	648	3	US-08-286-870A-4	Sequence 4, Appli
4	3373	89.7	719	3	US-09-003-217-2	Sequence 2, Appli
5	3368	89.6	719	3	US-09-218-943-2	Sequence 2, Appli
6	2800	74.5	535	3	US-08-286-870A-6	Sequence 6, Appli
7	2445.5	65.0	1229	1	US-08-107-709-4	Sequence 4, Appli
8	2445.5	65.0	1229	1	US-08-176-863-4	Sequence 4, Appli
9	2445.5	65.0	1229	1	US-08-474-038-4	Sequence 4, Appli
10	2445.5	65.0	1229	2	US-08-779-046-4	Sequence 4, Appli
11	2445.5	65.0	1229	2	US-08-681-340-4	Sequence 4, Appli
12	2340.5	62.2	488	1	US-08-448-170-10	Sequence 10, Appli
13	2340.5	62.2	488	3	US-08-961-803-10	Sequence 10, Appli
14	2264.5	60.2	1207	1	US-07-951-715A-7	Sequence 7, Appli
15	2264.5	60.2	1207	2	US-08-459-448A-7	Sequence 7, Appli
16	2264.5	60.2	1207	3	US-08-459-595A-7	Sequence 7, Appli
17	2264.5	60.2	1207	3	US-08-459-504B-7	Sequence 7, Appli
18	2264.5	60.2	1207	3	US-08-459-444-7	Sequence 7, Appli
19	2264.5	60.2	1207	3	US-09-053-549-8	Sequence 8, Appli
20	2264.5	60.2	1207	3	US-09-547-422-7	Sequence 7, Appli
21	2264.5	60.2	1207	4	US-09-988-462-7	Sequence 7, Appli
22	2263.5	60.2	1227	3	US-09-053-549-2	Sequence 2, Appli
23	2195.5	58.4	1227	1	US-08-448-170-8	Sequence 8, Appli
24	2195.5	58.4	1227	3	US-08-961-803-9	Sequence 9, Appli
25	2186.5	58.2	1227	4	US-09-661-322A-63	Sequence 63, Appli
26	2171.5	57.8	1186	3	US-09-178-252-23	Sequence 23, Appli
27	2171.5	57.8	1186	4	US-09-826-660-23	Sequence 23, Appli

Query Match 99.8%; Score 3752; DB 3; Length 719;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 717; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 M L K N Q D K H S F S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P F V S A S T I 60  
DB 1 M L K N Q D K H S F S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P F V S A S T I 60

QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K Q N O W E I F M E H V E I I N Q K I S T V A 120  
DB 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K Q N O W E I F M E H V E I I N Q K I S T V A 120

QY 121 R N K A L T D L K G L G D A L A V V H D S L E S W G N R N N T R A S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
DB 121 R N K A L T D L K G L G D A L A V V H D S L E S W G N R N N T R A S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180

QY 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V R A G D Y S D H C V K W Y S 240  
DB 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V R A G D Y S D H C V K W Y S 240

QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
DB 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300

QY 301 G T V H P H P S T S T T W N N N A P S F S A I E A A V V R N P H L D F L E Q V T I Y S L L S R S N T Q Y M N W 360  
DB 301 G T V H P H P S T S T T W N N N A P S F S A I E A A V V R N P H L D F L E Q V T I Y S L L S R S N T Q Y M N W 360

QY 361 G G H K L E F R T I G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
DB 361 G G H K L E F R T I G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420

QY 421 V D F H K F V T H P I A S D N F Y Y P G V G I G T O L Q D S E N L P P E A T Q P N Y E S Y S H R L S H I G L I S 480  
DB 421 V D F H K F V T H P I A S D N F Y Y P G V G I G T O L Q D S E N L P P E A T Q P N Y E S Y S H R L S H I G L I S 480

QY 481 A S H V K A L V S W T H R S A D R N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G D I L R R T N 540  
DB 481 A S H V K A L V S W T H R S A D R N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G D I L R R T N 540

QY 541 T G T F G D I R V N I N P P F A Q R V R I R Y A S T T D L O F H T S I N G K A I N Q G N F S A T M N R G D L D Y K 600  
DB 541 T G T F G D I R V N I N P P F A Q R V R I R Y A S T T D L O F H T S I N G K A I N Q G N F S A T M N R G D L D Y K 600

QY 601 T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E Y T Y A E Y D F E K A Q E K V 660  
DB 601 T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E Y T Y A E Y D F E K A Q E K V 660

QY 661 T A L F T S T N P R G L K T D V Q D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719  
DB 661 T A L F T S T N P R G L K T D V Q D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719

RESULT 2  
US-09-661-322A-42  
; Sequence 42, Application US/09661322A  
; Patent No. 6593293  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Ruper, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo  
; FILE REFERENCE: MECO201  
; CURRENT APPLICATION NUMBER: US/09/661,322A  
; CURRENT FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 42  
; LENGTH: 710  
; TYPE: PRT

ORGANISM: Bacillus thuringiensis  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (200)..(200)  
OTHER INFORMATION: No. 6593293-Coding  
US-09-661-322A-42

Query Match 92.4%; Score 3472.5; DB 4; Length 710;  
Best Local Similarity 92.4%; Pred. No. 1.9e-302;  
Matches 664; Conservative 15; Mismatches 31; Indels 9; Gaps 1;

QY 1 M L K N Q D K H S F S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P F V S A S T I 60  
DB 1 M L K N Q D K H S F S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P F V S A S T I 60

QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K Q N O W E I F M E H V E I I N Q K I S T V A 120  
DB 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K Q N O W E I F M E H V E I I N Q K I S T V A 120

QY 121 R N K A L T D L K G L G D A L A V V H D S L E S W G N R N N T R A S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
DB 121 R N K A L T D L K G L G D A L A V V H D S L E S W G N R N N T R A S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180

QY 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V R A G D Y S D H C V K W Y S 240  
DB 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N Q V R A G D Y S D H C V K W Y S 240

QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
DB 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300

QY 301 G T V H P H P S T S T T W N N N A P S F S A I E A A V V R N P H L D F L E Q V T I Y S L L S R S N T Q Y M N W 360  
DB 301 G T V H P H P S T S T T W N N N A P S F S A I E A A V V R N P H L D F L E Q V T I Y S L L S R S N T Q Y M N W 360

QY 361 G G H K L E F R T I G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
DB 361 G G H K L E F R T I G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420

QY 421 V D F H K F V T H P I A S D N F Y Y P G V G I G T O L Q D S E N L P P E A T Q P N Y E S Y S H R L S H I G L I S 480  
DB 421 V D F H K F V T H P I A S D N F Y Y P G V G I G T O L Q D S E N L P P E A T Q P N Y E S Y S H R L S H I G L I S 480

QY 481 A S H V K A L V S W T H R S A D R N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G D I L R R T N 540  
DB 481 A S H V K A L V S W T H R S A D R N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G D I L R R T N 540

QY 541 T G T F G D I R V N I N P P F A Q R V R I R Y A S T T D L O F H T S I N G K A I N Q G N F S A T M N R G D L D Y K 600  
DB 541 T G T F G D I R V N I N P P F A Q R V R I R Y A S T T D L O F H T S I N G K A I N Q G N F S A T M N R G D L D Y K 600

QY 601 T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E Y T Y A E Y D F E K A Q E K V 660  
DB 601 T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E Y T Y A E Y D F E K A Q E K V 660

QY 661 T A L F T S T N P R G L K T D V Q D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719  
DB 661 T A L F T S T N P R G L K T D V Q D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719

RESULT 3  
US-08-286-870A-4  
; Sequence 4, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: CUSHMAN DARBY & CUSHMAN

ADDRESSEE: Intellectual Property Group of  
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/286,870A  
FILING DATE: 05-AUG-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520228  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8910624.9  
FILING DATE: 09-MAY-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: PAUL N. KOKULIS  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 70608/220720  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 648 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-286-870A-4

Query Match 90.3%; Score 3394; DB 3; Length 648;  
Best Local Similarity 99.8%; Pred. No. 1.8e-295;  
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDTELQNHEDCLKMEYENVEPVSASTI 60  
DB 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDTELQNHEDCLKMEYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTLPVPPAGQVASYLSFTLGLWPKGKQWEIFMHEVVEIINOKISTYA 120  
DB 61 QTGIGIAGKILGTLPVPPAGQVASYLSFTLGLWPKGKQWEIFMHEVVEIINOKISTYA 120  
QY 121 RNKALTDLKGDLAVYHDSLSWVGNRNTRARSVVKSQYIALBELMFVQKLPSPAVSG 180  
DB 121 RNKALTDLKGDLAVYHDSLSWVGNRNTRARSVVKSQYIALBELMFVQKLPSPAVSG 180  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSISITFYNRQVRAGDYSCHVKWYS 240  
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSISITFYNRQVRAGDYSCHVKWYS 240  
QY 241 TGLNLRGNTNAESWRYNFRDRMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVTDAI 300  
DB 241 TGLNLRGNTNAESWRYNFRDRMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVTDAI 300  
QY 301 GTVHPHPSFTSTTYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQTMNMW 360  
DB 301 GTVHPHPSFTSTTYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQTMNMW 360  
QY 361 GGHKLEFRITGTLNISTOGSTNTSINPVTLPFTSDVTRTESLAGNLFLTPQVNGVPR 420  
DB 361 GGHKLEFRITGTLNISTOGSTNTSINPVTLPFTSDVTRTESLAGNLFLTPQVNGVPR 420  
QY 421 VDPHMKFVTHPTASDNFYPGYVIGITQLQDSNELPPEATGPNYESYSHRLSHIGLIS 480  
DB 421 VDPHMKFVTHPTASDNFYPGYVIGITQLQDSNELPPEATGPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGDIILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGDIILRRTN 540  
QY 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAIATMRGEDLDYK 600  
DB 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAIATMRGEDLDYK 600  
QY 601 TPRTVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTYE 648  
DB 601 TPRTVGFTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTYE 648  
RESULT 4  
US-09-003-217-2  
Sequence 2, Application US/09003217  
Patent No. 5956177  
GENERAL INFORMATION:  
APPLICANT: Osman, Yehia A.  
APPLICANT: Madkour, Magdy A.  
APPLICANT: Bulla, Lee A.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH  
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)  
STREET: 3605 Glenwood Ave. Suite 310  
CITY: Raleigh  
STATE: NC  
COUNTRY: US  
ZIP: 27622  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: US/09/003,217  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: 5718-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919 420 2202  
TELEFAX: 919 881 3175  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 719 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-003-217-2

Query Match 89.7%; Score 3373; DB 2; Length 719;  
Best Local Similarity 89.7%; Pred. No. 1.7e-293;  
Matches 645; Conservative 33; Mismatches 41; Indels 0; Gaps 0;  
QY 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDTELQNHEDCLKMEYENVEPVSASTI 60  
DB 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDTELQNHEDCLKMEYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTLPVPPAGQVASYLSFTLGLWPKGKQWEIFMHEVVEIINOKISTYA 120  
DB 61 QTGIGIAGKILGTLPVPPAGQVASYLSFTLGLWPKGKQWEIFMHEVVEIINOKISTYA 120  
QY 121 RNKALTDLKGDLAVYHDSLSWVGNRNTRARSVVKSQYIALBELMFVQKLPSPAVSG 180  
DB 121 RNKALTDLKGDLAVYHDSLSWVGNRNTRARSVVKSQYIALBELMFVQKLPSPAVSG 180  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSISITFYNRQVRAGDYSCHVKWYS 240

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181 BEVPLLIYAQAANLHLLLRDASIFKNGGLSASEISTFYNRQVTRDYSYHCVKWN 240
241 TGLNLEGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTD 300
241 TGLNLEGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTD 300
241 TGLNLEGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTD 300
301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVITYSLLSRWSNTQYNNMW 360
301 GTVDPNQALRSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVITYSLLSRWSNTQYNNMW 360
361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVPR 420
361 GGHLESPIGALNTSTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVPR 420
421 VDFHMKFVTHPIASDNFYPGYVIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480
421 VDFHMKFVTHPIASDNFYPGYVIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480
481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540
481 GSHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTK 540
541 TGTGFDIRVINPFPQAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600
541 TGTGFDIRVINPFPQAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600
601 TPTVTGFTTPTPSFSDVQSTFTTIGAWNFSSGNEVYIDRIEFVFPVEVYEAEDFEKAQEKV 660
601 TPTVTGFTTPTPSFSDVQSTFTTIGAWNFSSGNEVYIDRIEFVFPVEVYEAEDFEKAQEKV 660
661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFLDKRELFEIVKAKQIHIERNM 719
661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFLDKRELFEIVKAKQIHIERNM 719

RESULT 5
US-09-218-942-2
; Sequence 2, Application US/09218942
; Patent No. 6232439
; GENERAL INFORMATION:
; APPLICANT: Osmen, Yehia
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum
; FILE REFERENCE: CRYI
; CURRENT APPLICATION NUMBER: US/09/218,942
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/035,361
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: 09/003,217
; EARLIER FILING DATE: 1998-01-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; US-09-218-942-2

Query Match 89.6%; Score 3368; DB 3; Length 719;
Best Local Similarity 89.7%; Pred. No. 4.7e-293;
Matches 645; Conservative 33; Mismatches 41; Indels 0; Gaps 0;

QY 1 MGLKNDKHOSFSSNAKVDKISTDLKNETDIELQINHEHDCIKMSEYENVEPVFVSASTI 60
DB 1 MGLKNDKHQTLSSNAKVDKIATDSLKNETDIELKNNNEDYLKRMSEHESIDPFVSASTI 60
QY 61 QTGIGIAGKILGTGVFPAGVQASLYSIFILGELWPKGNQWEIFMEHVEIINQKISTVA 120
DB 61 QTGIGIAGKILGTGVFPAGVQASLYSIFILGELWPKGNQWEIFMEHVEIINQKISTVA 120
QY 121 RNKALTDLKGIDALAVVHDSLESWGNRNNTRARSVVKSQYIALELMFVQKLPSPAVSG 180
DB 121 RNKALTDLKGIDALAVVHDSLESWGNRNNTRARSVVKSQYIALELMFVQKLPSPAVSG 180

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181 BEVPLLIYAQAANLHLLLRDASIFKNGGLSASEISTFYNRQVTRDYSYHCVKWN 240
181 BEVPLLIYAQAANLHLLLRDASIFKNGGLSASEISTFYNRQVTRDYSYHCVKWN 240
241 TGLNLEGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTD 300
241 TGLNLEGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMYPIKTTAQLTREVYTD 300
301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVITYSLLSRWSNTQYNNMW 360
301 GTVDPNQALRSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVITYSLLSRWSNTQYNNMW 360
361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVPR 420
361 GGHLESPIGALNTSTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVPR 420
421 VDFHMKFVTHPIASDNFYPGYVIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480
421 VDFHMKFVTHPIASDNFYPGYVIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480
481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540
481 GSHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTK 540
541 TGTGFDIRVINPFPQAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600
541 TGTGFDIRVINPFPQAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600
601 TPTVTGFTTPTPSFSDVQSTFTTIGAWNFSSGNEVYIDRIEFVFPVEVYEAEDFEKAQEKV 660
601 TPTVTGFTTPTPSFSDVQSTFTTIGAWNFSSGNEVYIDRIEFVFPVEVYEAEDFEKAQEKV 660
661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFLDKRELFEIVKAKQIHIERNM 719
661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFLDKRELFEIVKAKQIHIERNM 719

RESULT 6
US-08-286-870A-6
; Sequence 6, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENN, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989

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; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-870A-6

Query Match 74.5%; Score 2800; DB 3; Length 535;
Best Local Similarity 99.8%; Pred. No. 2.6e-242;
Matches 534; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPFSASTI 60
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPFSASTI 60
QY 61 QTGIGTAGKILCTGLVPPFAGQVASYFLGELMPKGNQWEIFMEHVEEIIINOKISTYA 120
DB 61 QTGIGTAGKILCTGLVPPFAGQVASYFLGELMPKGNQWEIFMEHVEEIIINOKISTYA 120
QY 121 RNKALTDLKGDLALAVYHDSLSWVGNRNTRARSVVKSOYIALELMFVKQLPSFAVSG 180
DB 121 RNKALTDLKGDLALAVYHDSLSWVGNRNTRARSVVKSOYIALELMFVKQLPSFAVSG 180
QY 181 EEVPLLPPIVAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240
DB 181 EEVPLLPPIVAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240
QY 241 TGLNLRGNTNAESWVRYNQFRDWTLMVLVALPESYDTQMPYIKTTAQLTREVTDAI 300
DB 241 TGLNLRGNTNAESWVRYNQFRDWTLMVLVALPESYDTQMPYIKTTAQLTREVTDAI 300
QY 301 GTVHPHPSSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNW 360
DB 301 GTVHPHPSSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNW 360
QY 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPSTRSDVYRTESLAGLNLFQTQVNGVPR 420
DB 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPSTRSDVYRTESLAGLNLFQTQVNGVPR 420
QY 421 VDFHKKFVTHPIASDNFYYPGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHKKFVTHPIASDNFYYPGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVSWTHRSADRNTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDI 535
DB 481 ASHVKALVSWTHRSADRNTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
; Sequence 4, Application US/08100709
; Patent No. 5322687
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr. Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSES: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia

```

```

; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,709
; FILING DATE: 19930729
; CLASSIFICATION: S14
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-100-709-4

Query Match 65.0%; Score 2445.5; DB 1; Length 1229;
Best Local Similarity 65.6%; Pred. No. 6.6e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SNNAKVDKISTDSLKN-ETDIELQ-NINHEDECLKMEYENVEPFSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPTVSNPSTQMNLSPDARIEDSLCAEVNNDIPFVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPFAGQVASYFLGELMPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKG 130
DB 67 LGVLGVPPFAGQVASYFLGELMPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKG 126
QY 131 LGDALAVYHDSLSWVGNRNTRARSVVKSOYIALELMFVKQLPSFAVSGEEVPLLPPIYA 190
DB 127 LGRGYRSQQAALETWLDNENDARSIIILERYVALELDITAIPLPRIINEEVPLLMVYA 186
QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWSYSTGLNLRGNTN 250
DB 187 QAANLHLLLRDASIFGSEWGNASSDVNQYQEQIRYRTEYSNHCYQWYNTGLNLRGNTN 246
QY 251 AESSWRYNQFRDWTLMVLVALPESYDTQMPYIKTTAQLTREVTDAITGVHPHPSFT 310
DB 247 AESSWRYNQFRDWTLMVLVALPESYDTQMPYIKTTAQLTREVTDAITGVHPHPSFT 306
QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNWGGHKLFRIT 370
DB 307 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNWGGHKLFRIT 366
QY 371 GGTNLNISTQGST-NTSINPVTLPSTRSDVYRTESLAGLNLFQTQVNGVPRVDFHKKFVT 429
DB 367 GGTNLNISTQGST-NTSINPVTLPSTRSDVYRTESLAGLNLFQTQVNGVPRVDFHKKFVT 422
QY 430 HDIASDNFYYPG-----YVIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISAS 482
DB 423 --INPQNIYERGATTYSQYQVGIQDFSELPETTERPNYESYSHRLSHIGLIS 480
QY 483 HVKALVSWTHRSADRNTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTNTG 542
DB 481 TLRAPIVSWTHRSADRNTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTNTG 540
QY 543 TFGDIRVNIINPFAQRVRYRIYASTTDLQFHTSINGKAINOGNFSATWNRGSDLDYKTF 602
DB 541 TFGDIRLNIINPVLRSQRVRYRIYASTTDLQFHTSINGKAINOGNFSATWNRGSDLDYKTF 600
QY 603 RTVGTTTPPSFLDVQSTFTTIGAWNSSGNEVYIDIEFVPEVTEYAEYDFEKAQEKVTA 662
DB 601 RTAGFSTPFPNLAQSTFTTIGAWNSSGNEVYIDIEFVPEVTEYAEYDFEKAQEKVTA 659

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QY	663	LFTSTNPRGLKTDVYHIDQVNSLVESLDEYFVLDKRELFPIVYKAKQLHIERNM	719
Db	660	LFTSTNPRGLKTDVYHIDQVNSLVESLDEYFVLDKRELFPIVYKAKQLHIERNM	716
RESULT 8			
US-08-176-865-4			
Sequence 4, Application US/08176865			
Patent No. 5616319			
GENERAL INFORMATION:			
APPLICANT: Donovan, William P.			
APPLICANT: Tan, Yiping			
APPLICANT: Gonzalez Jr., Jose M.			
TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5			
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS			
NUMBER OF SEQUENCES: 5			
CORRESPONDENCE ADDRESS:			
ADDRESS: Panitch Schwarze Jacobs & Nadel c/o A.S.			
ADDRESS: Nadel			
STREET: 1601 Market Street, 36th Floor			
CITY: Philadelphia			
STATE: Pennsylvania			
COUNTRY: U.S.A.			
ZIP: 19103			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patent In Release #1.0, Version #1.25			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/176,865			
FILING DATE: 30-DEC-1993			
CLASSIFICATION: 435			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 08/100,709			
FILING DATE: 29-JUL-1993			
ATTORNEY/AGENT INFORMATION:			
NAME: Egoif, Christopher			
REGISTRATION NUMBER: 27633			
REFERENCE/DOCKET NUMBER: 7205-49			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: 215-757-1590			
INFORMATION FOR SEQ ID NO: 4:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 1229 amino acids			
TYPE: amino acid			
TOPOLOGY: linear			
MOLECULE TYPE: protein			
US-08-176-865-4			
Query Match			
Best Local Similarity 65.0%; Score 2445.5; DB 1; Length 1229;			
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;			
QY	13	SSNAKVDKISTDSLKN-ETDIEIQ-NINHEDCLKMEYENVEFPVSASTIQTGIGIAGKI	70
Db	7	NENEINALSIPVSNPSTQMNLSPARIEDSLCVAEVNNDPVSASTVQTGINIAGRI	66
QY	71	LGTGLVPFAGQASLYSIFLIGELWPKGNQWEIFMEHVEEINQKISTYARNKALTDLKG	130
Db	67	LGVLPFAGQASLYSIFLIGELWPKGNQWEIFMEHVEEINQKISTYARNKALTDLKG	126
QY	131	IGDALAVHDSLSWGNRNNTARSVKQYALSLMFMVKLPSPAVSGEEVPLPIYA	190
Db	127	LGRYRSYQALLETWLNDRNDAKRSILERYVALELDITTAIPLRINEEVPLLMVYA	186
QY	191	QAANLHLLLRDASIFGKEWGLSSSEISTFTYNQVERAGDYSDHCYKWTYSTGLNNLRGTN	250
Db	187	QAANLHLLLRDASLFGSEWGMASDDVQYQEQIRYTEYSNHCYKWTYSTGLNNLRGTN	246
QY	251	AESWVRNQFRDMLTGLVALFSPSYDTQMYPKTKTAQLTREVYTDALGTVHPHPST	310

Db	247	AESWVRNQFRDMLTGLVALFSPSYDTQMYPKTKTAQLTREVYTDALGTVHPHPST	306
QY	311	STTWNNNAPSFAIEAAVVRNPHLLDFLEOVITYSLLSRWSNTQYNNMGGHKLFRPTI	370
Db	307	STTNFNNNAPSFAIEAAI FRPPHLLDFPEQLITYSASSRWSSTQHMYVWGHRLNFRPI	366
QY	371	GGTNLNISTQGST-NTSINPVLTPTSRDVRVYRTESLAGLNLELTOPVNGVPRVDHFWKFT	429
Db	367	GGTNLNISTQGST-NTSINPVLTPTSRDVRVYRTESLAGLNLELTOPVNGVPRVDHFWKFT	422
QY	430	HPIASDNFYPG-----YVIGTQLODSNELPPEATGPNVYESYSHRLSHLGLISAS	482
Db	423	--INFQNIYERGATTYSQYQGVGLQFDSSELPETTERPNVYESYSHRLSHLGLIIGN	480
QY	483	HVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTWG	542
Db	481	TURAPVYSWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTVVGGPGFTGGDILRRNTWG	540
QY	543	TFGDIVNINPFPFAQRYVRIRYASTTDLOFHTSINGKAINQGFSAATMNRGEDIYKTF	602
Db	541	TFGDIVNINPFPFAQRYVRIRYASTTDLOFHTSINGKAINQGFSAATMNRGEDIYKTF	600
QY	603	RTVGVTFPESFLDVOSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYEAAYDEKAEKVTA	662
Db	601	RTAGFSTPFNFNAQSTFTLGAQSFN-QEVYIDRVEFPVPAEVTFEAEYDLERAQAVNA	659
QY	663	LFTSTNPRGLKTDVYHIDQVNSLVESLDEYFVLDKRELFPIVYKAKQLHIERNM	719
Db	660	LFTSTNPRGLKTDVYHIDQVNSLVESLDEYFVLDKRELFPIVYKAKQLHIERNM	716
RESULT 9			
US-08-474-038-4			
Sequence 4, Application US/08474038			
Patent No. 5679343			
GENERAL INFORMATION:			
APPLICANT: Donovan, William P.			
APPLICANT: Tan, Yiping			
APPLICANT: Gonzalez Jr., Jose M.			
TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5			
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS			
NUMBER OF SEQUENCES: 5			
CORRESPONDENCE ADDRESS:			
ADDRESS: Panitch Schwarze Jacobs & Nadel c/o A.S.			
ADDRESS: Nadel			
STREET: 1601 Market Street, 36th Floor			
CITY: Philadelphia			
STATE: Pennsylvania			
COUNTRY: U.S.A.			
ZIP: 19103			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patent In Release #1.0, Version #1.25			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/474,038			
FILING DATE: 07-JUN-1995			
CLASSIFICATION: 514			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 08/176,865			
FILING DATE: 30-DEC-1993			
APPLICATION NUMBER: US 08/100,709			
FILING DATE: 29-JUL-1993			
ATTORNEY/AGENT INFORMATION:			
NAME: Egoif, Christopher			
REGISTRATION NUMBER: 27633			
REFERENCE/DOCKET NUMBER: 7205-49			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: 215-757-1590			
INFORMATION FOR SEQ ID NO: 4:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 1229 amino acids			
TYPE: amino acid			
TOPOLOGY: linear			
MOLECULE TYPE: protein			
US-08-474-038-4			
Query Match			
Best Local Similarity 65.0%; Score 2445.5; DB 1; Length 1229;			
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;			



QY 543 TFGDIRVNIAPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATWNRGDLKYTF 602  
Db 541 TFGDIRLNIAPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATWNRGDLKYTF 600  
QY 603 RTVGFTTPEFSLDQSTFTTGAMNFFSGNEVYIDRIEFVVEVYEAAYDFEKAQKAVTA 662  
Db 601 RTAGFSTPFNLAQSTFTTGAQSFN-QEVYIDRIEFVVEVYEAAYDFEKAQKAVTA 659  
QY 663 LFTSTNPRGLKTDVYHIDQVSNVLSLSEDFYLDKRELFEIVKAKQLHIERNM 719  
Db 660 LFTSTNPRGLKTDVYHIDQVSNVLSLSEDFYLDKRELFEIVKAKQLHIERNM 716

RESULT 11  
US-08-881-340-4  
; Sequence 4, Application US/08881340  
; Patent No. 5942658  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yuping  
; APPLICANT: Jany, Christine S.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYE4 AND CRYE5  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
; ADDRESS: Nadel  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,340  
; FILING DATE: 24-JUN-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/100,709  
; FILING DATE: 29-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Egolf, Christopher  
; REGISTRATION NUMBER: 27633  
; REFERENCE/DOCKET NUMBER: 7205-49  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-757-1590  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1229 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-881-340-4

Query Match 65.0%; Score 2445.5; DB 2; Length 1229;  
Best Local Similarity 65.6%; Pred. No. 6.6e-210;  
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKLSLKN-ETDIEIQ-NINHEDCLKSEVENPFPFVASTIQTGIGIAGKI 70  
Db 7 NENEIINALISIPVSNPSTQMLSPDARIEDSLCAEVNNDPFSASTVQTGINIARI 66  
QY 71 LGTLGVFPAGQVASYSLFELGELWPKGNQWEIFMEHVEEIIINQKISTVARNKALTDLKG 130  
Db 67 LGVLGVFPAGQVASYSLFELGELWPKGNQWEIFMEHVEEIIINQKISTVARNKALTDLKG 126  
QY 131 LGDALVYHDSLSWTCNRRNTFARSVVKSQYIALELMFVQKLPSFAVSGEEVPLPIYA 190

Db 127 LGRGYRSQQALLETWLDNRNDARSRIILERYVALELDITTAIPLFRIRNEVEVPLLMVYA 186  
QY 191 QAAHLHLALLRDASTPGKMGWISSESEISTFYNQROVERAGDYSCHVKWYSTGLNLRGTN 250  
Db 187 QAAHLHLALLRDASTPGKMGWISSESEISTFYNQROVERAGDYSCHVKWYSTGLNLRGTN 246  
QY 251 ABSWRYNQFRDMTLMVLDLVALFPSTDTOMYPIKTTAQLTREYVYTDATGIVHPHPSFT 310  
Db 247 ABSWRYNQFRDMTLMVLDLVALFPSTDTOMYPIKTTAQLTREYVYTDATGIVHPHPSFT 306  
QY 311 STTWNNNAPSATBAAVVRPHLLDLEQVYIISLRSWNTQYMMWGGHKLERTI 370  
Db 307 STTWNNNAPSATBAAVVRPHLLDLEQVYIISLRSWNTQYMMWGGHKLERTI 366  
QY 371 CGTNAISTOGST-NTSINPVTLPFTSRDVRVRESLAGNLFLTQPVNGVPRVDFHWKFTV 429  
Db 367 CGTNAISTOGST-NTSINPVTLPFTSRDVRVRESLAGNLFLTQPVNGVPRVDFHWKFTV 422  
QY 430 HPIASDNFYYPG-----YVGIGTQLODSENELPEATGQNYSSYSHRLSHIGLISAS 482  
Db 423 --INPQNIYERGATTVSQYQGVIGLFDSETELPETTERPNYESYSHRLSHIGLISAS 480  
QY 483 HVKALVYSWTHRSADRTNTIENSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 542  
Db 481 TLRAPIYVSWTHRSADRTNTIENSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 540  
QY 543 TFGDIRVNIAPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATWNRGDLKYTF 602  
Db 541 TFGDIRLNIAPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATWNRGDLKYTF 600  
QY 603 RTVGFTTPEFSLDQSTFTTGAMNFFSGNEVYIDRIEFVVEVYEAAYDFEKAQKAVTA 662  
Db 601 RTAGFSTPFNLAQSTFTTGAQSFN-QEVYIDRIEFVVEVYEAAYDFEKAQKAVTA 659  
QY 663 LFTSTNPRGLKTDVYHIDQVSNVLSLSEDFYLDKRELFEIVKAKQLHIERNM 719  
Db 660 LFTSTNPRGLKTDVYHIDQVSNVLSLSEDFYLDKRELFEIVKAKQLHIERNM 716

RESULT 12  
US-08-448-170-10  
; Sequence 10, Application US/08448170  
; Patent No. 5723758  
; GENERAL INFORMATION:  
; APPLICANT: Payne, Jewel  
; APPLICANT: Cummings, David A.  
; APPLICANT: Cannon, Raymond J.C.  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Stelman, Steve  
; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted  
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes  
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/448,170  
; FILING DATE: 424  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/069,902  
; FILING DATE: 01-JUNE-1993  
; CLASSIFICATION: 424



```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Salivanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELEPHONE: (904) 372-5800
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-448-170-10

Query Match 62.2%; Score 2340.5; DB 1; Length 488;
Best Local Similarity 89.5%; Pred. No. 3.8e-201;
Matches 445; Conservative 13; Mismatches 30; Indels 9; Gaps 1;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMGEYENVEPFSASTI 60
DB 1 MMSKNQNMHQSLNNATVDKNFTGSLNNTNTELQNFH-----EGIEPFSVSTI 51
QY 61 QTGIGTAGKILGTGVPPAGQVASYLSFILGELWPKGKQWEIFMEHVEEINOKISTYA 120
DB 52 QTGIGIVGKILGNLGVPPAGQVASYLSFILGELWPKGKQWEIFMEHVEEINOKISTYA 111
QY 121 RNKALTDLKGDLALAVYHDSLSVGNRNTRARSVKVSQYIALELMFVKQLPSFAVSG 180
DB 112 RNKALADLKGDLALAVYHDSLSVGNRNTRARSVKVSQYIALELMFVKQLPSFAVSG 171
QY 181 EEPVLLPIVAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSCHCKWYS 240
DB 172 EEPVLLPIVAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSCHCKWYN 231
QY 241 TGLNLRGTNAESWVRYNQFRDMLTMDLVALPFSYDTQMYPIKTTAQLTREVYTDI 300
DB 232 TGLNLRGMNAESWVRYNQFRDMLTMDLVALPFSYDTQMYPIKTTAQLTREVYTDI 291
QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSQTQYNNW 360
DB 292 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSQTQYNNW 351
QY 361 GGHKLBFRTIGTLNISTOGSTNTSINPVTLPFTSRDVRTESLAGLNFLTOPVNGVPR 420
DB 352 GGHKLBFRTIGTLNISTOGSTNTSINPVTLPFTSRDVRTESLAGLNFLTOPVNGVPR 411
QY 421 VDFHMKFVTHPIASDNFYPGYVIGICTOLDSENELPPEATGQPNYESYSHRLSHGLIS 480
DB 412 VDFHMKFVTHPIASDNFYPGYVIGICTOLDSENELPPEATGQPNYESYSHRLSHGLIS 471
QY 481 ASHVKALVYSWTHRSAD 497
DB 472 ASHVKALVYSWTHRSAD 488

RESULT 13
US-08-961-803-10
; Sequence 10, Application US/08961803
; Patent No. 6150589
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 6150589e1 Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes

```

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; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,170
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: M/S 102DCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-961-803-10

Query Match 62.2%; Score 2340.5; DB 3; Length 488;
Best Local Similarity 89.5%; Pred. No. 3.8e-201;
Matches 445; Conservative 13; Mismatches 30; Indels 9; Gaps 1;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMGEYENVEPFSASTI 60
DB 1 MMSKNQNMHQSLNNATVDKNFTGSLNNTNTELQNFH-----EGIEPFSVSTI 51
QY 61 QTGIGTAGKILGTGVPPAGQVASYLSFILGELWPKGKQWEIFMEHVEEINOKISTYA 120
DB 52 QTGIGIVGKILGNLGVPPAGQVASYLSFILGELWPKGKQWEIFMEHVEEINOKISTYA 111
QY 121 RNKALTDLKGDLALAVYHDSLSVGNRNTRARSVKVSQYIALELMFVKQLPSFAVSG 180
DB 112 RNKALADLKGDLALAVYHDSLSVGNRNTRARSVKVSQYIALELMFVKQLPSFAVSG 171
QY 181 EEPVLLPIVAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSCHCKWYS 240
DB 172 EEPVLLPIVAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSCHCKWYN 231
QY 241 TGLNLRGTNAESWVRYNQFRDMLTMDLVALPFSYDTQMYPIKTTAQLTREVYTDI 300
DB 232 TGLNLRGMNAESWVRYNQFRDMLTMDLVALPFSYDTQMYPIKTTAQLTREVYTDI 291
QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSQTQYNNW 360
DB 292 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSQTQYNNW 351

```

Qy	361	GGHKLPRRTTGGTNTSTQSTWTSINPVTLPFTSRDVRVTTESLAGINLFLTOPVNGVPR	420
Db	352	GGHKLPRRTTGGTNTSTQSTWTSINPVTLPFTSRDVRVTTESLAGINLFLTOPVNGVPR	411
Qy	421	VDPHKVFTHPIASDNFYFGYVIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	480
Db	412	VDPHKVFTHPIASDNFYFGYVIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	471
Qy	481	ASHVKALVYSWTHRSAD	497
Db	472	ASHVKALVYSWTHRSAD	488
RESULT 14			
US-07-951-715A-7			
; Sequence 7, Application US/07951715A			
; Patent No. 5625136			
GENERAL INFORMATION:			
; APPLICANT: Koziel, Michael G.			
; APPLICANT: Desai, Nalini M.			
; APPLICANT: Lewis, Kelly S.			
; APPLICANT: Kramer, Vance C.			
; APPLICANT: Warren, Gregory W.			
; APPLICANT: Evola, Stephen V.			
; APPLICANT: Crossland, Lyle D.			
; APPLICANT: Wright, Martha S.			
; APPLICANT: Launis, Karen L.			
; APPLICANT: Rothstein, Steven J.			
; APPLICANT: Bowman, Cindy G.			
; APPLICANT: Dawson, John L.			
; APPLICANT: Dunder, Erik M.			
; APPLICANT: Pace, Gary M.			
; APPLICANT: Suttie, Janet L.			
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED			
INSECTICIDAL ACTIVITY IN MAIZE			
NUMBER OF SEQUENCES: 94			
CORRESPONDENCE ADDRESS:			
; ADDRESSEE: CIBA-GEIGY Corporation			
; STREET: 7 Skyline Drive			
; CITY: Hawthorne			
; STATE: New York			
; COUNTRY: USA			
; ZIP: 10532			
COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent In Release #1.0, Version #1.30B			
CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/07/951,715A			
; FILING DATE: 25-SEP-1992			
; CLASSIFICATION: 800			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/772,027			
; FILING DATE: 04-OCT-1991			
ATTORNEY/AGENT INFORMATION:			
; NAME: Sprull, W. Murray			
; REGISTRATION NUMBER: 32,943			
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP			
TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (919)541-8615			
; TELEFAX: (919)541-8689			
INFORMATION FOR SEQ ID NO: 7:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1207 amino acids			
; TYPE: amino acid			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-07-951-715A-7			
Query Match			
60.2%; Score 2264.5; DB 1; Length 1207;			

Best Local Similarity 64.3%; Pred. No. 1.1e-193;			
Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;			
Qy	40	EDCLKMSYENVEPVASSTTGTGTGAGKILGTGVFPAGVASLYSFLILGKWPKN	99
Db	10	EDSLCIAENNDPFPVSASTVQTGINIAGRIUGVGFAGQLASFYFLVGLWPRGD	69
Qy	100	QWEIFMEHVEEIIQKISTYARNKALTDLKGIGDALAVYHDSLESWVGVRNNTARSVVK	159
Db	70	QWEIFLEHVEQLINQOITENARNTALRLQGLGDSFRAYQQSLEDWLENRDDARTSVLY	129
Qy	160	SOYIALELMFVOKLPSPFAVSGEEVLLPIYAAANLHLLLDASIFGKEWGLSSEIST	219
Db	130	TOYIALELDLFLNAPLFAIRNQEVPLLMVYAAANLHLLLDASLFGSEFGLTQOEIQR	189
Qy	220	FYNROVERAGDYSDHCWKWYSTGLANNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSPYD	279
Db	190	YYERQVERTRDYSDYCVIEWINTGLNSLRGTNAASWVRYNQFRDLTLGVLDLVALFPSPYD	249
Qy	280	TQWYPIKTTAQLTREYVYTDAGTVHPHPSFTTTWYNNNAPSFAIEAAVVRNPHLLDPL	339
Db	250	TRYPINTSAQLTREYVYTDAGT--GVNMAWNNWNNNAPSFAIEAAAIIRSPHLLDPL	307
Qy	340	EQVTIYSLSRWSNTQYMMWNGHKLKLEPTIGTGLNISTQSTNTSINPVTLPFTSRDYY	399
Db	308	EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTSRDYY	367
Qy	400	RTESLAGLNLF--LTQPVNGVPRVDPHMKFVTHP-----IASDNFYFGYVIGTQLODS	452
Db	368	RTESYAGVLLWGIYLEPIHGVTVRNF--INPQNISDRGTANYSQP--YESPGLQLKDS	423
Qy	453	ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTPENSITQIDPL	512
Db	424	ETELPPEPPERPNYESYSHRLSHIGLILQSRVNVPIYSWTHRSADRTNTPGNRITQIDPM	483
Qy	513	VKAPNLSSGNAVVRGPGFTGDIILRTNTGTGDIRVWINPPFAQRYVRIRVASTDLOQ	572
Db	484	VKASELPQGTTVVRGPGFTGGDILRRTNTGGPGIRVTVNGELTQRYRIGFRYASTVDFD	543
Qy	573	FHTSINGKAINQGNFSATWNRGEDLDYKTRTVGFTTFFSFLDVQSTFTTIGAMNFSNGNE	632
Db	544	FFVSRGGTTVNNFRFLRTWNSGDELAYGNFVRAFTTPTFTTQIDIRTSIQGLSGNGE	603
Qy	633	VYIDRIEFVPEVYEAEDYFEKAQKVTALFTSTNPRGLKTDYKDYHDQVSNLVESLS	692
Db	604	VYIDKIEIIPVTATFEAYDLEAQAQAVNALFTNTNPRRLKTDVTDYHDQVSNLVACLS	663
Qy	693	DEFVLDEKRELFEIVKAKOLHIERNM	719
Db	664	DEFCLDEKRELLEKVKYAKLSDERNL	690
RESULT 15			
US-08-459-448A-7			
; Sequence 7, Application US/08459448A			
; Patent No. 5859336			
GENERAL INFORMATION:			
; APPLICANT: Koziel, Michael G.			
; APPLICANT: Desai, Nalini M.			
; APPLICANT: Lewis, Kelly S.			
; APPLICANT: Kramer, Vance C.			
; APPLICANT: Warren, Gregory W.			
; APPLICANT: Evola, Stephen V.			
; APPLICANT: Crossland, Lyle D.			
; APPLICANT: Wright, Martha S.			
; APPLICANT: Launis, Karen L.			
; APPLICANT: Rothstein, Steven J.			
; APPLICANT: Bowman, Cindy G.			
; APPLICANT: Dawson, John L.			
; APPLICANT: Dunder, Erik M.			
; APPLICANT: Pace, Gary M.			
; APPLICANT: Suttie, Janet L.			

[illegible]

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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:20:21 ; Search time 98.3514 Seconds  
(without alignments)  
2827.419 Million cell updates/sec

Title: US-10-019-823B-57

Perfect score: 3760

Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KELPEIVKAYAKQLHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseq1980s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001s:\*

5: Geneseq2002s:\*

6: Geneseq2003as:\*

7: Geneseq2003bs:\*

8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3760	100.0	719	4	AAB66910 Insectici
2	3760	100.0	719	6	AAB66910 Insectici
3	3756	99.9	719	4	AAB66908 Insectici
4	3756	99.9	719	6	AAB66908 Insectici
5	3756	99.9	719	8	ADR89421
6	3747	99.7	719	4	AAB66910 Insectici
7	3745	99.6	719	4	AAB66910 Insectici
8	3745	99.6	719	6	AAB66910 Insectici
9	3739	99.4	719	4	AAB66909 Insectici
10	3739	99.4	719	6	AAB66909 Insectici
11	3735	99.3	719	2	AAR08041
12	3724.5	99.1	718	6	AAB66907 Insectici
13	3718.5	98.9	718	4	AAB66907 Insectici
14	3547	94.3	719	7	ADM74717
15	3516	93.5	719	4	AAB66912 Insectici
16	3516	93.5	719	6	AAB66912 Insectici
17	3472.5	92.4	710	4	AAB66912 Insectici
18	3393	90.2	719	3	ABB07073
19	3373	89.7	719	2	AAB66909 Insectici
20	3287	87.4	1217	4	AAB66909 Insectici
21	2730	72.6	1208	8	ADK98489 B thuring
22	2447	65.1	1230	8	ADK98489 B thuring
23	2447	65.1	1230	8	ADK98489 B thuring
24	2447	65.1	1230	8	ADK98489 B thuring
25	2447	65.1	1230	8	ADK98489 B thuring

ALIGNMENTS

RESULT 1

AAB66910

ID AAB66910 standard; protein; 719 AA.

AC AAB66910;

DT 12-APR-2001 (first entry)

DE Insecticidal protein cryIIa4.

KW Insecticide; transgenic plant; insect-resistance.

OS Paecilomyces sp.

PN WO200100841-A1.

PD 04-JAN-2001.

PF 23-JUN-2000; 2000WO-GB002457.

PR 29-JUN-1999; 99GB-00015215.

PR 23-DEC-1999; 99GB-00030536.

XX (ZENE ) ZENECA LTD.

XX Griffin J., Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;

XX Vincent JL, Lee MD;

XX WPI; 2001-123015/13.

XX Novel insecticidal protein obtained from species of Paecilomyces for controlling insects, and for insect-resistant transgenic plant production.

XX Claim 14; Page 60-62; 72pp; English.

XX The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed

SQ Sequence 719 AA;

Query Match 100.0%; Score 3760; DB 4; Length 719;

Best Local Similarity 100.0%; Pred. No. 1.3e-290;

Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQINIHEDCLKMEYENVEPVSASTI 60  
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQINIHEDCLKMEYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTLGVPPAGQVASYFLGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTLGVPPAGQVASYFLGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
QY 121 RNKALTDLKGIDGALAVYHDSLESWGVRNNTARSVVKVSOYIALELMFVKQLPSFAVSG 180  
DB 121 RNKALTDLKGIDGALAVYHDSLESWGVRNNTARSVVKVSOYIALELMFVKQLPSFAVSG 180  
QY 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCKWYS 240  
DB 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCKWYS 240  
QY 241 TGLNLGATNAESWVRNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI 300  
DB 241 TGLNLGATNAESWVRNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI 300  
QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
DB 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
QY 361 GGHKLEFRTIGTTLNISTOGSTNTSINPVTLPPTSDRVYRTESLAGLNFLTOPVNGVPR 420  
DB 361 GGHKLEFRTIGTTLNISTOGSTNTSINPVTLPPTSDRVYRTESLAGLNFLTOPVNGVPR 420  
QY 421 VDFHWKFVTHPIASDNFYPGYVIGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFVTHPIASDNFYPGYVIGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
QY 481 ASHKVYVSWTHRSADRTNTEPNSITQIPLVKAFLNSGAAVVRGPGFTGGDILRTN 540  
DB 481 ASHKVYVSWTHRSADRTNTEPNSITQIPLVKAFLNSGAAVVRGPGFTGGDILRTN 540  
QY 541 TGTGDIRVNIINPPPAQRYRIRYASTTDLQFHTSINGKAINOGNFSATMNRGEDLDYK 600  
DB 541 TGTGDIRVNIINPPPAQRYRIRYASTTDLQFHTSINGKAINOGNFSATMNRGEDLDYK 600  
QY 601 TFRVTGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEAYDFEKAQEKV 660  
DB 601 TFRVTGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEAYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFLDEKRELFEIVKYAKQLHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFLDEKRELFEIVKYAKQLHIERNM 719

RESULT 2  
ID AAE36274 standard; protein; 719 AA.  
AC AAE36274;  
XX 26-JUN-2003 (first entry)  
DT  
XX B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa.  
DE Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
KW Bacillus thuringiensis.  
OS  
XX WO200298911-A2.  
PD 12-DEC-2002.  
XX 30-MAY-2002; 2002WO-GB002666.  
XX 07-JUN-2001; 2001GB-00013900.  
PR (SYGN ) SYNGENTA LTD.  
XX

Vincent JL, Viner R;  
WPI; 2003-175137/17.  
New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
Claim 12; Page 50-53; 67pp; English.  
The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
Sequence 719 AA;

Query Match 100.0%; Score 3760; DB 6; Length 719;  
Best Local Similarity 100.0%; Pred. No. 1.3e-290; Indels 0; Gaps 0;  
Matches 719; Conservative 0; Mismatches 0;  
QY 1 MKLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQINIHEDCLKMEYENVEPVSASTI 60  
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQINIHEDCLKMEYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTLGVPPAGQVASYFLGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTLGVPPAGQVASYFLGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
QY 121 RNKALTDLKGIDGALAVYHDSLESWGVRNNTARSVVKVSOYIALELMFVKQLPSFAVSG 180  
DB 121 RNKALTDLKGIDGALAVYHDSLESWGVRNNTARSVVKVSOYIALELMFVKQLPSFAVSG 180  
QY 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCKWYS 240  
DB 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCKWYS 240  
QY 241 TGLNLGATNAESWVRNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI 300  
DB 241 TGLNLGATNAESWVRNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI 300  
QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
DB 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
QY 361 GGHKLEFRTIGTTLNISTOGSTNTSINPVTLPPTSDRVYRTESLAGLNFLTOPVNGVPR 420  
DB 361 GGHKLEFRTIGTTLNISTOGSTNTSINPVTLPPTSDRVYRTESLAGLNFLTOPVNGVPR 420  
QY 421 VDFHWKFVTHPIASDNFYPGYVIGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFVTHPIASDNFYPGYVIGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
QY 481 ASHKVYVSWTHRSADRTNTEPNSITQIPLVKAFLNSGAAVVRGPGFTGGDILRTN 540  
DB 481 ASHKVYVSWTHRSADRTNTEPNSITQIPLVKAFLNSGAAVVRGPGFTGGDILRTN 540  
QY 541 TGTGDIRVNIINPPPAQRYRIRYASTTDLQFHTSINGKAINOGNFSATMNRGEDLDYK 600  
DB 541 TGTGDIRVNIINPPPAQRYRIRYASTTDLQFHTSINGKAINOGNFSATMNRGEDLDYK 600  
QY 601 TFRVTGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEAYDFEKAQEKV 660  
DB 601 TFRVTGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEAYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFLDEKRELFEIVKYAKQLHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFLDEKRELFEIVKYAKQLHIERNM 719

RESULT 3		
ID	AAB66908	standard; protein; 719 AA.
XX	AAAB66908;	
AC	AAAB66908;	
DT	12-APR-2001	(first entry)
XX		
DE	Insecticidal protein cryIIa2.	
XX		
KW	Insecticide; transgenic plant; insect-resistance.	
XX		
OS	Paecilomyces sp.	
PN	WO200100841-A1.	
PD	04-JAN-2001.	
XX		
PF	23-JUN-2000;	2000WO-GB002457.
XX		
PR	29-JUN-1999;	99GB-00015215.
PR	23-DEC-1999;	99GB-00030536.
XX		
PA	(ZENE ) ZENECA LTD.	
XX		
PI	Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;	
PI	Vincent JL, Lee MD;	
XX		
DR	WPI; 2001-123015/13.	
XX		
PT	Novel insecticidal protein obtained from species of Paecilomyces for	
PT	controlling insects, and for insect-resistant transgenic plant	
PT	production.	
XX		
PS	Claim 14; Page 55-57; 72pp; English.	
XX		
CC	The present invention relates to novel insecticidal proteins obtained	
CC	from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The	
CC	insecticidal proteins can be used to produce transgenic plants, which are	
CC	insect-resistant. Also, the insecticidal proteins are useful for	
CC	controlling insects by providing them at a locus where insects feed	
XX		
SQ	Sequence 719 AA;	
Query Match		
Best Local Similarity 99.9%; Score 3756; DB 4; Length 719;		
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYEYENVEPVSASTI 60
DB	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYEYENVEPVSASTI 60
QY	61	QTGIGIAGKILGTLGVPPAGQVAVSLYSFILGELWPKGKQWEIFMHEVBEIINOKISTYA 120
DB	61	QTGIGIAGKILGTLGVPPAGQVAVSLYSFILGELWPKGKQWEIFMHEVBEIINOKISTYA 120
QY	121	RNKALTDLKGLDALAVYHDSLESWGNRNTRARSVKVKSQYIALSLMFVKLPSFAVSG 180
DB	121	RNKALTDLKGLDALAVYHDSLESWGNRNTRARSVKVKSQYIALSLMFVKLPSFAVSG 180
QY	181	EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSCHVKWYS 240
DB	181	EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSCHVKWYS 240
QY	241	TGLNNLRGTNAESWRYNQFRDMTLMVLVDLVALFPSYDTQMPYIKTTAQLTREVYTDAI 300
DB	241	TGLNNLRGTNAESWRYNQFRDMTLMVLVDLVALFPSYDTQMPYIKTTAQLTREVYTDAI 300
QY	301	GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNW 360
DB	301	GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNW 360
Query Match		
Best Local Similarity 99.9%; Score 3756; DB 6; Length 719;		
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	361	GGHKLFRFTIGTGLNISTQGSTNTSINPVTLPTSRDVRVYRTESLAGLNFLTPQVNGVPR 420
DB	361	GGHKLFRFTIGTGLNISTQGSTNTSINPVTLPTSRDVRVYRTESLAGLNFLTPQVNGVPR 420
QY	421	VDFHWKFVTHPIASDNFYPGVVGIGTOLQDSNELPPEATGPNVYESYSHRLSHIGLIS 480
DB	421	VDFHWKFVTHPIASDNFYPGVYGAGIGTOLQDSNELPPEATGPNVYESYSHRLSHIGLIS 480
QY	481	ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB	481	ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY	541	TCTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
DB	541	TCTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY	601	TPRTVGFTTPSFQSTFTIGAWNFGSGNEVYIDRIEFVPEVTEAYEAYDPEKAQEKV 660
DB	601	TPRTVGFTTPSFQSTFTIGAWNFGSGNEVYIDRIEFVPEVTEAYEAYDPEKAQEKV 660
QY	661	TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB	661	TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
RESULT 4		
ID	AAE36272	standard; protein; 719 AA.
XX	AAE36272;	
AC	AAE36272;	
DT	26-JUN-2003	(first entry)
XX		
DE	B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.	
XX		
KW	Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.	
XX		
OS	Bacillus thuringiensis.	
XX		
PN	WO200298911-A2.	
XX		
PD	12-DEC-2002.	
XX		
PF	30-MAY-2002;	2002WO-GB002666.
XX		
PR	07-JUN-2001;	2001GB-00013900.
XX		
PA	(SYGN ) SYNGENTA LTD.	
XX		
PI	Vincent JL, Viner R;	
XX		
DR	WPI; 2003-175137/17.	
XX		
PT	New insecticidal protein comprising an X-glycine motif at the amino-	
PT	terminus, useful as an active ingredient of a pesticide.	
XX		
PS	Claim 12; Page 44-47; 67pp; English.	
XX		
CC	The invention relates to insecticidal protein comprising an X-glycine	
CC	motif at the amino-terminus. Polynucleotide or DNA constructs of the	
CC	invention are useful for producing plants or plant parts that are	
CC	resistant to insects. The protein or synergistic combination is useful as	
CC	an active ingredient of a pesticide or for controlling insects.	
CC	Antibodies raised to the insecticidal proteins can be used to identify	
CC	other proteins with insecticidal activity. The present sequence is	
CC	Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This	
CC	sequence is used in the invention	
XX		
SQ	Sequence 719 AA;	
Query Match		
Best Local Similarity 99.9%; Score 3756; DB 6; Length 719;		
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		

QY	1	MKLKQDKHQSFSNAKVDKISTDSLKNETDIELQININHEDCMKSEYENVEFPVGSASTI	60	PR	20-FEB-2003; 2003US-0448632P.
DB	1	MKLKQDKHQSFSNAKVDKISTDSLKNETDIELQININHEDCMKSEYENVEFPVGSASTI	60	PR	20-FEB-2003; 2003US-0448633P.
QY	61	QTGIGIAGKILGTGVPPAGQVSLYSFILGELWPKGKNQWEIFMEHVEIINQKISTYA	120	PR	20-FEB-2003; 2003US-0448797P.
DB	61	QTGIGIAGKILGTGVPPAGQVSLYSFILGELWPKGKNQWEIFMEHVEIINQKISTYA	120	PR	20-FEB-2003; 2003US-0448806P.
QY	121	RNKALTDLKGIDALAVYHDSLESWGVRNNTARSVVKSQYIALELMFVKQLPSPAVSG	180	PR	20-FEB-2003; 2003US-0448810P.
DB	121	RNKALTDLKGIDALAVYHDSLESWGVRNNTARSVVKSQYIALELMFVKQLPSPAVSG	180	PR	20-FEB-2003; 2003US-0448812P.
QY	181	EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGYSYDHCWKWYS	240	PR	19-FEB-2004; 2004US-00781979.
DB	181	EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGYSYDHCWKWYS	240	PR	19-FEB-2004; 2004US-00782020.
QY	241	TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI	300	PR	19-FEB-2004; 2004US-00782096.
DB	241	TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI	300	PR	19-FEB-2004; 2004US-00782141.
QY	301	GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW	360	PR	19-FEB-2004; 2004US-00782570.
DB	301	GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW	360	PR	19-FEB-2004; 2004US-00783417.
QY	361	GGHKLFRPTIGTTLNISTQGSTNTSINPVTLPFTSRDVRTERSLAGLNLFITQPVNGVPR	420	XX	(ATHE-) ATHENIX CORP.
DB	361	GGHKLFRPTIGTTLNISTQGSTNTSINPVTLPFTSRDVRTERSLAGLNLFITQPVNGVPR	420	XX	Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
QY	421	VDFHMKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	480	XX	WPI; 2004-635574/61.
DB	421	VDFHMKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	480	XX	New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
QY	481	ASHVKALVYSWTHRSADRTNTIENSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN	540	XX	and polypeptides, useful for killing lepidopteran or coleopteran pests or
DB	481	ASHVKALVYSWTHRSADRTNTIENSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN	540	XX	for producing organisms with pesticide resistance.
QY	541	TGTFGDIIRVNPPAQRYRVRIRVASTDLOQHTSINGKAINQGNFSATNWRGEDLDYK	600	XX	Example 6; SEQ ID NO 33; 178pp; English.
DB	541	TGTFGDIIRVNPPAQRYRVRIRVASTDLOQHTSINGKAINQGNFSATNWRGEDLDYK	600	XX	This sequence represents a delta-endotoxin crystal protein. This protein
QY	601	TPRTVGFTTFFSLDVQSTFTIGAMNFSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV	660	XX	is included in the scope of the invention as a comparison to the delta-
DB	601	TPRTVGFTTFFSLDVQSTFTIGAMNFSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV	660	XX	endotoxins of the invention. Some of the delta-endotoxin coding sequences
QY	661	TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELPEIVKAYAKOLHIERNM	719	XX	of the invention have alternative start codons, producing more than one
DB	661	TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELPEIVKAYAKOLHIERNM	719	XX	protein from a single open reading frame. The nucleic acid sequences of
RESULT 5					the invention are useful in DNA constructs or expression cassettes for
ID	ADR89421	standard; protein; 719 AA.			transformation and expression in plants and bacteria. The nucleic acids
XX	ADR89421;				and corresponding polypeptides are useful for killing lepidopteran or
XX	18-NOV-2004 (first entry)				coleopteran pests. Compositions containing the delta-endotoxins of the
DT	crylla.				invention, and methods for their production, are useful for the
XX	delta-endotoxin; delta-endotoxin associate polypeptide;				production of organisms with pesticide resistance, specifically bacteria
XX	expression cassette; transformation; transgenic; plant; bacteria;				and plants. These organisms are useful for generating altered or improved
KW	lepidoptera; coleoptera; pest; pesticide; resistance;				delta-endotoxin or delta-endotoxin-associated proteins that have
KW	pesticidal activity.				pesticidal activity, or for detecting the presence of delta-endotoxin or
XX	Bacillus thuringiensis.				delta-endotoxin-associated proteins or nucleic acids in products or
XX	WO2004074462-A2.				organisms.
XX	02-SEP-2004.				Sequence 719 AA;
XX	20-FEB-2004; 2004WO-US005829.				Query Match 99.9%; Score 3756; DB 8; Length 719;
XX					Best Local Similarity 99.9%; Pred. No. 2.7e-290;
XX					Mismatches 1; Indels 0; Gaps 0;
XX					Matches 718; Conservative 0;



Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNFLTPQVNGVPR 420  
QY 421 VDFHWKFVTHPIASDNFYYPGVYIGTQLQDSNELPPEATGPNVYESYSHRLSHIGLIS 480  
Db 421 VDFHWKFVTHPIASDNFYYPGVYIGTQLQDSNELPPEATGPNVYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
Db 481 ASHVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMRGEDLDYK 600  
Db 541 TGTFGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMRGEDLDYK 600  
QY 601 TPTVTGFTTTPFSLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVVEYEAEDPEKAQEKV 660  
Db 601 TPTVTGFTTTPFSLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVVEYEAEDPEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 6

AAU02095  
ID AAU02095 standard; protein; 719 AA.

AC AAU02095;  
XX  
DT 07-SEP-2001 (first entry)

DE Bacillus thuringiensis partial mutant CryIIa.  
XX  
XX Crystal protein; CryIIa; CryIIa; moth; butterfly; Colorado potato beetle;  
XX mutant; mutein.

XX Bacillus thuringiensis.

OS  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= Signal\_peptide  
FT Protein /label= Mature\_CryIIa

FT EP1099760-A1.  
PN  
XX  
XX  
PD 16-MAY-2001.

XX 09-NOV-1999; 99EP-00203723.  
XX  
XX 09-NOV-1999; 99EP-00203723.

XX (CPRO-) CPRO-DLO CENT PLANTENVERDEDELINGS REPROD.

XX De Maagd RA, Bosch HJ;  
XX WPI: 2001-337141/36.  
XX N-PSDB; AAS04855.

XX New hybrid Bacillus thuringiensis hybrid toxins comprising structural  
FT domains derived from at least 2 different crystal proteins, such as  
PT CryIIa and CryIIa, and having insecticidal activity, useful for combating  
PT insects.

XX Example; Page 30-32; 43pp; English.

XX The sequence is B. thuringiensis (8t) crystal protein CryIIa, the DNA  
CC encoding which was mutated to allow cloning of domain III or domains I  
CC and II, to make the hybrid protoxins of the invention. The hybrid toxins  
CC of the invention, having structural domains I, II and III in this order  
CC starting from the N-terminal derived from at least 2 different crystal  
CC proteins, are useful for protecting plants against pest insects, e.g.

CC moths, butterflies and Colorado potato beetle or for combating insects  
XX Sequence 719 AA;

Query Match 99.7%; Score 3747; DB 4; Length 719;  
Best Local Similarity 99.7%; Pred. No. 1.4e-289; Indels 0; Gaps 0;  
Matches 717; Conservative 0; Mismatches 2;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLNKNETDTELQNIHEDCLKMSYENVEFVSASTI 60  
Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLNKNETDTELQNIHEDCLKMSYENVEFVSASTI 60

QY 61 QTGIGIAGKILGTGLVPFAGQVASLYSFTLGBELPKGKQWEIFMEHVBEIINQKISTYA 120  
Db 61 QTGIGIAGKILGTGLVPFAGQVASLYSFTLGBELPKGKQWEIFMEHVBEIINQKISTYA 120

QY 121 RNKALTDLKGLGDALAVYHDSLESVWGNRNNTRAKSVKVSQVYALRLMFPVKLPSFAVSG 180  
Db 121 RNKALTDLKGLGDALAVYHDSLESVWGNRNNTRAKSVKVSQVYALRLMFPVKLPSFAVSG 180

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSVHCYKWS 240  
Db 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSVHCYKWS 240

QY 241 TGLNNLRGTNASSWVRVYNOFRDMLMVLVDLVALPSPSYDTQMPYPIKTTAQLTREVYTDI 300  
Db 241 TGLNNLRGTNASSWVRVYNOFRDMLMVLVDLVALPSPSYDTQMPYPIKTTAQLTREVYTDI 300

QY 301 GTVHPHPSFTSTWYNNNAPSFAEAAVVRPHLLDLEQVTIYSLLSRWSNTQVNMW 360  
Db 301 GTVHPHPSFTSTWYNNNAPSFAEAAVVRPHLLDLEQVTIYSLLSRWSNTQVNMW 360

QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNFLTPQVNGVPR 420  
Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNFLTPQVNGVPR 420

QY 421 VDFHWKFVTHPIASDNFYYPGVYIGTQLQDSNELPPEATGPNVYESYSHRLSHIGLIS 480  
Db 421 VDFHWKFVTHPIASDNFYYPGVYIGTQLQDSNELPPEATGPNVYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
Db 481 ASHVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540

QY 541 TGTFGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMRGEDLDYK 600  
Db 541 TGTFGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATMRGEDLDYK 600

QY 601 TPTVTGFTTTPFSLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVVEYEAEDPEKAQEKV 660  
Db 601 TPTVTGFTTTPFSLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVVEYEAEDPEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 7

AA866911  
ID AA866911 standard; protein; 719 AA.

XX AA866911;

DT 12-APR-2001 (first entry)

XX Insecticidal protein cryIIa5.

XX Insecticide; transgenic plant; insect-resistance.

XX Paecilomyces sp.

XX WO200100841-A1.

XX

PD 04-JAN-2001.  
XX 23-JUN-2000; 2000WO-GB002457.  
XX 29-JUN-1999; 99GB-00015215.  
XX 23-DEC-1999; 99GB-00030536.  
XX (ZENE ) ZENECA LTD.  
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
XX Vincent JL, Lee MD;  
XX WPI; 2001-123015/13.  
XX Novel insecticidal protein obtained from species of Paecilomyces for  
XX controlling insects, and for insect-resistant transgenic plant  
XX production.  
XX Claim 14; Page 62-64; 72pp; English.  
XX The present invention relates to novel insecticidal proteins obtained  
XX from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
XX insecticidal proteins can be used to produce transgenic plants, which are  
XX insect-resistant. Also, the insecticidal proteins are useful for  
XX controlling insects by providing them at a locus where insects feed  
XX  
XX Sequence 719 AA;  
SQ  
Query Match 99.6%; Score 3745; DB 4; Length 719;  
Best Local Similarity 99.4%; Pred. No. 2e-289;  
Matches 715; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MCLKNQDKHQSFSNAKVDKISTSLKNETDIELQINNHEDCLKMSYENVEPVSASTI 60  
DB 1 MCLKNQDKHQSFSNAKVDKISTSLKNETDIELQINNHEDCLKMSYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQISTYA 120  
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQISTYA 120  
QY 121 RNKALTDLKGLGDALAVYHDSLESWGNNRNNTRARSVVKSOYIALELMFVKLPSPFVSG 180  
DB 121 RNKALTDLKGLGDALAVYHDSLESWGNNRNNTRARSVVKSOYIALELMFVKLPSPFVSG 180  
QY 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGDYSCHVKWYS 240  
DB 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGDYSCHVKWYS 240  
QY 241 TGLANLRGTNAESWRYNQFRDMLVLDLVALFPSSYDTQMPYIKTTAQLTREVTYDAI 300  
DB 241 TGLANLRGTNAESWRYNQFRDMLVLDLVALFPSSYDTQMPYIKTTAQLTREVTYDAI 300  
QY 301 GTVHPHPSFTSTWNNNAPSFAIEAAVVRNPHLLDLEQVITYSLLSRNSNTQYNNMW 360  
DB 301 GTVHPHPSFTSTWNNNAPSFAIEAAVVRNPHLLDLEQVITYSLLSRNSNTQYNNMW 360  
QY 361 GGHKLEERTIGTGLNISQGSNTSINPVTLPFTSRDVRYESLAGNLFITQPVGVPYR 420  
DB 361 GGHKLEERTIGTGLNISQGSNTSINPVTLPFTSRDVRYESLAGNLFITQPVGVPYR 420  
QY 421 VDFHWKFVTHPIASDNFYYPYVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFVTHPIASDNFYYPYVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRADRNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVYSWTHRADRNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNNPPAQRRVRIRVASTTDLQFHTSINGKAINQGNFATMNRGBDLYK 600  
DB 541 TGTFGDIRVNNPPAQRRVRIRVASTTDLQFHTSINGKAINQGNFATMNRGBDLYK 600  
QY 601 TPTRTVGFTTTPFSLDVQSTFTTIGANNFSSGNEVYIDRIEFVFEVTEYAEYDFEKAQEKV 660

DB 601 TERTVGTFTTTPFSLDVQSTFTTIGANNFSSGNEVYIDRIEFVFEVTEYAEYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDYHIDOVSNLVESLSDFYLDKRELFEIVKYAKOLHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDYHIDOVSNLVESLSDFYLDKRELFEIVKYAKOLHIERNM 719  
RESULT 8  
AAE36275  
ID AAE36275 standard; protein; 719 AA.  
XX AC  
XX AAE36275;  
XX 26-JUN-2003 (first entry)  
XX B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa5.  
XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
XX Bacillus thuringiensis.  
XX WO200298911-A2.  
XX 12-DEC-2002.  
XX 30-MAY-2002; 2002WO-GB002666.  
XX 07-JUN-2001; 2001GB-00013900.  
XX (SYGN ) SYNGENTA LTD.  
XX Vincent JL, Viner R;  
XX WPI; 2003-175137/17.  
XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
XX Claim 12; Page 53-56; 67pp; English.  
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
XX Sequence 719 AA;  
Query Match 99.6%; Score 3745; DB 6; Length 719;  
Best Local Similarity 99.4%; Pred. No. 2e-289;  
Matches 715; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MCLKNQDKHQSFSNAKVDKISTSLKNETDIELQINNHEDCLKMSYENVEPVSASTI 60  
DB 1 MCLKNQDKHQSFSNAKVDKISTSLKNETDIELQINNHEDCLKMSYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQISTYA 120  
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQISTYA 120  
QY 121 RNKALTDLKGLGDALAVYHDSLESWGNNRNNTRARSVVKSOYIALELMFVKLPSPFVSG 180  
DB 121 RNKALTDLKGLGDALAVYHDSLESWGNNRNNTRARSVVKSOYIALELMFVKLPSPFVSG 180  
QY 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGDYSCHVKWYS 240  
DB 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGDYSCHVKWYS 240

QY 241 TGLNLRGTTNAESKVRVYNQFRDWTLMVLDFALFVSYDTQMPYPIKTTAQLTREVTDAI 300  
DB 241 TGLNLRGTTNAESKVRVYNQFRDWTLMVLDFALFVSYDTQMPYPIKTTAQLTREVTDAI 300  
QY 301 GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMNW 360  
DB 301 GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMNW 360  
QY 361 GGHKLEFRTIGTGLNLTSTQSTNTSINPVTLPFTSRDVRTESLAGLNLFLTOPVNGVPR 420  
DB 361 GGHKLEFRTIGTGLNLTSTQSTNTSINPVTLPFTSRDVRTESLAGLNLFLTOPVNGVPR 420  
QY 421 VDFHMKFVTHPIASDNFYYPGYGIGTQLQDSENELPPEATGPNYESYSHRLSHIGLIS 480  
DB 421 VDFHMKFVTHPIASDNFYYPGYGIGTQLQDSENELPPEATGPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDIILRTN 540  
DB 481 ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDIILRTN 540  
QY 541 TGTFGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
DB 541 TGTFGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
QY 601 TFRVTGFTTFFSFLDVQSTFTTICAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
DB 601 TFRVTGFTTFFSFLDVQSTFTTICAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLTKDVKDHYDQVSNLVESLSEDFYLDKRELFELVYKAKQLHIERNM 719  
DB 661 TALFTSTNPRGLTKDVKDHYDQVSNLVESLSEDFYLDKRELFELVYKAKQLHIERNM 719

RESULT 9

AAB66909  
ID AAB66909 standard; protein; 719 AA.  
XX AAB66909;  
AC AC  
DT 12-APR-2001 (first entry)  
XX Insecticidal protein cryIIa3.  
DE Insecticide; transgenic plant; insect-resistance.  
XX  
XX Paecilomyces sp.  
OS  
XX WO200100841-A1.  
PN  
XX 04-JAN-2001.  
XX 23-JUN-2000; 2000WO-GB002457.  
XX  
PR 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX  
XX (ZENE ) ZENECA LTD.  
XX  
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX WPI; 2001-123015/13.  
XX  
PT Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PT production.  
XX  
XX Claim 14; Page 57-59; 72pp; English.  
XX  
XX The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for

CC controlling insects by providing them at a locus where insects feed  
XX  
SQ Sequence 719 AA;  
Query Match 99.4%; Score 3739; DB 4; Length 719;  
Best Local Similarity 99.4%; Pred. No. 6e-289;  
Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MKLKNQDKHQSSNAKVDKISTDSLKNKTDIELQNIHEDCLKMEYENVEFPVSASTI 60  
DB 1 MKLKNQDKHQSSNAKVDKISTDSLKNKTDIELQNIHEDCLKMEYENVEFPVSASTI 60  
QY 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELMPKQKQWEIFMEHVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELMPKQKQWEIFMEHVEEIIINQKISTYA 120  
QY 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNRTRARSVVKVQSYIALBLMFVQKLPSPAVSG 180  
DB 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNRTRARSVVKVQSYIALBLMFVQKLPSPAVSG 180  
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSVHCWKYS 240  
DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSVHCWKYS 240  
QY 241 TGLNLRGTNAESWVRVYNQFRDWTLMVLDFALFVSYDTQMPYPIKTTAQLTREVTDAI 300  
DB 241 TGLNLRGTNAESWVRVYNQFRDWTLMVLDFALFVSYDTQMPYPIKTTAQLTREVTDAI 300  
QY 301 GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMNW 360  
DB 301 GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMNW 360  
QY 361 GGHKLEFRTIGTGLNLTSTQSTNTSINPVTLPFTSRDVRTESLAGLNLFLTOPVNGVPR 420  
DB 361 GGHKLEFRTIGTGLNLTSTQSTNTSINPVTLPFTSRDVRTESLAGLNLFLTOPVNGVPR 420  
QY 421 VDFHMKFVTHPIASDNFYYPGYGIGTQLQDSENELPPEATGPNYESYSHRLSHIGLIS 480  
DB 421 VDFHMKFVTHPIASDNFYYPGYGIGTQLQDSENELPPEATGPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDIILRTN 540  
DB 481 ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDIILRTN 540  
QY 541 TGTFGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
DB 541 TGTFGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
QY 601 TFRVTGFTTFFSFLDVQSTFTTICAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
DB 601 TFRVTGFTTFFSFLDVQSTFTTICAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLTKDVKDHYDQVSNLVESLSEDFYLDKRELFELVYKAKQLHIERNM 719  
DB 661 TALFTSTNPRGLTKDVKDHYDQVSNLVESLSEDFYLDKRELFELVYKAKQLHIERNM 719  
RESULT 10  
AAB66273  
ID AAB66273 standard; protein; 719 AA.  
XX AAB66273;  
AC AC  
DT 26-JUN-2003 (first entry)  
XX  
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.  
XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
XX Bacillus thuringiensis.  
OS  
XX WO200298911-A2.  
PN  
XX

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PD 12-DEC-2002.
XX PF 30-MAY-2002; 2002WO-GB002666.
XX PR 07-JUN-2001; 2001GB-00013900.
XX PA (SYGN ) SYNGENTA LTD.
XX PI Vincent JL, Viner R;
XX WPI; 2003-175137/17.
XX DE New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX PT Claim 12; Page 47-50; 67pp; English.
XX CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.
XX CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is
XX CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
XX SQ Sequence 719 AA;

Query Match 99.4%; Score 3739; DB 6; Length 719;
Best Local Similarity 99.4%; Pred. No. 6e-289;
Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVSASTI 60
DB 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGGLDALAYVHDSLESWGVRNNTARSVVKSQYIALELMFVKLPSPFAVSG 180
DB 121 RNKALTDLKGGLDALAYVHDSLESWGVRNNTARSVVKSQYIALELMFVKLPSPFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNRQVERAGDYSCHVKWYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNRQVERAGDYSCHVKWYS 240
QY 241 TGLNLRGTNAESWVRVYNQFRDMLVLDLVALFPSYDTQWPIKTTAQLTREVTYDAI 300
DB 241 TGLNLRGTNAESWVRVYNQFRDMLVLDLVALFPSYDTQWPIKTTAQLTREVTYDAI 300
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRNSNTQYNNMW 360
DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRNSNTQYNNMW 360
QY 361 GGHKLEPRTTGCTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLFLOPVNGVPR 420
DB 361 GGHKLEPRTTGCTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLFLOPVNGVPR 420
QY 421 VDFHWKFTVTHPIASDNFYPGYVIGTQLODSENELPPEATQPNYESYSHRISHIGLIS 480
DB 421 VDFHWKFTVTHPIASDNFYPGYVIGTQLODSENELPPEATQPNYESYSHRISHIGLIS 480
QY 481 ASHKALVYSWTHESADRTNTEIENSITQPLVKAFLNSGAAVVRGPGFTGGDILRTN 540
DB 481 ASHKALVYSWTHESADRTNTEIENSITQPLVKAFLNSGAAVVRGPGFTGGDILRTN 540
QY 541 TGTGDIRVINPFPQRYRVRIRYASTTDILOFHTSINGKAINQGNFSATWNRGEDLDYK 600
DB 541 TGTGDIRVINPFPQRYRVRIRYASTTDILOFHTSINGKAINQGNFSATWNRGEDLDYK 600

601 TFRVTGFTTFFSFLDVQSTFTTICAMNPFSSNGNEVYIDRIEFVPVEVYTYEARDFEKAQEKV 660
601 TFRVTGFTTFFSFLDVQSTFTTICAMNPFSSNGNEVYIDRIEFVPVEVYTYEARDFEKAQEKV 660
661 TALFTSTNPRGLKTDVKYHIDOVSNLVSLSDEFYLDKRELFEIVKAKQLHIERNM 719
661 TALFTSTNPRGLKTDVKYHIDOVSNLVSLSDEFYLDKRELFEIVKAKQLHIERNM 719

RESULT 11
AAR08041
ID AAR08041 standard; protein; 719 AA.
XX AC AAR08041;
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 27-FEB-1991 (first entry)
XX 81 kD endotoxin deduced from DNA carried on pJH12.
XX Crystal; insecticide; toxin; delta endotoxin.
XX Bacillus thuringiensis; JHCC 4353 and 4835.
XX WO9013651-A.
XX 15-NOV-1990.
XX 09-MAY-1989; 89GB-00010624.
XX 09-MAY-1989; 89GB-00010624.
XX (ICIL ) IMPERIAL CHEM IND PLC.
XX Blenk RG, Ely S, Tailor RH, Tippet JM;
XX WPI; 1990-361486/48.
XX N-PSDB; AAQ06636.
XX Bacillus thuringiensis strains - used for producing an endotoxin for protecting plants against insects, partic. Lepidoptera and Coleoptera.
XX Claim 5; Fig 5-10; 66pp; English.
XX The sequence carried on pJH12 which was isolated from B. thuringiensis strains JHCC4835 and JHCC 4353 (NCIB 40091 and 40090 resp.). The DNA can be used to produce transformants E. coli strain MCL2022/pJH12 (NCIB 40278, or Bacteriophage EMBL4 vector (NCIB 40279) or E. coli strain BL21/pJH11 (NCIB 40275). The delta-endo-toxin produced by the transformants can be used in formulations for combatting Lepidoptera and Coleoptera pests.
XX (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
XX Sequence 719 AA;

Query Match 99.3%; Score 3735; DB 2; Length 719;
Best Local Similarity 99.4%; Pred. No. 1.3e-288;
Matches 715; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVSASTI 60
DB 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGGLDALAYVHDSLESWGVRNNTARSVVKSQYIALELMFVKLPSPFAVSG 180
DB 121 RNKALTDLKGGLDALAYVHDSLESWGVRNNTARSVVKSQYIALELMFVKLPSPFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYS 240
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Db 181 EVELLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVRAGDYSYHCVKWTYS 240  
Qy 241 TGLNLRGTNAESWVRYNQFRDMLTMDLVALPFSYDTOMYPIKTTAQLTREVYTDAI 300  
Db 241 TGLNLRGTNAESWVRYNQFRDMLTMDLVALPFSYDTOMYPIKTTAQLTREVYTDAI 300  
Qy 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQTMNMW 360  
Db 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQTMNMW 360  
Qy 361 GGHKLEFRITGTLNISTOGSTNTSINPVTLPFTSRDVRVTSAGLNLFLEQVNGVPR 420  
Db 361 GGHKLEFRITGTLNISTOGSTNTSINPVTLPFTSRDVRVTSAGLNLFLEQVNGVPR 420  
Qy 421 VDFHMKFVTHPIASDNFYYPGVYIGITQLODSNELPPEATGQPNYESYSHRLSHIGLIS 480  
Db 421 VDFHMKFVTHPIASDNFYYPGVYIGITQLODSNELPPEATGQPNYESYSHRLSHIGLIS 480  
Qy 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
Db 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
Qy 541 TGTFGDIRVINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYK 600  
Db 541 TGTFGDIRVINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYK 600  
Qy 601 TFRVTGFTTPFSLDQVSTFTIGAMNPFSSGNEVYIDRIEFPVPEVTEAEYDPEKAQEKV 660  
Db 601 TFRVTGFTTPFSLDQVSTFTIGAMNPFSSGNEVYIDRIEFPVPEVTEAEYDPEKAQEKV 660  
Qy 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFELFEIVKAKQLHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFELFEIVKAKQLHIERNM 719

RESULT 12  
AAE36271  
ID AAE36271 standard; protein; 718 AA.  
XX  
AC AAE36271;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa1.  
XX  
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
XX  
OS Bacillus thuringiensis.  
XX  
PN WO200298911-A2.  
XX  
PD 12-DEC-2002.  
XX  
PF 30-MAY-2002; 2002WO-00002666.  
XX  
PR 07-JUN-2001; 2001GB-00013900.  
XX  
PA (SYGN ) SYNGENTA LTD.  
XX  
PI Vincent JL, Viner R;  
XX  
DR WPI; 2003-175137/17.  
XX  
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
PT  
PS Claim 12; Page 42-44; 67pp; English.  
XX  
CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as

CC an active ingredient of a pesticide or for controlling insects.  
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
XX  
SQ Sequence 718 AA;  
Query Match 99.1%; Score 3724.5; DB 6; Length 718;  
Best Local Similarity 99.4%; Pred. No. 8.6e-288;  
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
Qy 1 MKLKNQDKHQSFSSNAKVDKISTDSLNKNETDIQLQINHEHEDCLKMSYENVPFVSASTI 60  
Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLNKNETDIQLQINHEHEDCLKMSYENVPFVSASTI 60  
Qy 61 QTGIGTAGKILGTGVFPFAGQVASYLSFYLGLMPPKGNQWEIFMEHVEEIIINOKISTYA 120  
Db 61 QTGIGTAGKILGTGVFPFAGQVASYLSFYLGLMPPKGNQWEIFMEHVEEIIINOKISTYA 120  
Qy 121 RNKALTDLKGGLDALAVYHDSLSWVGNRNNTARSVVKSQYIALELMFVQKLPSFAVSG 180  
Db 121 RNKALTDLKGGLDALAVYHDSLSWVGNRNNTARSVVKSQYIALELMFVQKLPSFAVSG 180  
Qy 181 BEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVRAGDYSYHCVKWTYS 240  
Db 181 BEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVRAGDYSYHCVKWTYS 240  
Qy 241 TGLNLRGTNAESWVRYNQFRDMLTMDLVALPFSYDTOMYPIKTTAQLTREVYTDAI 300  
Db 241 TGLNLRGTNAESWVRYNQFRDMLTMDLVALPFSYDTOMYPIKTTAQLTREVYTDAI 300  
Qy 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQTMNMW 360  
Db 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQTMNMW 360  
Qy 361 GGHKLEFRITGTLNISTOGSTNTSINPVTLPFTSRDVRVTSAGLNLFLEQVNGVPR 420  
Db 361 GGHKLEFRITGTLNISTOGSTNTSINPVTLPFTSRDVRVTSAGLNLFLEQVNGVPR 420  
Qy 421 VDFHMKFVTHPIASDNFYYPGVYIGITQLODSNELPPEATGQPNYESYSHRLSHIGLIS 480  
Db 421 VDFHMKFVTHPIASDNFYYPGVYIGITQLODSNELPPEATGQPNYESYSHRLSHIGLIS 480  
Qy 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
Db 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
Qy 541 TGTFGDIRVINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYK 600  
Db 541 TGTFGDIRVINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYK 600  
Qy 601 TFRVTGFTTPFSLDQVSTFTIGAMNPFSSGNEVYIDRIEFPVPEVTEAEYDPEKAQEKV 660  
Db 601 TFRVTGFTTPFSLDQVSTFTIGAMNPFSSGNEVYIDRIEFPVPEVTEAEYDPEKAQEKV 660  
Qy 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFELFEIVKAKQLHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFELFEIVKAKQLHIERNM 719  
RESULT 13  
AAE66907  
ID AAE66907 standard; protein; 718 AA.  
XX  
AC AAE66907;  
XX  
DT 12-APR-2001 (first entry)  
XX  
DE Insecticidal protein cryIIa1.  
XX  
KW Insecticide; transgenic plant; insect-resistance.  
XX

OS Paecilomyces sp.  
XX WO200100841-A1.  
XX 04-JAN-2001.  
XX 23-JUN-2000; 2000WO-GB002457.  
XX 29-JUN-1999; 99GB-00015215.  
XX 23-DEC-1999; 99GB-00030536.  
XX (ZENEC) ZENEC LTD.  
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
XX Vincent JL, Lee MD;  
XX WPI; 2001-123015/13.  
XX Novel insecticidal protein obtained from species of Paecilomyces for  
XX controlling insects, and for insect-resistant transgenic plant  
XX production.  
XX Claim 14; Page 53-55; 72pp; English.  
XX The present invention relates to novel insecticidal proteins obtained  
XX from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
XX insecticidal proteins can be used to produce transgenic plants, which are  
XX insect-resistant. Also, the insecticidal proteins are useful for  
XX controlling insects by providing them at a locus where insects feed  
XX  
XX Sequence 718 AA;  
SQ  
Query Match 98.9%; Score 3718.5; DB 4; Length 718;  
Best Local Similarity 99.3%; Pred. No. 2.6e-287;  
Matches 714; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N E V P F V S A S T I 60  
DB 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N E V P F V S A S T I 60  
QY 61 Q T G I G I A K I L G T L G V P P A G V A S I Y S F I L G E L M P K G N Q W E I P M E H V E E I I N Q K I S T Y A 120  
DB 61 Q T G I G I A K I L G T L G V P P A G V A S I Y S F I L G E L M P K G N Q W E I P M E H V E E I I N Q K I S T Y A 120  
QY 121 R N K A L T D L K G D A L A V H D S I E S W G N N R N T R A S V V K S O V I A L E M F V Q K L P S F A V S G 180  
DB 121 R N K A L T D L K G D A L A V H D S I E S W G N N R N T R A S V V K S O V I A L E M F V Q K L P S F A V S G 180  
QY 181 E E V P L L P I Y A Q A N L H L L L L R D A S I F G K E W G L S S E I S T F Y N Q R V A G D Y S D R C V K W Y S 240  
DB 181 E E V P L L P I Y A Q A N L H L L L L R D A S I F G K E W G L S S E I S T F Y N Q R V A G D Y S H C V K W Y S 240  
QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D I V A L F P S Y D T O M Y I K T T A Q L T R E V Y T D A I 300  
DB 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D I V A L F P S Y D T O M Y I K T T A Q L T R E V Y T D A I 300  
QY 301 G T V H P H P S F T S T T W N N N A P S F A E A A V R N P H L L D F L E Q V T I Y S L L S R N S T Q Y M N W 360  
DB 301 G T V H P H P S F T S T T W N N N A P S F A E A A V R N P H L L D F L E Q V T I Y S L L S R N S T Q Y M N W 360  
QY 361 G G H K L E F R T I G T L N I S T G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F T Q P V N G V P R 420  
DB 361 G G H K L E F R T I G T L N I S T G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F T Q P V N - V P R 419  
QY 421 V D F H K F V T H P T A S N F Y P G V G I G T O L D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
DB 420 V D F H K F V T H P T A S N F Y P G V G I G T O L D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 479  
QY 481 A S H K A L V Y S W T H R A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G F T G G D I L R E T N 540  
DB 480 A S H K A L V Y S W T H R A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G F T G G D I L R E T N 539  
QY 541 T C T F G D I R V N I N P P F A Q R Y R V I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T W N R G E D L D Y K 600

DB 540 T C T F G D I R V N I N P P F A Q R Y R V I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T W N R G E D L D Y K 599  
QY 601 T F R T V G F T T P P S F L D V Q S T F T I C A N N F S S G N E V Y I D R I E F V P V E Y T Y E A E Y D F E K A Q E K V 660  
DB 600 T F X T V G F T T P P S L L D V Q S T F T I C A N N F S S G N E V Y I D R I E F V P V E Y T Y E A E Y D F E K A Q E K V 659  
QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S I D E F V L D E K R E L F E I V K Y A K Q L H I E R N M 719  
DB 660 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S I D E F V L D E K R E L F E I V K Y A K Q L H I E R N M 718  
RESULT 14  
ADM74717  
ID ADM74717 standard; protein; 719 AA.  
XX ADM74717;  
XX 03-JUN-2004 (first entry)  
XX B. thuringiensis cryIIel SEQ ID NO:2.  
XX cryI; toxicity; lepidoptera; cryIab; cryIba; coleoptera; diptera;  
XX cryIIel.  
XX Bacillus thuringiensis.  
XX CN1401772-A.  
XX 12-MAR-2003.  
XX 20-AUG-2001; 2001CN-00124163.  
XX 20-AUG-2001; 2001CN-00124163.  
XX (PLAN-) PLANT PROTECTION INST CHINESE ACAD AGRIC.  
XX Song F, Zhang J, Huang D;  
XX WPI; 2003-442339/42.  
XX N-PSDB; ADM74716.  
XX Bacillus thuringiensis cryI gene, expression vector, nucleotide sequence  
XX with high-toxicity to lepidoptera pests, encoded protein, primer  
XX sequences and the shuttle vector pSXY422b, useful as a pesticide.  
XX Example 3; SEQ-ID NO 2; 29pp; Chinese.  
XX The invention relates to a novel Bacillus thuringiensis cryI gene, gene  
XX combination, expression vector, nucleotide sequence of the B  
XX thuringiensis cryI gene with high-toxicity to lepidoptera pests and the  
XX amino acid sequence of the protein encoded by it, cooperative use of the  
XX cryI gene with the expression product of cryIab or cryIba, primer  
XX sequences for expressing the genes, and the constructed shuttle vector  
XX pSXY422b. The gene in combination with the cryIab or cryIba genes  
XX displays high toxicity to the lepidoptera, coleoptera and diptera pests.  
XX The present sequence represents the cryIIel protein.  
XX Sequence 719 AA;  
SQ  
Query Match 94.3%; Score 3547; DB 7; Length 719;  
Best Local Similarity 93.5%; Pred. No. 1.2e-273;  
Matches 672; Conservative 26; Mismatches 21; Indels 0; Gaps 0;  
QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N E V P F V S A S T I 60  
DB 1 M K L K N P K H S L S S N A K V D K I A T D S L K N E T D I E L K N I N H E D F L R M S E S I D P F V S A S T I 60  
QY 61 Q T G I G I A K I L G T L G V P P A G V A S I Y S F I L G E L M P K G N Q W E I P M E H V E E I I N Q K I S T Y A 120  
DB 61 Q T G I G I A K I L G T L G V P P A G V A S I Y S F I L G E L M P K G S Q W E I P M E H V E E L I D Q K I S T Y A 120  
QY 121 R N K A L T D L K G L D A L A V H D S I E S W G N N R N T R A S V V K S O V I A L E M F V Q K L P S F A V S G 180

Db 121 RNTALADLKGDLAVYHESLSWIKRNNARATSVVKSQYIALELLFVQKLPSPAVSG 180  
QY 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTEYNNQVRAGDYSVHCVKWYS 240  
Db 181 EEVPLPIYAQAANLHLLLRDASVFGKEWGLSNSQISTEYNNQVTSYDYSVHCVKWYS 240  
QY 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALPFSYDQYPIKTTAQLTREVTDAI 300  
Db 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLIALPFSYDQYPIKTTSLTREVTDAI 300  
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDPLEQVITYSLLSRWSNTQYNNMW 360  
Db 301 GTVHPNASFSTWYNNNAPSFAIESAVVRNPHLLDPLEQVITYSLLSRWSNTQYNNMW 360  
QY 361 GGHKLEFRTIGTGLNTSTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420  
Db 361 GGHKLEFRTIGGLVNTSTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420  
QY 421 VDFHMKFVTHPIASDNFYGYGIGTQLQDSENELPPEATGQPNYESYSHRSLHIGLIS 480  
Db 421 VDFHMKFATLPIASDNFYLYGAGVGTQLQDSENELPPEATTGQPNYESYSHRSLHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
Db 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
QY 541 TGTFTGDIRVNIINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEBLDYK 600  
Db 541 TGTFTGDIRVNIINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEBLDYK 600  
QY 601 TFRVTGFTTFFSFDVQSTFTTIGAMNFFSSGNEVYIDRIEFPVPEVTEYAEYDFEKAQEKV 660  
Db 601 TFRVTGFTTFFSFDVQSTFTTIGAMNFFSSGNEVYIDRIEFPVPEVTEYAEYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFVIVKAKQIHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFVIVKAKQIHIERNM 719

RESULT 15

AAB66912 standard; protein; 719 AA.

ID AAB66912;

DT 12-APR-2001 (first entry)

XX Insecticidal protein cryIb1.

DE Insecticide; transgenic plant; insect-resistance.

XX Paecilomyces sp.

XX WO200100841-A1.

XX 04-JAN-2001.

XX 23-JUN-2000; 2000WO-GB002457.

XX 29-JUN-1999; 99GB-00015215.

XX 23-DEC-1999; 99GB-00030536.

XX (ZENE ) ZENECA LTD.

XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;

XX Vincent JL, Lee WD;

XX WPI; 2001-123015/13.

PT Novel insecticidal protein obtained from species of Paecilomyces for

PT controlling insects, and for insect-resistant transgenic plant

PT production.

XX Claim 14; Page 64-66; 72pp; English.

XX The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX Sequence 719 AA;

Query Match 93.5%; Score 3516; DB 4; Length 719;  
Best Local Similarity 92.8%; Pred. No. 3,7e-271;  
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSSNAKVDKISTDSLKNKTDTELONIHEDCLKMEYENVEBPFVASTI 60

Db 1 MKLKNQDKHQSSNAKVDKISTDSLKNKTDTELONIHEDCLKMEYENVEBPFVASTI 60

QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELMPKQKQWEIFMEHVEEIIINQKISTYA 120

Db 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELMPKQKQWEIFMEHVEEIIINQKILTYA 120

QY 121 RNKALTDLKGLDALAVYHDSLESWGNRNTRARSVVKVQYIALELMFVQKLPSPAVSG 180

Db 121 RNKALSDDLKGLDALAVYHDSLESWGNRNTRARSVVKVQYIALELMFVQKLPSPAVSG 180

QY 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTEYNNQVRAGDYSVHCVKWYS 240

Db 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTEYNNQVRAGDYSVHCVKWYN 240

QY 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALPFSYDQYPIKTTAQLTREVTDAI 300

Db 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALPFSYDQYPIKTTSLTREVTDAI 300

QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDPLEQVITYSLLSRWSNTQYNNMW 360

Db 301 GTVHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDPLEKVITYSLLSRWSNTQYNNMW 360

QY 361 GGHKLEFRTIGTGLNTSTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420

Db 361 GGHKLEFRTIGGLVNTSTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420

QY 421 VDFHMKFVTHPIASDNFYGYGIGTQLQDSENELPPEATGQPNYESYSHRSLHIGLIS 480

Db 421 VDFHMKFPTLPIASDNFYLYGAGVGTQLQDSENELPPEATTGQPNYESYSHRSLHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540

Db 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540

QY 541 TGTFTGDIRVNIINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEBLDYK 600

Db 541 TGTFTGDIRVNIINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEBLDYK 600

QY 601 TFRVTGFTTFFSFDVQSTFTTIGAMNFFSSGNEVYIDRIEFPVPEVTEYAEYDFEKAQEKV 660

Db 601 TFRVTGFTTFFSFDVQSTFTTIGAMNFFSSGNEVYIDRIEFPVPEVTEYAEYDFEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFVIVKAKQIHIERNM 719

Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFVIVKAKQIHIERNM 719

Search completed: February 14, 2005, 20:50:34  
Job time : 102.351 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2005, 17:22:50 ; Search time 70.6029 Seconds  
(without alignments)  
3350.901 Million cell updates/sec

Title: US-10-019-823B-57

Perfect score: 3760

Sequence: 1 MKLNQDKHQSFSNAKVDK.....KRELFEIVKYAKQLHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*

2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*

4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*

5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*

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18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*

19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3756	99.9	719	16	US-10-782-020-10
2	3756	99.9	719	16	US-10-782-141-8
3	3472.5	92.4	710	15	US-10-428-961-42
4	2277.5	60.6	1228	16	US-10-809-953-10
5	2264.5	60.2	1207	10	US-09-988-462-7
6	2186.5	58.2	1227	15	US-10-428-961-63
7	2171.5	57.8	1186	9	US-09-826-660-23
8	2115	56.2	1228	15	US-10-428-961-38
9	2115	56.2	1228	15	US-10-614-524-2
10	1932.5	51.4	643	9	US-09-826-660-25
11	1724.5	45.9	1167	14	US-10-089-678-1
12	1680.5	44.7	653	15	US-10-428-961-6
13	1669.5	44.4	1157	16	US-10-782-141-16

14	1510	40.2	1206	13	US-10-032-717-2	Sequence 2, Appli
15	1510	40.2	1206	14	US-10-414-637-2	Sequence 2, Appli
16	1510	40.2	1206	15	US-10-606-320-2	Sequence 2, Appli
17	1494	39.7	1210	13	US-10-032-717-4	Sequence 4, Appli
18	1494	39.7	1210	14	US-10-414-637-4	Sequence 4, Appli
19	1494	39.7	1210	15	US-10-606-320-4	Sequence 4, Appli
20	1487.5	39.6	1156	14	US-10-099-285-72	Sequence 72, Appli
21	1487.5	39.6	1156	15	US-10-428-961-28	Sequence 28, Appli
22	1465	39.0	1155	9	US-09-756-643-2	Sequence 2, Appli
23	1465	39.0	1155	10	US-09-988-462-9	Sequence 9, Appli
24	1465	39.0	1155	15	US-10-136-998A-2	Sequence 2, Appli
25	1465	39.0	1177	14	US-10-035-060-6	Sequence 6, Appli
26	1465	39.0	1181	10	US-09-988-462-11	Sequence 11, Appli
27	1465	39.0	1181	10	US-09-988-462-13	Sequence 13, Appli
28	1465	39.0	1181	10	US-09-988-462-15	Sequence 15, Appli
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36	1458	38.8	1177	14	US-10-035-060-8	Sequence 8, Appli
37	1457	38.8	1177	14	US-10-102-469-24	Sequence 24, Appli
38	1447.5	38.5	1176	16	US-10-782-141-6	Sequence 6, Appli
39	1424.5	37.9	1176	11	US-09-837-961-2	Sequence 2, Appli
40	1424.5	37.9	1176	16	US-10-825-751-2	Sequence 2, Appli
41	1398	37.2	1167	15	US-10-428-961-40	Sequence 40, Appli
42	1377	36.6	1177	9	US-09-873-873-26	Sequence 26, Appli
43	1377	36.6	1177	10	US-09-916-956A-26	Sequence 26, Appli
44	1377	36.6	1177	10	US-09-997-914-26	Sequence 26, Appli
45	1377	36.6	1177	14	US-10-365-645-26	Sequence 26, Appli

#### ALIGNMENTS

RESULT 1

US-10-782-020-10

; Sequence 10, Application US/10782020

; Publication No. US20040197916A1

; GENERAL INFORMATION:

; APPLICANT: Carozzi, Nadine

; APPLICANT: Hargiss, Tracy

; APPLICANT: Koziel, Michael G.

; APPLICANT: Duck, Nicholas B.

; APPLICANT: Carr, Brian

; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and

; TITLE OF INVENTION: Methods for Its Use

; FILE REFERENCE: 045600/274139

; CURRENT APPLICATION NUMBER: US/10/782.020

; PRIOR FILING DATE: 2004-02-19

; PRIOR APPLICATION NUMBER: 60/448,810

; PRIOR FILING DATE: 2003-02-20

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 10

; LENGTH: 719

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

; US-10-782-020-10

Query Match 99.9%; Score 3756; DB 16; Length 719;

Best Local Similarity 99.9%; Pred. No. 1.2e-308;

Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLNQDKHQSFSNAKVDKISTSLKNETDIELQNHEDCLKMSYENVEPFSASTI 60

Db 1 MKLNQDKHQSFSNAKVDKISTSLKNETDIELQNHEDCLKMSYENVEPFSASTI 60

Qy 61 QTGIGIAGKILGTGVFPAGQVASLYSFLGELPKGNQWEIEMHVEEIIINQKISTYA 120

Db 61 QTGIGIAGKILGTGVFPAGQVASLYSFLGELPKGNQWEIEMHVEEIIINQKISTYA 120

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QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSYIALELMFVQKLPSPAVSG 180
Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSYIALELMFVQKLPSPAVSG 180
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Db 181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCVKWS 240
QY 241 TGLNLRGTAESWVRYNQFRDMLVLDLVALFPYSYDTQMPYIKTTAQLTREVTDAI 300
Db 241 TGLNLRGTAESWVRYNQFRDMLVLDLVALFPYSYDTQMPYIKTTAQLTREVTDAI 300
QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420
QY 421 VDEHMKFVTHPIASDNFYPGVIGITQDSENELPPEATGQPNYESYSHRSHIGLIS 480
Db 421 VDEHMKFVTHPIASDNFYPGVIGITQDSENELPPEATGQPNYESYSHRSHIGLIS 480
QY 481 ASHKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
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Db 541 TGTFGDIRVNINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600
QY 601 TTRTVGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660
Db 601 TTRTVGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 2
US-10-782-141-8
; Sequence 8, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-8

Query Match 99.9%; Score 3756; DB 16; Length 719;
Best Local Similarity 99.9%; Pred. No. 1.2e-308;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDLSKNETDIELQNIHEDCLKMSSEYENVEPVSASTI 60

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Db 61 QTGIGIACKILGTLPFPAGOVASLYSIFILGELWPKGNQWEIIFMEHVVEEIIINOKISTYA 120
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Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSYIALELMFVQKLPSPAVSG 180
QY 181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCVKWS 240
Db 181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCVKWS 240
QY 241 TGLNLRGTAESWVRYNQFRDMLVLDLVALFPYSYDTQMPYIKTTAQLTREVTDAI 300
Db 241 TGLNLRGTAESWVRYNQFRDMLVLDLVALFPYSYDTQMPYIKTTAQLTREVTDAI 300
QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420
QY 421 VDEHMKFVTHPIASDNFYPGVIGITQDSENELPPEATGQPNYESYSHRSHIGLIS 480
Db 421 VDEHMKFVTHPIASDNFYPGVIGITQDSENELPPEATGQPNYESYSHRSHIGLIS 480
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Db 481 ASHKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
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Db 541 TGTFGDIRVNINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600
QY 601 TTRTVGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660
Db 601 TTRTVGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 3
US-10-428-961-42
; Sequence 42, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; FEATURE:

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NAME/KEY: misc\_feature  
LOCATION: (2007)..(200)  
OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid  
US-10-428-961-42

Query Match 92.4%; Score 3472.5; DB 15; Length 710;  
Best Local Similarity 92.4%; Pred. No. 1.2e-284; Mismatches 31; Indels 9; Gaps 1;  
Matches 664; Conservative 15; Mismatches 284; Indels 9; Gaps 1;

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Db 52 QTGIGIAGKILGTLGVPAGVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 111  
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Db 112 RNKALTDLKGLDALAVVHDSLESVWGNRNTRASVVKSOVIALELMFVKLPFAVSG 171  
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Db 352 GGHKLEFRTIGTLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFITQPVNGVPR 411  
Qy 421 VDFHWKVFTHPIASDNFYPGVIGTGLODSENELPPEATQPNYESYSHRLSHIGLIS 480  
Db 412 VDFHWKVFTHPIASDNFYPGVIGTGLODSENELPPEATQPNYESYSHRLSHIGLIS 471  
Qy 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540  
Db 472 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 531  
Qy 541 TGTGDIRVNIAPPQAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATWNRGDLDYK 600  
Db 532 TGTGDIRVNIAPPQAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATWNRGDLDYK 591  
Qy 601 TFRVGTFTPFSLDVQSTFTTIGAMNFSNGNEVIDRIEFVPEVVEYEAEDFEKAQEV 660  
Db 592 TFRVGTFTPFSLDVQSTFTTIGAMNFSNGNEVIDRIEFVPEVVEYEAEDFEKAQEV 651  
Qy 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDFEYLDKEKELFEIVKYAKQLHIERN 719  
Db 652 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDFEYLDKEKELFEIVKYAKQLHIERN 710

RESULT 4  
US-10-809-953-10  
Sequence 10, Application US/10809953  
Publication No. US20040181825A1  
GENERAL INFORMATION:  
APPLICANT: Van Mellaert, Herman  
APPLICANT: Botterman, Johan  
APPLICANT: Van Rie, Jeroen  
APPLICANT: Joos, Henk  
TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTICIDAL PROTEINS  
FILE REFERENCE: 021565-078  
CURRENT APPLICATION NUMBER: US/10/809,953  
CURRENT FILING DATE: 2004-03-26  
PRIOR APPLICATION NUMBER: US/09/661,016

PRIOR FILING DATE: 2000-09-13  
PRIOR APPLICATION NUMBER: PCT/EP90/00905  
PRIOR FILING DATE: 1990-05-30  
PRIOR APPLICATION NUMBER: GB 89401499.2  
FILING DATE: 1989-05-31  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 10  
LENGTH: 1228  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis  
US-10-809-953-10

Query Match 60.6%; Score 2277.5; DB 16; Length 1228;  
Best Local Similarity 62.7%; Pred. No. 4e-183;  
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

Qy 23 TDSLKNETDIELQNFH-----ECLKMSYENVEPVSASTIOTGIGIAGKI 70  
Db 2 TSNRNENEIINAVSNHSAQMDLPDARIEDSLCIAEGNIDPFVSASTVQTGINIAGRI 61  
Qy 71 LGTLGVPAGVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130  
Db 62 LGTLGVPAGVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 121  
Qy 131 LGDALAVVHDSLESVWGNRNTRASVVKSOVIALELMFVKLPFAVSGBEVPLPIYA 190  
Db 122 LGDSFRAYQOQSLDLEWLENRRDARTSVLHTQVIALELDFLNAAMPLFAIRNQEVPPLMVA 181  
Qy 191 QAANLHLLLDASIFGKXWGLSDSEISTFYNRQVERAGDSDHCVKWYSGLNLRGTN 250  
Db 182 QAANLHLLLDASIFGKXWGLSDSEISTFYNRQVERAGDSDHCVKWYSGLNLRGTN 241  
Qy 251 AESWVRYNQFRDMLVLDLVALPSPYDQMPYPIKTTAQLTREYVTDATGTVHPHPSFT 310  
Db 242 AESWVRYNQFRDMLVLDLVALPSPYDQMPYPIKTTAQLTREYVTDATGTVHPHPSFT 299  
Qy 311 STTWYNNAPSFSAIEAAVVRNPHLLDLEQVITYSLLSRNSNTQYNNMWGKHLEFRTI 370  
Db 300 STTWYNNAPSFSAIEAAVVRNPHLLDLEQVITYSLLSRNSNTQYNNMWGKHLEFRTI 359  
Qy 371 GGTNLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFITQPVNGVPRVDFHWK 428  
Db 360 GGTNLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFITQPVNGVPRVDFHWK 416  
Qy 429 THP-----IASDNFYPGVIGTGLODSENELPPEATQPNYESYSHRLSHIGLISASH 483  
Db 417 THP-----IASDNFYPGVIGTGLODSENELPPEATQPNYESYSHRLSHIGLISASH 475  
Qy 484 VKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 543  
Db 476 VNVFVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 535  
Qy 544 FGDTRVNIAPPQAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATWNRGDLDYK 603  
Db 536 FGDTRVNIAPPQAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATWNRGDLDYK 595  
Qy 604 TVGFTTTPFSLDVQSTFTTIGAMNFSNGNEVIDRIEFVPEVVEYEAEDFEKAQEV 663  
Db 596 TVGFTTTPFSLDVQSTFTTIGAMNFSNGNEVIDRIEFVPEVVEYEAEDFEKAQEV 655  
Qy 664 FTSTNPRGLKTDVVDYHIDQVSNLVESLSDFEYLDKEKELFEIVKYAKQLHIERN 719  
Db 656 FTSTNPRGLKTDVVDYHIDQVSNLVESLSDFEYLDKEKELFEIVKYAKQLHIERN 711

RESULT 5  
US-09-988-462-7  
Sequence 7, Application US/09988462  
Publication No. US20030046726A1  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
Desai, Nalini M.

Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Launis, Karen L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Syngenta Biotechnology, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/09/988,462  
APPLICATION NUMBER: US/20030046726A1-2001  
FILING DATE: 20-NO. US20030046726A1-2001  
CLASSIFICATION DATA: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/547,422  
FILING DATE: 11-APR-2000  
APPLICATION NUMBER: US 08/459,504  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-188051  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7  
Query Match 60.2%; Score 2264.5; DB 10; Length 1207;  
Best Local Similarity 64.3%; Pred. No. 4.9e-182;  
Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;  
QY 40 EDCLKMSEYENVEPVASSTIQTGIGIAGKILGTLGVPFAGQVAVSLYFSLGELWPKGN 99  
DB 10 EDSLCLAEAGNNIDFPVSGASTVQTGINAGRLGVLGVPFAGQLASFYSFLVGLWPRGRD 69  
QY 100 QWEIFMEHVEEIIQKISTYARNKALTDLKGGLDALAVYHDSLESWVGNRNTARSVVK 159  
DB 70 QWEIFLEHVEQLNQIQTENARNALALQGLGDSFRAYQOSLEDWLENRDDARTSVLY 129  
QY 160 QYIALELMFVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSIST 219  
DB 130 QYIALELDLFLNAPLFAIRQVEPMLLVYAQAANLHLLLRDASLFGSEGLTSQIQOR 189  
QY 220 FYNROVERAGDYSCHVCWKYSTGLNLRGTNAESWVRYNQFRDMLWLDLVALFPSYD 279  
DB 190 YTERQVERTRDYSYCVENYNTGLNSLGTNAASWVRYNQFRDLTLGLVLDLVALFPSYD 249  
QY 280 TQMPYIKTTAQLTREYVYDAIGTVHPHFSFTTWNNNAPSFAIEAAVVRNPHLLDFL 339

DB 250 TETYPINTSAQLTREYVYDAIGAT--GVNMAVMWNNAPSPFSAIEAAAIRSHLLDFL 307  
QY 340 EQVTIYLLSRWSNTQYNNMAGGKHLERTIGTLNISTOGSTNTSINPVTLPFTSRDYY 399  
DB 308 EQLTIFSSASRWSNTRHMTYWRGHTIQSRPLGGGLNTSTHGATNTSINPVTLPFASRDY 367  
QY 400 RTESLAGLNLF--LTQPVNGVRVDFHWKFVTHP-----IASDNFYFPGYVIGITQLODS 452  
DB 368 RTESVAGVLLWGIYLEPIHGVTVRNF--TNPNISDRGTANYSQP--YESPGLQLKDS 423  
QY 453 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTPNSITQIPL 512  
DB 424 ETELPPETTERPNYESYSHRLSHIGIILQSRVNVVSVWTHRSADRTNTPNRTQIPM 483  
QY 513 VKAFNLSSGAAVVRGPGTGGDILARTNTGTGDIRVNVNPPFAQRYRVRIRYASTTDLQ 572  
DB 484 VKASLPQGTTVVRGPGTGGDILARTNTGTGDIRVNVNPPFAQRYRVRIRYASTVDFD 543  
QY 573 FHTSINGKAINQGNFSATNWRGEDLDYKTFRTVGTTPFSELDVQSTFTIGAWNFSSGNE 632  
DB 544 FVSRGGTTVNNFRFLRTWNSGDELKYGNFVRRFTTPTFTQIQDIIRTSIQGLSGNGE 603  
QY 633 VIIDRIEFVPEVVEYAEYDEKAKQKVTALFTSNPRGLKTDVKDYHIDQVSNLVESLS 692  
DB 604 VYIDKIEIIPVTATPEAYDLEAQAVALFTNPNRELKTDVTDYHIDQVSNLVACLS 663  
QY 693 DEFYLDKRELFEIVKYAKQLHIERNM 719  
DB 664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 6  
US-10-428-961-63  
Sequence 63, Application US/10428961  
Publication No. US20030237111A1  
GENERAL INFORMATION:  
APPLICANT: Baum, James A.  
APPLICANT: Chu, Chih-Rei  
APPLICANT: Donovan, William P.  
APPLICANT: Gilmer, Amy J.  
APPLICANT: Rupar, Mark J.  
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)  
FILE REFERENCE: MECO201-1  
CURRENT APPLICATION NUMBER: US/10/428,961  
CURRENT FILING DATE: 2003-05-02  
PRIOR APPLICATION NUMBER: 09/661,322  
PRIOR FILING DATE: 2000-09-13  
PRIOR APPLICATION NUMBER: 60/153,995  
PRIOR FILING DATE: 1999-09-15  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 63  
LENGTH: 1227  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis  
US-10-428-961-63

Query Match 58.2%; Score 2186.5; DB 15; Length 1227;  
Best Local Similarity 59.2%; Pred. No. 2e-175;  
Matches 423; Conservative 105; Mismatches 173; Indels 13; Gaps 3;  
QY 13 SNAKVDKISTDSLKN-----ETDIELONINHEDECLMSEYENVEPVASSTIQTGIG 65  
DB 7 NENEINALSIPAVSNHSAQNNLSTDARI-----EDSLCIAEGNNIDFPVSGASTVQTGIN 61  
QY 66 IAGKILGTLGVPFAGQVAVSLYFSLGELWPKGNQWEIFMEHVEEIIQKISTYARNKAL 125  
DB 62 IAGRLGVLGVPFAGQVAVSLYFSLGELWPKGRDPWEIFLEHVEEIIQKISTYARNKAL 121  
QY 126 TDLKGLGDALAVYHDSLESWVGNRNTARSVVKQYIALELMFVQKLPSFAVSGEEVPL 185



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; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; US-10-614-524-2

Query Match      56.2%; Score 2115; DB 15; Length 1228;
Best Local Similarity 59.5%; Pred. No. 2.3e-169;
Matches 424; Conservative 98; Mismatches 181; Indels 10; Gaps 7;

13 SNAKVDKISTSLKN-ETDIELQ-NINHEDCMKSEVENPEFVSASTIQTGIGIAGKI 70
7 NENEIINALSPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINAGRI 66
71 LGTLGVPPAGOVASLYFSLGELMPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKG 130
67 LGVLGVPPAGQIASFISFLVGLMFGPRDQWEIFLEHVEQLINQOITENARNALARLOG 126
131 LGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKQLPSFAVSGSEVPLPIYA 190
127 LGDSPRAYQOSLEDWLENRDARTRSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYA 186
191 QAAHLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDYSRCHVKWYSTGLNNLRGTN 250
187 QAAHLHLLLRDASLFGSEFGLTSQEIORYYERQVEQTRDYSYCVWEYNTGLNSLRGTN 246
251 AESWRYNQFRDRLTGLVLDLVALFPSYDTQWPIKTTAQLTREYVYDAIGAT--GVNMA 304
247 AASWRYNQFRDRLTGLVLDLVALFPSYDTQWPIKTTAQLTREYVYDAIGAT--GVNMA 304
311 STTWYNNAPSPSAIAEAAVVRNPHLLDFLEQVITYLSLRSWNTQYMMWGGHKLFRTI 370
305 SMWYNNAPSPSAIAETAVIRSPHLLDFLEQVITYLSLRSWNTQYMMWGGHKLFRTI 364
371 GGTINISTQGSTNTINPVTLPFTSRDVRVTESLAGLNL--LTQPVNGVPRVDFHWKFV 428
365 GGLNTSTHGSTNTINPVLSPFRDVRVYTESYAGVLLGWIYLEPIHGVTFRFNRNP 424
429 --THPIASDNFYPGYVIGTQLQDSNELPPATQPNYSYSHRLSHIGLISASHVKA 486
425 QNTFERGTANYSQP--YESPGLQKDSSETLPPETTERPNYESYSHRLSHIGLISASHV 483
487 LVYSWTHRSADRTNTEPNSITQIPLKAFNLSSGAAVVRGPGFTGGDILRRNTGTFGD 546
484 PVSWSWTHRSADRTNTEPNSITQIPLKAFNLSSGAAVVRGPGFTGGDILRRNTGTFGD 543
547 IRVNIWPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYKTFRTVG 606
544 MGLNFNTSLQRYVRVRYAASQTMVLRTVVGSTTTFDQGPSTMSANESLTSQSFRFAE 603
607 FTTFPFSLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQKVTALFTS 666
604 FPVGISASGSQ--TAGISISNNAAGRTQTFHDKIEFIPITATFEAYDLERAQAVNALFTN 662
667 TNPRLKTDVVDYHIDQVSNLVESLSDFEVLDEKRELFEIVKAKQLHIERNM 719
663 TNPRLKTDVVDYHIDQVSNLVESLSDFEVLDEKRELFEIVKAKQLHIERNM 715

RESULT 9
US-10-614-524-2
; Sequence 2, Application US/10614524
; Publication No. US20040016020A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
; FILE REFERENCE: NEWBTSUS2
; CURRENT APPLICATION NUMBER: US/10/614,524
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/739,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28

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; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 25
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-25

Query Match      51.4%; Score 1932.5; DB 9; Length 643;
Best Local Similarity 57.7%; Pred. No. 2.3e-154;
Matches 371; Conservative 100; Mismatches 159; Indels 13; Gaps 3;

QY 13 SSNAKVDKISTSLKN-----ETDIELQNIHEDCLKMSYEYVPEFVSASTIQTGIG 65
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
7 NENEIINALSPAVSNHSAQMNLSLDARI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61

QY 66 TAGKILGTLGVPAGOVASLYSFLGELWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 125
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 TAGRILGVLGVFPAGQIASFYSFLVGLWPRGRDWEIFLEHVEQLIRQQVTNTRDTAL 121

QY 126 TDLKGLGDALAYVHDSLSWGNRNTRARSVVKSOYIALELMFVKLPSPAVSGEEVPL 185
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
122 ARLOGLGNSFRAYQOSLEDWLENRDDARTSRVLYTYQYIALELDLFNAPLFAIRNQEVPL 181

QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNN 245
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
182 LMWYAQAANLHLLLRDASLFGSEFLTSQELQRYRYERQVEKREYSDYCARWYNTGLNN 241

QY 246 LGRTVAESWVRYNQPRDMLVLDLVALFPSTYDTQMTPIKTAQLTREVYTDALGTVHP 305
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
242 LGRTVAESWLRYNQPRDMLTGLVLDLVALFPSTYDRVYPMNTSAQLTREIYTDPIGRTNA 301

QY 306 HPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLRWSNTQYNNMVGHKL 365
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
302 PSGFASTWNNFNNAPSFSAIEAAVVRNPHLLDFPEQLTIFSVLSRWSNTQYNNMVGHRL 361

QY 366 EPRFTIGTLNISTQGSTNTSINPVLTPFTSRDVRVTESLAGLNLFLTPVANGVPRVDFHW 425
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
362 ESRTIRGSLSTHGTNTSINPVLQFTSRDVRVTESLAGLNLFLTPVANGVPRVDFHW 421

QY 426 KPVTHPIASDNFPYGYGIGTQLOQDSNELPPEATGQPNYESYSHRLSHIGLISASHVK 485
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
422 RNPLNSLRGSLLYTIGYTGVTGQTLDFSETLPPETTERPNYESYSHRLSNIRLISGNTLR 481

QY 486 ALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRRTNTGFG 545
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
482 APVYSWTHRSADRTNTIISDSITQIPLVKSFLNLSGTSVSGPGTGGDILRRRTNNGSVL 541

QY 546 DIRVINPFPQRYRIRYASTTDLQFHTSINGKAINQGNFSAATNRGDEDLDYKTFRTV 605
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
542 SMGLNFNNTSLQRYRVRVRYAASQTMVLVRVTVGSGSTTFDQGPSTMSANESITSGSFRFA 601

QY 606 GFTTPFSLDVQSTTIGAWNFSSGNEVVDRIEFPVPEVTEYE 648
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
602 EFPVGISAGSQ-TAGISISNAGRQTGFHDKIEPIPTATILE 643

RESULT 11
US-10-089-678-1
; Sequence 1, Application US/10089678
; Publication No. US20030017967A1
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shinichi
; TITLE OF INVENTION: NOXIOUS ORGANISM-HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A
; TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
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; FILE REFERENCE: Q68821
; CURRENT APPLICATION NUMBER: US/10/089,678
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: JP 2000-236140
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/JP01/06660
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-089-678-1

Query Match      45.9%; Score 1724.5; DB 14; Length 1167;
Best Local Similarity 48.1%; Pred. No. 2.4e-136;
Matches 362; Conservative 125; Mismatches 220; Indels 45; Gaps 11;

QY 1 MKLKNQDKHQ---SPSSNAKVDKISTDLSKNETDIELQNIHEDCLKMSYEY-----NV 51
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MSPNNQNEYEILDASSSTVSVDNSVRYPLANDQTTLLQNMNYKYDLRMSEGENPELFGNP 60

QY 52 EPPVSASTIQTGIGTAGKILGTLGVPAGOVASLYSFLGELWPKGK-NQWEIFMEHVEE 110
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 ETFISSSTVQTGIGIVGQVLGALGVFPAGQIASFYSFIVGQLWPSSTVSWEMIMKQVED 120

QY 111 IINOKIYARANKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFV 170
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121 LIDQKITSVKRTALAGLOGLDVYQKSLKNWLENDRNTRARSVVVTVYIALELDFV 180

QY 171 QKLPFAVSGEVEPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGD 230
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
181 AKIPSAISQGEVPLLSVYAQAANLHLLLRDASIFGAEGFTGCEISTFYDRQVTRTAQ 240

QY 231 YSDCHVKWYSGLNLRGTNAESWVRYNQPRDMLVLDLVALFPSTYDTQMTPIKTTAQ 290
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
241 YSDYCVKRYNTGLDKLGKTNAAASWLYKHQPRFEMTLVLDLVALFPNTDTRTPLETTAQ 300

QY 291 LTRVYVTDIAGTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLS- 349
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
301 LTRVYVTDPIVNRBETSGGFCRWSLNSDIFSSEVASIRSPHLFDLSEIEFTYTRAG 360

QY 350 -RWSNTQTMNMWGHKLEFRITIGTGLNISTQGSTNTSINPVLTPFTSRDVRVTESL-AGL 407
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
361 LPLNNTLEYWVGHSIKYKNTNASSALERNYGTITSNKIKYDLANKDIQVRSIGADL 420

QY 408 NLPLTOPVNGVPRVDFHWKFTHPFIASDNFPYYPGVVG-----IGTQLOQDSNE 455
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
421 ANYYQAQ-YGVYPYASF-----TLDDKNTGSGSVGGFTYSKPHTTWQVCTQNTYNTIDE 471

QY 456 LPPEATGQPNYESYSHRLSHIGLIS-----ASHVKALVYSWTHRSADRTNTIEPNSI 507
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
472 IPPE--NEPLSRGYSHRLSHITSYFSKVASPSARYGNLVPFAWTHRSADVTNTVYSDKI 529

QY 508 TQIPLVKAFLNLSGAAVVRGPGTGGDILRRRTNTGFGDIRVINPFPQRYRVRIRYAS 567
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
530 TQIPLVKAHTLVSGTTVIKGPGFTGGNLLKRTSSGPLAYTSVSVKSPLSQRYRIRYAS 589

QY 568 TTDIQQFHTSINGKAINQGNFSAATNRGDEDLDYKTFRTVGTTPFSPFLDVQSTFTIGANNF 627
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
590 TTNLRLFVTTISGTRIYSINVNKTMKGGDILFTNTFDLATIGTAFTFSSYSDSLTVDGDSF 649

QY 628 SSGNEVYIDRIEFVPVEVTEAEYDFAKQSKVLTALFTSTNPRGLKTDVQKVDHIDQVSNL 687
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
650 ASGGEVYVDKELIPVNATFEABEDLDVAKAVNGLFTSKKD-ALQTSVTDYQVQNAANL 708

QY 688 VESLSDEFYLDKRELFEIVKAYAKQLHIERNM 719
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
709 VECLSDLEYPNKRMMLMDVAKEAKELVQARNL 740

RESULT 12
```

US-10-428-961-6  
; Sequence 6, Application US/10428961  
; Publication No. US2003023711A1  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Rugar, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
; FILE REFERENCE: Polynucleotides, Compositions, and Methods of Use (Amended)  
; CURRENT APPLICATION NUMBER: US/10/428,961  
; CURRENT FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: 09/661,322  
; PRIOR FILING DATE: 2000-09-13  
; PRIOR APPLICATION NUMBER: 60/153,995  
; PRIOR FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 653  
; TYPE: PRP  
; ORGANISM: Bacillus thuringiensis  
US-10-428-961-6

Query Match 44.7%; Score 1680.5; DB 15; Length 653;  
Best Local Similarity 51.5%; Pred. No. 5.1e-133; Mismatches 173; Indels 47; Gaps 14;  
Matches 346; Conservative 106

QY 13 SSNAVKDIXTSLKN---ETDIELQINIHEDCLMKSEYENVEPVASSTIQTGIGIAGK 69  
DB 2 NENEIINALSPAVNSHQAQMDLSL-DARIEDSLCIAEGNNINPLVASSTVQTGINIAGR 60

QY 70 ILGTGVPAGVAVSLYFGLGELWPKQKQWEIFMEHVEELINQKISTYARNKALTDLK 129  
DB 61 ILGVLGVPAGVAVSLYFGLGELWPKQKQWEIFMEHVEELINQKISTYARNKALTDLK 120

QY 130 GIGDALVYHDSLEWGNRNTRARSVVVKSQVIALELMFVKQLPSFAVSGEVEPLPIY 189  
DB 121 GUGRVYRVSQALETWLDNRNDARSIIILERYVALELDITTAIPLFRINEVEPLLMVY 180

QY 190 AQAAHLHLLLRDASIFGKWEGLSSEISTFTYRQVERAGDYSDCHVXWYSTGLNLRGT 249  
DB 181 AQAAHLHLLLRDASIFGSEWGMASDDVNYQOEQIRYEEYSNCHVCQWYNTGLNLRGT 240

QY 250 NAESVRYNQPRDMLVLDVALPSPYDTOMYIKITTAQTLTREYVYDAIGTVHPHPSF 309  
DB 241 NAESVRYNQPRDMLVLDVALPSPYDTOMYIKITTAQTLTREYVYDAIGTVHPHPSF 300

QY 310 TSTWYNNAPSAFSAEAAVAVRNPHLLDLEQVITYSLSRNSNTQYMMWGHKLEPRT 369  
DB 301 ASTNFWNNAPSAFSAEAAVAVRNPHLLDLEQVITYSLSRNSNTQYMMWGHKLEPRT 360

QY 370 IGGTLNISTQGST-NTSINPVLTPF-TSRDVTYRTSLAGLNLFLTPVNGVPRVDFHMKF 427  
DB 361 IGGTLNISTQGST-NTSINPVLTPF-TSRDVTYRTSLAGLNLFLTPVNGVPRVDFHMKF 418

QY 428 VTHPIASDNFYYP-----GVVGIGTQIQSENELPEATGQPNYESYSHRLSHIG-- 477  
DB 419 ITLRIFKMEAPLTVNRIELGFNYLIQKLNHOK-----QQNDQIMNHIVIDISYR 470

QY 478 LISASHVKALVSWTHRSADRTNTEPNISITQIPLVKAFLNLSGAAVVRPGFTGDIILR 537  
DB 471 LIIGNTLAPVSWTHRSADRTNTEPNISITQIPLVKAFLNLSGAAVVRPGFTGDIILR 529

QY 538 -RTNCTGF---GDIRVIN-PPFAQRYRVRIRYASTDLDQHTSINGKAINQGNFSATWN 592  
DB 530 LNRNNGNIQNRGIEVPIQFTSTSTRYRVRIRYASTDLDQHTSINGKAINQGNFSATWN 589

QY 593 RGEDLYKTRFTVGTTPSPFLDQVSTFT-----LGANNESGNEVYIDRFEFVEVT 646  
DB 590 SLDNLQ-----SGDFGYVEINNAFTSATGNIVGARNFSANAEEVYIDRFEFIPVTAT 640

QY 647 YEAEYDFEKAQE 658  
DB 641 FEVEYDLERAQK 652

RESULT 13  
US-10-782-141-16  
; Sequence 16, Application US/10782141  
; Publication No. US20040197917A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Kozziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for its Use  
; FILE REFERENCE: 045600/274143  
; CURRENT APPLICATION NUMBER: US/10/782,141  
; CURRENT FILING DATE: 2004-02-20  
; PRIOR APPLICATION NUMBER: 60/448,632  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 1157  
; TYPE: PRP  
; ORGANISM: Bacillus thuringiensis  
US-10-782-141-16

Query Match 44.4%; Score 1669.5; DB 16; Length 1157;  
Best Local Similarity 49.1%; Pred. No. 1.1e-131; Mismatches 230; Indels 57; Gaps 18;  
Matches 371; Conservative

QY 1 MKLKNQDKHQSFSSNAVKDIXTDS---LKNVETDIELQINIHEDCLMKSEYE-----N 50  
DB 1 MSPNQNEYEIIIDATPST-SVSSDNRYPPANETFDALQNNYKDYLKMSGGENPELFGN 59

QY 51 VEPFVSASTIQTGIGIAGKILGTGVPAGVAVSLYFGLGELWPKQKQWEIFMEHVE 109  
DB 60 PETFISSSTIQTGIGIAGKILGTGVPAGVAVSLYFGLGELWPKQKQWEIFMEHVE 119

QY 110 EIIQNKISTYARNKALTDLKGLDALVYHDSLEWGNRNTRARSVVVKSQVIALELMF 169  
DB 120 ELVDQKIEKYVKDIALAEKGLGNALDYQOSLEDWLENRDARTSRVSVNQFIALDLNF 179

QY 170 VKQLPSFAVSGEVEPLPIYAAQANLHLLLRDASIFGKWEGLSSEISTFTYRQVERAG 229  
DB 180 VSSIPSFVAVSGEVEPLPIYAAQANLHLLLRDASIFGKWEGLSSEISTFTYRQVERAG 239

QY 230 DYSKHCVKWYSTGLNLRGNTNAESVRYNQPRDMLVLDVALPSPYDTOMYIKITTA 289  
DB 240 EYSDYCVKWKYIGLDKLGKTTSKSLNLYHQFRRMTLLVLDLVALFPNYDTHMYPETTA 299

QY 290 QLTREYVYDAIGTVHPHPSFTST-----TWYNNAPSAFSAEAAVAVRNPHLLDLEQVITY 345  
DB 300 QLTREYVYDAIGTVHPHPSFTST-----TWYNNAPSAFSAEAAVAVRNPHLLDLEQVITY 355

QY 346 SLLSR-----WNTQYMMWGHKLEFR-----TIGTLNISTQGSTNTSINPVLTPFTR 396  
DB 356 T--SGGGLTNDAYINTWSGHTLKRYRTADSTVITYTANYGRIITSEKNS-----PALEDR 408

QY 397 DYTERTESLAGLNLFLTPVNGVPRVDFHMKFVTHPIASDNFY-----YGVVGIGTQIQLOD 451  
DB 409 DIFEINSTVANLANLYYQKAYGVPGSWFH--VYKRGTSSTTAYLYSKHTALQGC-TQYVE 465

QY 452 SENEPLPPEATGQPNYESYSHRLSHI-----GLISASHVKALVSWTHRSADRTNTE 503  
DB 466 SDEIPLDRT-VPVAESYSHRLSHITSHSFKNKG--SAYGSPFVFWVTHHSADLNNTIY 522

QY 504 PNIISQIPLVKAFLNLSGAAVVRPGFTGDIILRTNTGTGDIRVINPPEPFAQRYRVI 563  
DB 504 PNIISQIPLVKAFLNLSGAAVVRPGFTGDIILRTNTGTGDIRVINPPEPFAQRYRVI 563



Db 523 SDKITQIPAVKCDMLYLGSSVVOGCGFTGGDILKKTNPBSILCTFAVTNGSLSQRYRVI 582  
Qy 564 RYASTDDQFHTSINGKAINQGNFATMNRGBDLDYKTRIVGFTTTPFSLDVQSTFTIG 623  
Db 583 RYASTDTEF-TLYLGDITKRNFKTMDNGASLTFTYFKFASFTDQFRETQDKILLS 641  
Qy 624 AWPSSGNEVYIDRIEFVVEVYAEVDFEKAQKVTALFTSTNPRGLKTDVQKDYHIDQ 683  
Db 642 MGFSSGGEVYIDRIEFIPVDETYAEQDLEAAKAVNALFTNKD-GLRPGVTDYEVNQ 700  
Qy 684 VSNLVESLSDEFYDLKRELFEIVKAKQLHIERNM 719  
Db 701 AANLVECLSDLLYPNEKRLLPDAVREAKRLSARNL 736

RESULT 14  
US-10-032-717-2  
; Sequence 2, Application US/10032717  
; Publication No. US20020151709A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/032,717  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/242,838  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1206  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-032-717-2

Query Match 40.2%; Score 1510; DB 13; Length 1206;  
Best Local Similarity 44.3%; Pred. No. 3.6e-118;  
Matches 337; Conservative 130; Mismatches 229; Indels 64; Gaps 22;  
Qy 1 MKLKNQDKHGFSSNAKVDKISTDS---LKNETDIELQNINHEDECLM-----SEYE-N 50  
Db 1 MSPNNQNEYIIDATPST-SVSNDSNRYPPFANEPTNALQNMDYKDYLKMSAGNASEYPGS 59  
Qy 51 VEPFVSA-STIQTGTIGIAGKILGTLPVFPAGQVASLYSFIILGELWPKG-KNQWEIFMEHV 108  
Db 60 PEVLVSGQDAAKAADIIVGKLLSGLGVFPVGVPIVSLYTLQIDILWPSGEKSQWEIFMEQV 119  
Qy 109 BEINQKISTVARNKALTDLKGDLALAVYHDSLESVGNRNNTARSVVKSOYTALEM 168  
Db 120 BELNQKIAEYARNKALSELEGLGNVQYLYLTALLEEWEENPNNGSRALDRVRNREILDSL 179  
Qy 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSISFTYNQVERA 228  
Db 180 FTQYMPSPRVNTFEVFLTVYAMAANLHLLLRDASIFGEEWGSTTTINNYIDQMKLT 239  
Qy 229 GDYSDHCVKYKYSTGLNNLRTNAESWRYNFRDMTLMVLVDLVALFPSTQYTPYIKTT 288  
Db 240 AEYSDHCVKYKYSTGLKLGTSKQWVDYNQFRREMTLAVLDVVALFPYDTRTPMETK 299  
Qy 289 AQLTREVTDAIGTVHPHPSFTSTWYNNAPSPAIAAIVRNPHLLDFLEQVITYSL 348  
Db 300 AQLTREVTDPGLGAVNV---SIGSWY-DKAPSGFVIESSVIRPPHVDYITGLTVYTSQ 355  
Qy 349 SRWNTQYNNWGGHKLFRITGGTLNISTOGSTNTSINPV-TLPFTSRDYVRESLAGL 407  
Db 356 RSISARYIRHWAGHQISYHVRVSRGSLQOQMYGTNQNLHSTSTFDFTNYDIKTLKSDAV 415

Qy 408 NLFLTQP-----VNGVPRVDFHWKFVTHPIASDN---PYYPGYGIGTQLQDSENELPPE 459  
Db 416 LLDIVPGYTYIFFGMEPEF---FMVQNLNTRKTLKYNPVSKDIIIASTRDSELELPPE 472  
Qy 460 ATGQNVESYSHRLSHIGLISAS-HVKAL--VYSWTHRSADRTNTIEPNSITQIPLVKAF 516  
Db 473 TSDQNVESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNIYSKTIQIPAVKWCW 532  
Qy 517 NLSGAAVVRGPGFTGGDILR-RNWTGTFGDI---RVNINPPFAQRYRIRIYASTTDIQ 572  
Db 533 DNLFPVPVVGPGHTGGDLLQVNRSTGSGVTLFLARYGLALEKAGKYRVLRYATDADIV 592  
Qy 573 PHTSINGKAINQGNFATMNRGBDLDYKTR-----TVGFTTTPSF-----DVQST 619  
Db 593 LH--VNDAAQI---QMPKTMNPGEDLTSTKTFKVADAITLNLATDSSLAKHNLGEDPNST 647  
Qy 620 FTIGAWNFSSGNEVYIDRIEFVVEVYAEVDFEKAQKVTALFTSTNPRGLKTDVQDY 679  
Db 648 LS-----GIVYVDRIEFIPVDETYAEQDLEAAKAVNALFTNKD-GLRPGVTDY 697  
Qy 680 HIDQVSNLVESLSDEFYDLKRELFEIVKAKQLHIERNM 719  
Db 698 EVNQAAANLVECLSDLLYPNEKRLLPDAVREAKRLSARNL 737

RESULT 15  
US-10-414-637-2  
; Sequence 2, Application US/10414637  
; Publication No. US20030177528A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/414,637  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: US/10/032,717  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/242,838  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1206  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-414-637-2

Query Match 40.2%; Score 1510; DB 14; Length 1206;  
Best Local Similarity 44.3%; Pred. No. 3.6e-118;  
Matches 337; Conservative 130; Mismatches 229; Indels 64; Gaps 22;  
Qy 1 MKLKNQDKHGFSSNAKVDKISTDS---LKNETDIELQNINHEDECLM-----SEYE-N 50  
Db 1 MSPNNQNEYIIDATPST-SVSNDSNRYPPFANEPTNALQNMDYKDYLKMSAGNASEYPGS 59  
Qy 51 VEPFVSA-STIQTGTIGIAGKILGTLPVFPAGQVASLYSFIILGELWPKG-KNQWEIFMEHV 108  
Db 60 PEVLVSGQDAAKAADIIVGKLLSGLGVFPVGVPIVSLYTLQIDILWPSGEKSQWEIFMEQV 119  
Qy 109 BEINQKISTVARNKALTDLKGDLALAVYHDSLESVGNRNNTARSVVKSOYTALEM 168  
Db 120 BELNQKIAEYARNKALSELEGLGNVQYLYLTALLEEWEENPNNGSRALDRVRNREILDSL 179  
Qy 169 FVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSISFTYNQVERA 228  
Db 180 FTQYMPSPRVNTFEVFLTVYAMAANLHLLLRDASIFGEEWGSTTTINNYIDQMKLT 239





Thu Mar 10 14:26:05 2005

Query Match 99.8%; Score 3752; DB 3; Length 719;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 717; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 M K L K N Q D K H O S F S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60  
DB 1 M K L K N Q D K H O S F S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60  
QY 61 Q T G I G A K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K Q W E I F M H V E E I I N Q K I S T Y A 120  
DB 61 Q T G I G A K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K Q W E I F M H V E E I I N Q K I S T Y A 120  
QY 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
DB 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R Q V R A G D Y S D H C V K W Y S 240  
DB 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R Q V R A G D Y S D H C V K W Y S 240  
QY 241 T G L N N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
DB 241 T G L N N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
QY 301 G T V H P H P S F T S T T W Y N N N A P S F A I E A A V V R N P H L L D F L E Q V T T Y S L L S R S N T Q Y M N M W 360  
DB 301 G T V H P H P S F T S T T W Y N N N A P S F A I E A A V V R N P H L L D F L E Q V T T Y S L L S R S N T Q Y M N M W 360  
QY 361 G G H K L E F R T I G T L N I S T O G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
DB 361 G G H K L E F R T I G T L N I S T O G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
QY 421 V D F H W K F V T H P I A S D N F Y P G V G I G T Q L O D S E N E L P P E A T Q P N Y E S Y S H R L S H I G L I S 480  
DB 421 V D F H W K F V T H P I A S D N F Y P G V G I G T Q L O D S E N E L P P E A T Q P N Y E S Y S H R L S H I G L I S 480  
QY 481 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540  
DB 481 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540  
QY 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
DB 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
QY 601 T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
DB 601 T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719  
DB 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719

RESULT 2  
US-09-661-322A-42  
; Sequence 42, Application US/09661322A  
; Patent No. 6593293  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Mark J.  
; APPLICANT: Rugar, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos  
; FILE REFERENCE: MECO201  
; CURRENT APPLICATION NUMBER: US/09/661,322A  
; CURRENT FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 42  
; LENGTH: 710  
; TYPE: PRT

ORGANISM: Bacillus thuringiensis  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (200)..(200)  
OTHER INFORMATION: No. 6593293-Coding  
US-09-661-322A-42  
Query Match 92.4%; Score 3472.5; DB 4; Length 710;  
Best Local Similarity 92.4%; Pred. No. 1.9e-302;  
Matches 664; Conservative 15; Mismatches 31; Indels 9; Gaps 1;  
QY 1 M K L K N Q D K H O S F S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60  
DB 1 M K S K N Q N H Q S L S N A T V D K N F T G S L E N N T N T E L Q N F N H -----E G I E P F V S V S T I 51  
QY 61 Q T G I G A K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K Q W E I F M H V E E I I N Q K I S T Y A 120  
DB 61 Q T G I G A K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K Q W E I F M H V E E I I N Q K I S T Y A 111  
QY 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
DB 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A S V V K S Q Y I A L E M F V Q K L P S F A V S G 171  
QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R Q V R A G D Y S D H C V K W Y S 240  
DB 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R Q V R A G D Y S D H C V K W Y N 231  
QY 241 T G L N N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
DB 241 T G L N L M G N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 291  
QY 301 G T V H P H P S F T S T T W Y N N N A P S F A I E A A V V R N P H L L D F L E Q V T T Y S L L S R S N T Q Y M N M W 360  
DB 301 G T V H P H P S F T S T T W Y N N N A P S F T I E A A V V R N P H L L D F L E Q V T T Y S L L S R S N T Q Y M N M W 351  
QY 361 G G H K L E F R T I G T L N I S T O G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
DB 361 G G H K L E F R T I G T L N I S T O G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 411  
QY 421 V D F H W K F V T H P I A S D N F Y P G V G I G T Q L O D S E N E L P P E A T Q P N Y E S Y S H R L S H I G L I S 480  
DB 421 V D F H W K F V T H P I A S D N F Y P G V G I G T Q L O D S E N E L P P E A T Q P N Y E S Y S H R L S H I G L I S 471  
QY 481 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540  
DB 481 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 531  
QY 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
DB 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 591  
QY 601 T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
DB 601 T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E E V 651  
QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 719  
DB 652 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 710

RESULT 3  
US-08-286-870A-4  
; Sequence 4, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

```

; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286.870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-870A-4

Query Match          90.3%; Score 3394; DB 3; Length 648;
Best Local Similarity 99.8%; Pred. No. 1.8e-295;
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCLKNQDKHQSFSNAKVDKISTSLKNETDIELQNIHEDCLKXSEYENVEPVSASTI 60
Db 1 MCLKNQDKHQSFSNAKVDKISTSLKNETDIELQNIHEDCLKXSEYENVEPVSASTI 60
Qy 61 QTGIGIAGKILGTLGVPPAGQVASLYSFLGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTLGVPPAGQVASLYSFLGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Qy 121 RNKALTDLKGGLDALAVYHDSLESWGNGNRRNTRARSVVKVQYIALELMFVKLPFAVSG 180
Db 121 RNKALTDLKGGLDALAVYHDSLESWGNGNRRNTRARSVVKVQYIALELMFVKLPFAVSG 180
Qy 181 BEVPLLPYIAQAANLHLLLDASIFGKEWGLSSEISTFFYNQVERAGDYSRHCVKWYS 240
Db 181 BEVPLLPYIAQAANLHLLLDASIFGKEWGLSSEISTFFYNQVERAGDYSRHCVKWYS 240
Qy 241 TGLNLRGTNAESWVRVYNQFRDMLVLDLVALFPSYDTQWPKTKTAQLTREVIYTDAI 300
Db 241 TGLNLRGTNAESWVRVYNQFRDMLVLDLVALFPSYDTQWPKTKTAQLTREVIYTDAI 300
Qy 301 GTVHPHPSFTSTTWNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
Db 301 GTVHPHPSFTSTTWNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360
Qy 361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420
Db 361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420
Qy 421 VDFHWKFWTHPIASDNFYPCYVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFWTHPIASDNFYPCYVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

; 481 ASHKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAANVRGPGFTGCDILRRTN 540
; 481 ASHKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAANVRGPGFTGCDILRRTN 540
; 541 TGTFGDIRVWINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 600
; 541 TGTFGDIRVWINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 600
; 601 TFRVTGFTTSPFLDVQSTFTTGAWNFSGNEVYIDRIEFVPEVYTYE 648
; 601 TFRVTGFTTSPFLDVQSTFTTGAWNFSGNEVYIDRIEFVPEVYTYE 648

RESULT 4
US-09-003-217-2
; Sequence 2, Application US/09003217
; Patent No. 5986177
; GENERAL INFORMATION:
; APPLICANT: Osman, Yehia A.
; APPLICANT: Madkour, Megdy A.
; APPLICANT: Bulla, Lee A.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
; TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
; STREET: 3605 Glenwood Ave. Suite 310
; CITY: Raleigh
; STATE: NC
; COUNTRY: US
; ZIP: 27622
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003.217
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 5718-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2202
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-003-217-2

Query Match          89.7%; Score 3373; DB 2; Length 719;
Best Local Similarity 89.7%; Pred. No. 1.7e-293;
Matches 645; Conservative 33; Mismatches 41; Indels 0; Gaps 0;

Qy 1 MCLKNQDKHQSFSNAKVDKISTSLKNETDIELQNIHEDCLKXSEYENVEPVSASTI 60
Db 1 MCLKNQDKHQSFSNAKVDKISTSLKNETDIELQNIHEDCLKXSEYENVEPVSASTI 60
Qy 61 QTGIGIAGKILGTLGVPPAGQVASLYSFLGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTLGVPPAGQVASLYSFLGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Qy 121 RNKALTDLKGGLDALAVYHDSLESWGNGNRRNTRARSVVKVQYIALELMFVKLPFAVSG 180
Db 121 RNKALTDLKGGLDALAVYHDSLESWGNGNRRNTRARSVVKVQYIALELMFVKLPFAVSG 180
Qy 181 BEVPLLPYIAQAANLHLLLDASIFGKEWGLSSEISTFFYNQVERAGDYSRHCVKWYS 240
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Db 181 EEPVLLPIYAQAANLHLLLRDASIFKNGGLSASEISTFYNRQVTRDRYSVHCVKWN 240  
Qy 241 TGLNLRGTNAESVRYNQFRDWTMLVLDLVALFSPYDTQMPYIKTTAQLTREVTDAI 300  
Db 241 TGLNLRGTNAESVRYNQFRDWTMLVLDLVALFSPYDTQMPYIKTTAQLTREVTDAI 300  
Qy 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYLSLSRWSNTQYMNW 360  
Db 301 GTVDPNQALRSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYLSLSRWSNTQYMNW 360  
Qy 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTOPVNGVPR 420  
Db 361 GGHLESRPICGALNTSTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTOPVNGVPR 420  
Qy 421 VDFHKKFTHPIASDNFYGYGVGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480  
Db 421 VDFHKKFTHPIASDNFYGYGVGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480  
Qy 481 ASHVKALVYSWTHRSADRTNTEPNSTIQPLVKAFNLSSGAAVVRGPGFTGGHILRRTN 540  
Db 481 GSHVKALVYSWTHRSADRTNTEPNSTIQPLVKAFNLSSGAAVVRGPGFTGGHILRRTK 540  
Qy 541 TGTFGDIRVNINPPPAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGCDLYK 600  
Db 541 TGTFGDIRVNINPPPAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGCDLYK 600  
Qy 601 TPTVGTFTTFFSFDVQSTFTIGAMNFFSGNEVYIDRIEFVPVEVTEAEYDPEKAQEKV 660  
Db 601 TPTVGTFTTFFSFDVQSTFTIGAMNFFSGNEVYIDRIEFVPVEVTEAEYDPEKAQEKV 660  
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFLDEKRELFELVYKAKQIHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFLDEKRELFELVYKAKQIHIERNM 719

RESULT 5  
US-09-218-942-2  
; Sequence 2, Application US/09218942  
; Patent No. 6232439  
; GENERAL INFORMATION:  
; APPLICANT: Osman, Yehia  
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum  
; FILE REFERENCE: CryII  
; CURRENT APPLICATION NUMBER: US/09/218,942  
; EARLIER FILING DATE: 1998-12-22  
; EARLIER APPLICATION NUMBER: 60/035,361  
; EARLIER FILING DATE: 1997-01-10  
; EARLIER APPLICATION NUMBER: 09/003,217  
; EARLIER FILING DATE: 1998-01-06  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-09-218-942-2

Query Match 89.6%; Score 3368; DB 3; Length 719;  
Best Local Similarity 89.7%; Pred. No. 4.7e-293;  
Matches 645; Conservative 33; Mismatches 41; Indels 0; Gaps 0;

Qy 1 MGLKNQDKHOSFSSNAKVDKISTDSLKNETDIELQINIHEDCLMKSEYENVEPVSASTI 60  
Db 1 MGLKNPKHQTLSSNAKVDKIATDSLKNETDIELKWNNDYLRMSEHESIDPVSASTI 60  
Qy 61 QTGIGIAGKILGTGVFPAGVASLYSFIIGELMPKKNQWEIFMEHVEIINQKISTYA 120  
Db 61 QTGIGIAGKILGTGVFPAGVASLYSFIIGELMPKKNQWEIFMEHVEIINQKISTYA 120  
Qy 121 RNKALTDLKIGDALAVYHDSLESWGNRNTRARSVVKQYIALELMFVQKLPSPAVSG 180  
Db 121 RNKALTDLKIGDALAVYHDSLESWGNRNTRARSVVKQYIALELMFVQKLPSPAVSG 180

Qy 181 EEPVLLPIYAQAANLHLLLRDASIFKNGGLSASEISTFYNRQVTRDRYSVHCVKWS 240  
Db 181 EEPVLLPIYAQAANLHLLLRDASIFKNGGLSASEISTFYNRQVTRDRYSVHCVKWN 240  
Qy 241 TGLNLRGTNAESVRYNQFRDWTMLVLDLVALFSPYDTQMPYIKTTAQLTREVTDAI 300  
Db 241 TGLNLRGTNAESVRYNQFRDWTMLVLDLVALFSPYDTQMPYIKTTAQLTREVTDAI 300  
Qy 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYLSLSRWSNTQYMNW 360  
Db 301 GTVDPNQALRSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYLSLSRWSNTQYMNW 360  
Qy 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTOPVNGVPR 420  
Db 361 GGHLESRPICGALNTSTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTOPVNGVPR 420  
Qy 421 VDFHKKFTHPIASDNFYGYGVGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480  
Db 421 VDFHKKFTHPIASDNFYGYGVGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480  
Qy 481 ASHVKALVYSWTHRSADRTNTEPNSTIQPLVKAFNLSSGAAVVRGPGFTGGHILRRTN 540  
Db 481 ASHVKALVYSWTHRSADRTNTEPNSTIQPLVKAFNLSSGAAVVRGPGFTGGHILRRTK 540  
Qy 541 TGTFGDIRVNINPPPAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGCDLYK 600  
Db 541 TGTFGDIRVNINPPPAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGCDLYK 600  
Qy 601 TPTVGTFTTFFSFDVQSTFTIGAMNFFSGNEVYIDRIEFVPVEVTEAEYDPEKAQEKV 660  
Db 601 TPTVGTFTTFFSFDVQSTFTIGAMNFFSGNEVYIDRIEFVPVEVTEAEYDPEKAQEKV 660  
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFLDEKRELFELVYKAKQIHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFLDEKRELFELVYKAKQIHIERNM 719

RESULT 6  
US-08-286-870A-6  
; Sequence 6, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989







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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-038-4

Query Match      65.0%; Score 2445.5; DB 1; Length 1229;
Best Local Similarity 65.6%; Pred. No. 6.6e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

Qy 13 SSNAKVDKISDLSKN-ETDIELQ-NINHEDECLMSEYENVEPVFSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCVAEVNNDPFSASTVQTGINIAGRI 66
Qy 71 LGTLGVFPAGQVASYLFILGELWPKGNQWEIFMEHVEEIIINQKISYARKNALTDLKG 130
Db 67 LGVLGVFPAGQVASYLFILGELWPKGNQWEIFMEHVEEIIINQKISYARKNALTDLKG 126
Qy 131 LGDALAVYHDSLEWGNRNTRARSVVKSVYIALELMFVQKLPFAVSGEVEPLPIYA 190
Db 127 LGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPLFRIRNEVEPLLMVYA 186
Qy 191 QAANLHLLLRDASIFGKESGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNLRGTN 250
Db 187 QAANLHLLLRDASIFGKESGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNLRGTN 246
Qy 251 AESWVRYNQFRDRLTGLVDLVALFPPSYDTOMYPIKTAQLTREYVTDATGTVHPHPSFT 310
Db 247 AESWLRYNQFRDRLTGLVDLVALFPPSYDTOMYPIKTAQLTREYVTDATGTVHPHPSFT 306
Qy 311 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMGGHKLFRPTI 370
Db 307 STWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMGGHKLFRPTI 366
Qy 371 GGTNLNISTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLELFTQPVNGVPRVDFHKEVT 429
Db 367 GGTNLNISTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLELFTQPVNGVPRVDFHKEVT 422
Qy 430 HPIASDNFYYPG-----YVIGTQLQDSNELPPPEATGPNYVESYSHRSLHGLISAS 482
Db 423 --INPQNIYERGATTYSQPYQGVIGLFDSETELPPETTERPNYVESYSHRSLHGLIGN 480
Qy 483 HVKALVYSWTHRSADRTNITPNSITQIPVKAFNLSGAAVVRGPGFTGGDILRRNTG 542
Db 481 TLRAVYSWTHRSADRTNITPNSITQIPVKAFNLSGAAVVRGPGFTGGDILRRNTG 540
Qy 543 TFGDIRVNINPPFAQVRVIRYASTTDLQPHTSINGKAINQGNFSATMARGEDLDYKTF 602
Db 541 TFGDIRVNINPPFAQVRVIRYASTTDLQPHTSINGKAINQGNFSATMARGEDLDYKTF 600
Qy 603 RTVGFTTFFSLDQSTFTIGANNFSGNEVYIDRIEFVPEVVEYAEYDEKAQEKVTA 662
Db 601 RTAGFTTFFFLNQAQSTFTLGAQFSN-QEVIIDRVFVPAEVTFEAYDILERAQKAVNA 659
Qy 663 LFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIYKVAQKLIHERNM 719
Db 660 LFTSTNPRGLKTDVKYHIDQVSNVACLSDDEFCLDEKRELFEIYKVAKRLSDERNL 716

RESULT 10
US-08-779-046-4
; Sequence 4, Application US/08779046
; Patent No. 5854053
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jan, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYETA AND CRYETS
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
```

```
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,046
; FILING DATE: 06-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-779-046-4

Query Match      65.0%; Score 2445.5; DB 2; Length 1229;
Best Local Similarity 65.6%; Pred. No. 6.6e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

Qy 13 SSNAKVDKISDLSKN-ETDIELQ-NINHEDECLMSEYENVEPVFSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCVAEVNNDPFSASTVQTGINIAGRI 66
Qy 71 LGTLGVFPAGQVASYLFILGELWPKGNQWEIFMEHVEEIIINQKISYARKNALTDLKG 130
Db 67 LGVLGVFPAGQVASYLFILGELWPKGNQWEIFMEHVEEIIINQKISYARKNALTDLKG 126
Qy 131 LGDALAVYHDSLEWGNRNTRARSVVKSVYIALELMFVQKLPFAVSGEVEPLPIYA 190
Db 127 LGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPLFRIRNEVEPLLMVYA 186
Qy 191 QAANLHLLLRDASIFGKESGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNLRGTN 250
Db 187 QAANLHLLLRDASIFGKESGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNLRGTN 246
Qy 251 AESWVRYNQFRDRLTGLVDLVALFPPSYDTOMYPIKTAQLTREYVTDATGTVHPHPSFT 310
Db 247 AESWLRYNQFRDRLTGLVDLVALFPPSYDTOMYPIKTAQLTREYVTDATGTVHPHPSFT 306
Qy 311 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMGGHKLFRPTI 370
Db 307 STWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMGGHKLFRPTI 366
Qy 371 GGTNLNISTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLELFTQPVNGVPRVDFHKEVT 429
Db 367 GGTNLNISTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLELFTQPVNGVPRVDFHKEVT 422
Qy 430 HPIASDNFYYPG-----YVIGTQLQDSNELPPPEATGPNYVESYSHRSLHGLISAS 482
Db 423 --INPQNIYERGATTYSQPYQGVIGLFDSETELPPETTERPNYVESYSHRSLHGLIGN 480
Qy 483 HVKALVYSWTHRSADRTNITPNSITQIPVKAFNLSGAAVVRGPGFTGGDILRRNTG 542
Db 481 TLRAVYSWTHRSADRTNITPNSITQIPVKAFNLSGAAVVRGPGFTGGDILRRNTG 540
Qy 543 TFGDIRVNINPPFAQVRVIRYASTTDLQPHTSINGKAINQGNFSATMARGEDLDYKTF 602
Db 541 TFGDIRVNINPPFAQVRVIRYASTTDLQPHTSINGKAINQGNFSATMARGEDLDYKTF 600
Qy 603 RTVGFTTFFSLDQSTFTIGANNFSGNEVYIDRIEFVPEVVEYAEYDEKAQEKVTA 662
Db 601 RTAGFTTFFFLNQAQSTFTLGAQFSN-QEVIIDRVFVPAEVTFEAYDILERAQKAVNA 659
Qy 663 LFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIYKVAQKLIHERNM 719
Db 660 LFTSTNPRGLKTDVKYHIDQVSNVACLSDDEFCLDEKRELFEIYKVAKRLSDERNL 716
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543 TFGDIRVNPPFAQVRVIRYASTTDLQFHTSINGKAINQNFSAWNRGDLDYKTF 602  
 541 TFGDIRVNPPFAQVRVIRYASTTDLQFHTSINGKAINQNFSAWNRGDLDYKTF 600  
 603 RTVGFTTFFSFLDVQSTFTTGANNFSSGNEVYIDRIEFVPEVTEAEYDEKAKQKVT 662  
 601 RTAGFSTFPNLAQSTFTLGAQSFN-QEVYIDRIEFVPEVTEAEYDEKAKQKVT 659  
 663 LFTSTNPRGLKTDVYDHYDQVSNVLSDEFLDEKRELFEIVKAKQLHIERNM 719  
 660 LFTSTNPRRLKTDVTDYDHYDQVSNVACLSDFLDEKRELFEIVKAKQLSDERNL 716

RESULT 11  
 US-08-861-340-4  
 ; Sequence 4, Application US/08881340  
 ; Patent No. 5942658  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yiping  
 ; APPLICANT: Jan, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS cvYET4 AND crYET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESSES: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/881,340  
 ; FILING DATE: 24-JUN-1997  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/100,709  
 ; FILING DATE: 29-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egolf, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1229 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-861-340-4

Query Match 65.0%; Score 2445.5; DB 2; Length 1229;  
 Best Local Similarity 65.6%; Pred. No. 6.6e-210;  
 Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;  
 13 SSNAKVDKISTDLKN-ETDTELO-NINHECLAKMSEYENVEPVSAVSTTQTGTGAGKI 70  
 7 NENEIINLSIPTVSNPSTQNLSPDARIEDSLCAEVNNDIPVSAVSTVQTGTGAGRI 66  
 71 LCTLGVPFAGVASYFILGELWPKGNQKQWEIWEHVEEILNQKISTYARNKALDTLKG 130  
 67 LGVLGVPFAGQLASFSYFLVGLWPSGRDPWEIIEHVEEILNQKISTYARNKALDTLKG 126  
 131 LGDALVYHDSLESVWGNRNTRARVVKVKSQVIALELMFVQKLPFAVSGEVEFLPIYA 190

127 LGRGYSYQOALETWLNRNDARSRIILERYVALELDITTAIPLFIRNEEYVPLLMVYA 186  
 191 QAAHLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSCHVCWYSGTGLNLRGTN 250  
 187 QAAHLHLLLRDASLFGSEWGMASDVQYQEQIRYTEESNHCQWYNTGLNLRGTN 246  
 251 AESWVRVYNQFRDMLVLDLVALFPSPYDTQMPYIKTAQLTREVTYDAIGTVHPHPSFT 310  
 247 AESWLRVYNQFRDMLVLDLVALFPSPYDTQMPYIKTAQLTREVTYDAIGTVHPHPSFT 306  
 311 STTWNNAPSFSAIEAAVAVNPHLLDPLEQVITYSLLSRWNSNTQYNNMGGHLEPRTI 370  
 307 STNWFNNAPSFSAIEAAVAVNPHLLDPLEQVITYSLLSRWNSNTQYNNMGGHLEPRTI 366  
 371 GGTNLISQTGST-NITSINPVTLPFTSRDVRVYTESLAGNLFTOPVNCVPRVDFHMKFTV 429  
 367 GGTNLISQTGST-NITSINPVTLPFTSRDVRVYTESLAGNLFTOPVNCVPRVDFHMKFTV 422  
 430 HPIASDNFYYPG-----YVIGTLODSENELPPEATGQPNVYESYSHRLSHIGLISAS 482  
 423 --INPQNIYERGATTYSQPYQGVGILQFDSSETLPPETTERPNYESYSHRLSHIGLIS 480  
 483 HVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTWTG 542  
 481 TRAPVSWTHRSADRTNTEPNSITQIPLVKALHSGVTVGGFGTGGDILRTWTG 540  
 543 TFGDIRVNPPFAQVRVIRYASTTDLQFHTSINGKAINQNFSAWNRGDLDYKTF 602  
 541 TFGDIRVNPPFAQVRVIRYASTTDLQFHTSINGKAINQNFSAWNRGDLDYKTF 600  
 603 RTVGFTTFFSFLDVQSTFTTGANNFSSGNEVYIDRIEFVPEVTEAEYDEKAKQKVT 662  
 601 RTAGFSTFPNLAQSTFTLGAQSFN-QEVYIDRIEFVPEVTEAEYDEKAKQKVT 659  
 663 LFTSTNPRGLKTDVYDHYDQVSNVLSDEFLDEKRELFEIVKAKQLHIERNM 719  
 660 LFTSTNPRRLKTDVTDYDHYDQVSNVACLSDFLDEKRELFEIVKAKQLSDERNL 716

RESULT 12  
 US-08-448-170-10  
 ; Sequence 10, Application US/08448170  
 ; Patent No. 5723758  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Payne, Jewel  
 ; APPLICANT: Cummings, David A.  
 ; APPLICANT: Cannon, Raymond J.C.  
 ; APPLICANT: Narva, Kenneth E.  
 ; APPLICANT: Stelman, Steve  
 ; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted  
 ; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes  
 ; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: David R. Saliwanchik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/448,170  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/069,902  
 ; FILING DATE: 01-JUNE-1993  
 ; CLASSIFICATION: 424

;; PRIOR APPLICATION DATA: 62.2%; Score 2340.5; DB 1; Length 488;  
;; APPLICATION NUMBER: US 07/759,247  
;; FILING DATE: 13-SEPT-1991  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Saliwanchik, David R.  
;; REGISTRATION NUMBER: 31,794  
;; REFERENCE/DOCKET NUMBER: M/S 102D.C1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (904) 375-8100  
;; TELEFAX: (904) 372-5800  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 488 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-448-170-10

Query Match 62.2%; Score 2340.5; DB 1; Length 488;  
Best Local Similarity 89.5%; Pred. No. 3.8e-201;  
Matches 445; Conservative 13; Mismatches 30; Indels 9; Gaps 1;  
  
Qy 1 MKLKNQDKHQSFSSNAKVDTSLDKNETDIELQNIHEDCLKSEYENVEPPFVSASTI 60  
Db 1 MKSKNNQNHQSLSNNATVDKNTGSLNNTNTELFQNFH-----EGIEPPFVSASTI 51  
  
Qy 61 QTGIGIAGKILGTLCVPPAGQVASYLSFILGELWPKGNQWEI FMEHVEEII NQKISTYA 120  
Db 52 QTGIGIVCKILGNLGVPPAGQVASYLSFILGELWPKGKSQWEI FMEHVEEII NQKISTYA 111  
  
Qy 121 RNKALTDLKGGLDALAVYHDSLESWVGNNRNRTRRSVVKSOYIALELMFVKLPSPFAVSG 180  
Db 112 RNKALADLKGGLDALAVYHESLESWENNRNRTRRSVVKSOYITLELMFVQSLPFAVSG 171  
  
Qy 181 BEVPLLPITYAQAANLHLLLRDASIFGKEMWGLSSSEISTFTYNNRQVERAGDYSCHCKWYS 240  
Db 172 BEVPLLPITYAQAANLHLLLRDASIFGKXWGLSDSEISTFTYNNRQSGKSEYSDHCVKWYN 231  
  
Qy 241 TGLNLRGTNAESWRYNQFRDMTLMVLDLVALPSPYDTQMYPIKTTAQLTREVYTDAT 300  
Db 232 TGLNLRGNNAESWRYNQFRDMTLMVLDLVALPSPYDTQMYPIKTTAQLTREVYTDAT 291  
  
Qy 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 360  
Db 292 GTVHPHPSFTTWTNNNAPSFTIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 351  
  
Qy 361 GGHKLEFRTIGTTLNISTQSTNTSINPVTLPTFSRDVYRTESLAGLNLFTQPVNGVPR 420  
Db 352 GGHKLEFRTIGTTLNISTQSTNTSINPVTLPTFSRDVYRTESLAGLNLFTQPVNGVPR 411  
  
Qy 421 VDFHWKFTVHTPIASDNFYYPGVGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLIS 480  
Db 412 VDFHWKFTVHTPIASDNFYYPGVAGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLIS 471  
  
Qy 481 ASHKVLYVSWTHRSAD 497  
Db 472 ASHKVLYVSWTHRSAD 488

RESULT 13  
US-08-961-803-10  
; Sequence 10, Application US/08961803  
; Patent No. 6150589  
; GENERAL INFORMATION:  
; APPLICANT: Payne, Jewel  
; APPLICANT: Cummings, David A.  
; APPLICANT: Cannon, Raymond J.C.  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Stelman, Steve  
; TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted  
; ; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes

;; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
;; NUMBER OF SEQUENCES: 10  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Jay M. Sanders  
;; STREET: 2421 N.W. 41st Street, Suite A-1  
;; CITY: Gainesville  
;; STATE: Florida  
;; COUNTRY: USA  
;; ZIP: 32606  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/961.803  
;; FILING DATE: 31-OCT-1997  
;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/069,902  
;; FILING DATE: 01-JUNE-1993  
;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/759,247  
;; FILING DATE: 13-SEPT-1991  
;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/448,170  
;; FILING DATE: 23-MAY-1995  
;; CLASSIFICATION: 800  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sanders, Jay M.  
;; REGISTRATION NUMBER: 39,355  
;; REFERENCE/DOCKET NUMBER: M/S 102DCD1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (352) 375-8100  
;; TELEFAX: (352) 372-5800  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 488 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-961-803-10

Query Match 62.2%; Score 2340.5; DB 3; Length 488;  
Best Local Similarity 89.5%; Pred. No. 3.8e-201;  
Matches 445; Conservative 13; Mismatches 30; Indels 9; Gaps 1;  
  
Qy 1 MKLKNQDKHQSFSSNAKVDTSLDKNETDIELQNIHEDCLKSEYENVEPPFVSASTI 60  
Db 1 MKSKNNQNHQSLSNNATVDKNTGSLNNTNTELFQNFH-----EGIEPPFVSASTI 51  
  
Qy 61 QTGIGIAGKILGTLCVPPAGQVASYLSFILGELWPKGNQWEI FMEHVEEII NQKISTYA 120  
Db 52 QTGIGIVCKILGNLGVPPAGQVASYLSFILGELWPKGKSQWEI FMEHVEEII NQKISTYA 111  
  
Qy 121 RNKALTDLKGGLDALAVYHDSLESWVGNNRNRTRRSVVKSOYIALELMFVKLPSPFAVSG 180  
Db 112 RNKALADLKGGLDALAVYHESLESWENNRNRTRRSVVKSOYITLELMFVQSLPFAVSG 171  
  
Qy 181 BEVPLLPITYAQAANLHLLLRDASIFGKEMWGLSSSEISTFTYNNRQVERAGDYSCHCKWYS 240  
Db 172 BEVPLLPITYAQAANLHLLLRDASIFGKXWGLSDSEISTFTYNNRQSGKSEYSDHCVKWYN 231  
  
Qy 241 TGLNLRGTNAESWRYNQFRDMTLMVLDLVALPSPYDTQMYPIKTTAQLTREVYTDAT 300  
Db 232 TGLNLRGNNAESWRYNQFRDMTLMVLDLVALPSPYDTQMYPIKTTAQLTREVYTDAT 291  
  
Qy 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 360  
Db 292 GTVHPHPSFTTWTNNNAPSFTIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 351

Best Local Similarity 64.3%; Pred. No. 1.1e-193; Indels 13; Gaps 5;  
Matches 442; Conservative 78; Mismatches 154;

40 EDCLKMSEVNEPVSASTIOTGIGIAGKILGTLPVFPAGQVSLYFIFLGEIWPVKGN 99  
10 EDSCICAGNNIDPVSASTVQTGINAGRIILGVLPFAGQVSLYFIFLGEIWPVKGN 69  
100 QWEIFMEHVEEIIINOKISTYARNKALTDLKGGLDALAVYHDSLESWGNRNNTARSVVK 159  
70 QWEIFLEHVEQLINQIITENARNALARLQGLGDSFRAYQQSLDNLWENLDDARTSRVLY 129  
160 SOYIALELMFVOKLPSPAVSGEEVPLLPYAAQANLHLLLRDASIFPKWGLSSSEIST 219  
130 TOYIALELDFLNAFLFAIRNOQEVPLLPYAAQANLHLLLRDASLFGSEFGLTSQEIQR 189  
220 FYNROVERAGDYSDHCWKWYSTGLNLRGTAESWVRYNQFRDMTLLVLDLVALFPSPYD 279  
190 YERQVERTRDYCYVWYNTGLNSLRTGTAASWVRYNQFRDLTLGLVLDLVALFPSPYD 249  
280 TOMYPIKTTAQLTREYVYDAIGTVHPHSFTTWWNNAPSFAIEAAVVRNPHLLDFL 339  
250 TRTYPINTSAQLTREYVYDAIGAT--GVNMAKNWNNAPSFAIEAAVVRNPHLLDFL 307  
340 EQVTIYLLSRWSNTQYMMWGHKLEFRTIGTILNISTQGSTNTSINPVTLPFTSRDVI 399  
308 EQLTIFSASSRWSNTRHMTYWRGHTIOSRPIGGGLNTSTHGATNTSINPVTLPFTSRDVI 367  
400 RTESLAGLMLF--LTQPVNGVRVDPHMKFVTHP-----IASDNFYPGVIGITQLODS 452  
368 RTESYAGVLLWGIYLPPIHGVPTVRNF--TNPQNISDRGTANYSQP-YESFGLQLODS 423  
453 ENELPPEATQCPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPL 512  
424 ETELPPEATQCPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPL 483  
513 VKAFNLSSGAAVVRGPGFTGGDILRRTNTGTGDIRVNIWNPFAQYRVRIRVASTDLO 572  
484 VKASELPQGTIVVRGPGFTGGDILRRTNTGTGDIRVNIWNPFAQYRVRIRVASTDLO 543  
573 PHTSINKAINQGNFSATMRGEDLDYKTRTVGFTTPESFLOVQSTFTIGAMNFSSGNE 632  
544 PFVSRGGTIVNFRFLTNMSGDELKYGNFVRRAFTTPTFTQIQRISIOGLSGNGE 603  
633 VYIDRIEFPVVEVTEAEYDPEKAQEKVATLFTSTNPRGLTKDVKYHIDQVSNLVESLS 692  
604 VYIDKIELIPVATFAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACL 663  
693 DEFYLDKRELFETVYKAKQLHIERNM 719  
664 DEFCLDEKRELFETVYKAKQLHIERNM 690

RESULT 15  
US-08-459-448A-7  
; Sequence 7, Application US/08459448A  
; Patent No. 5859336  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.

361 GGKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRVYRTESLAGLNLFLTOPVNGVPR 420  
352 GGKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRVYRTESLAGLNLFLTOPVNGVPR 411  
421 VDFHWKFTVTHIASDNFYPGYVIGITQLODSNELPPEATQCPNYESYSHRLSHIGLIS 480  
412 VDFHWKFTVTHIASDNFYPGYVIGITQLODSNELPPEATQCPNYESYSHRLSHIGLIS 471  
481 ASHKALVYSWTHRSAD 497  
472 ASHKALVYSWTHRSAD 488

RESULT 14  
US-07-951-715A-7  
; Sequence 7, Application US/07951715A  
; Patent No. 5625136  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/951,715A  
; FILING DATE: 25-SEP-1992  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8615  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1207 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-951-715A-7



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2005, 20:11:42 ; Search time 81.1112 Seconds  
(without alignments)  
4539.261 Million cell updates/sec

Title: US-10-019-823B-58

Perfect score: 3761

Sequence: 1 MKLKNQKHQSFSSNAKVDK.....KRELFEIVKYANELHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3724	99.0	719	1	CIIA_BACTK
2	3724	99.0	719	2	Q6X181
3	3719	98.9	719	2	Q93NJ5
4	3718	98.9	719	2	O85796
5	3589	95.4	719	2	O8KY61
6	3517	93.5	719	2	Q9F0P8
7	3484	92.6	719	1	C1IB_BACTE
8	3363	89.4	719	1	C1ID_BACTU
9	3341	88.8	719	1	C1IC_BACTU
10	2417.5	64.3	1229	1	C1BB_BACTU
11	2417.5	64.3	1233	1	C1BC_BACTM
12	2250.5	59.8	1228	2	Q93775
13	2248.5	59.6	1228	2	C1BA_BACTK
14	2240.5	59.6	1228	2	Q93NM5
15	2166.5	57.6	849	2	O6PYW8
16	2166.5	57.6	1227	1	C1BE_BACTU
17	2083.5	55.4	1231	2	O8KXZ2
18	2078.5	55.3	1231	1	C1BD_BACTZ
19	1971.5	52.4	1215	1	C1KA_BACTM
20	1876	49.9	381	2	Q45740
21	1643.5	43.7	1157	1	C8AA_BACUK
22	1630	43.3	1144	2	O8KZL7
23	1466	39.0	1157	1	C9CA_BACTO
24	1460.5	38.8	1169	1	C8BA_BACUK
25	1458.5	38.8	1166	1	C1GA_BACTU
26	1455	38.7	1169	1	C1FB_BACTM
27	1451	38.6	1167	1	C1JA_BACTU
28	1449	38.5	1174	2	Q457I9
29	1443	38.4	1155	1	C1AB_BACTK
30	1443	38.4	1155	2	Q7BE98
31	1443	38.4	1155	2	Q9F296

32	1441	38.3	1118	2	Q9AM83	Q9am83 bacillus th
33	1438	38.2	1156	2	Q6GUA7	Q6gua7 bacillus th
34	1433	38.1	1177	2	Q6EIX3	Q6eix3 bacillus th
35	1431	38.0	1155	2	Q93T21	Q93t21 bacillus th
36	1430.5	38.0	793	2	Q6PYW7	Q6pyw7 bacillus th
37	1430.5	38.0	1180	2	Q9S5V8	Q9s5v8 bacillus th
38	1429.5	38.0	1176	2	Q7WZT9	Q7wzt9 bacillus th
39	1425.5	37.9	1181	1	C1AE_BACTL	Q45736 bacillus th
40	1423.5	37.8	1176	2	Q45736	P02965 bacillus th
41	1419.5	37.7	1176	1	C1AA_BACTK	Q45736 bacillus th
42	1419.5	37.7	1176	2	Q9RC30	Q9rc30 bacillus th
43	1411.5	37.5	1169	2	O8GHE8	O8ghe8 bacillus th
44	1407.5	37.4	1179	1	C1AD_BACTA	Q03744 bacillus th
45	1404.5	37.3	1169	1	C1GB_BACTZ	Q9zaz6 bacillus th

ALIGNMENTS

RESULT 1  
CIIA\_BACTK  
ID\_CIIA\_BACTK STANDARD; PRT; 719 AA.  
AC Q45752: P71092; Q45750; Q45751; Q45756;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Pestidical crystal protein cryIIa (Insecticidal delta-endotoxin  
DE CryII(a)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
GN Name-cryIIa; Synonyms-CGCryV, cryII(a), cryV, cryVI;  
OS Bacillus thuringiensis (subsp. kurstaki).  
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=29339;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSIR732;  
RX MEDLINE=93298009; PubMed=8517758;  
RA Gleave A.P., Williams R., Hedges R.J.;  
RT "Screening by polymerase chain reaction of Bacillus thuringiensis  
RT serotypes for the presence of cryV-like insecticidal protein genes and  
RT characterization of a cryV gene cloned from B. thuringiensis subsp.  
RT kurstaki";  
RL Appl. Environ. Microbiol. 59:1683-1687(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JHCC4835;  
RX MEDLINE=92269582; PubMed=1588820;  
RA Tailor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;  
RT "Identification and characterization of a novel Bacillus thuringiensis  
RT delta-endotoxin entomocidal to coleopteran and lepidopteran larvae";  
RL Mol. Microbiol. 6:1211-1217(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HD-1;  
RX MEDLINE=95314293; PubMed=7793960;  
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;  
RT "Distribution of cryV-type insecticidal protein genes in Bacillus  
RT thuringiensis and cloning of cryV-type genes from Bacillus  
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.  
RT entomocidus";  
RL Appl. Environ. Microbiol. 61:2402-2407(1995).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AB88;  
RX MEDLINE=96178985; PubMed=8606196;  
RA Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,  
RA Craig J.A., Kozel M.G., Estruch J.J.;  
RT "Cloning of a cryV-type insecticidal protein gene from Bacillus  
RT thuringiensis: the cryV-encoded protein is expressed early in  
RT stationary phase";  
RL J. Bacteriol. 178:2141-2144(1996).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=61;

RA Selvapandian A., Bhatnagar R.K.;  
RT "Isolation, cloning and expression of cryV gene.";  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Promotes colloidomotic lysis by binding to the midgut  
CC epithelial cells of certain coleopteran and lepidopteran species.  
CC CC Active on Plutella xylostella and Bombyx mori.  
CC -1- DEVELOPMENTAL STAGE: The crystal protein is produced during  
CC sporulation and is accumulated both as an inclusion and as part of  
CC the spore coat.  
CC -1- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
CC terminus.  
CC -1- SIMILARITY: Belongs to the delta endotoxin family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; M98544; AA22354.1; -;  
CC EMBL; X62821; CAA44833.1; -;  
CC EMBL; L36338; AAC36999.1; -;  
CC EMBL; L49391; AAB00958.1; -;  
CC EMBL; Y08920; CAA70124.1; -;  
CC PIR; I39815; I39815.  
CC PIR; S25383; S25383.  
CC HSP; P02965; 1CIY.  
CC InterPro; IPR001178; Endotoxin.  
CC InterPro; IPR005638; endotoxin\_C.  
CC InterPro; IPR005639; endotoxin\_N.  
CC InterPro; IPR008979; Gal bind like.  
CC Pfam; PF03944; Endotoxin\_C; 1.  
CC Pfam; PF00555; Endotoxin\_M; 1.  
CC Pfam; PF03945; Endotoxin\_N; 1.  
KW Sporulation; Toxin; 159 K -> R (in strain 61);  
FT VARIANT 233 233 D -> Y (in strain JHC4835 and strain HD-  
FT 1).  
FT VARIANT 443 712 A -> V (in strain AB88).  
FT VARIANT 711 712 KQ -> NE (in strain HD-1 and strain 61).  
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;  
  
Query Match 99.0%; Score 3724; DB 1; Length 719;  
Best Local Similarity 99.3%; Pred. No. 5.1e-252;  
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;  
  
QY 1 MCLKNQKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKMSEYENVEPVSASTI 60  
DB 1 MCLKNQKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKMSEYENVEPVSASTI 60  
  
QY 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
DB 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
  
QY 120 ARNKALTDLKGDLALAVYHDSLESWGNNRNTARSVRSQYIALELMFVKLPSPFVS 179  
DB 120 ARNKALTDLKGDLALAVYHDSLESWGNNRNTARSVRSQYIALELMFVKLPSPFVS 179  
  
QY 180 GEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSDHCVKWY 239  
DB 180 GEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSDHCVKWY 239  
  
QY 240 STGLNNRGNTNAESWRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTREYVYTD 299  
DB 240 STGLNNRGNTNAESWRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTREYVYTD 299  
  
QY 300 IGVHPPSPFTSTWYNNNAPSFAIEAAVVRNPHLLDFEQVTIYSLSRWSNTQYMMN 359  
DB 300 IGVHPPSPFTSTWYNNNAPSFAIEAAVVRNPHLLDFEQVTIYSLSRWSNTQYMMN 359  
  
QY 360 WGGHKLFRITGGTINISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTQPVNGVP 419

DB 360 WGGHKLFRITGGTINISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTQPVNGVP 419  
QY 420 RVDFWKFPVTHPIASDNFYFPGYAGIGTQLODSENELPPEATGQPNVSEYSHRLSHIGLI 479  
DB 420 RVDFWKFPVTHPIASDNFYFPGYAGIGTQLODSENELPPEATGQPNVSEYSHRLSHIGLI 479  
QY 480 SASHVKALVYSWTHRSADRTWTIIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
DB 480 SASHVKALVYSWTHRSADRTWTIIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
QY 540 NTGTFGDIRVNNPPFAQRYRVRIRYASTTDLQHTSINGKAINQGNFSATMNGEDLDY 599  
DB 540 NTGTFGDIRVNNPPFAQRYRVRIRYASTTDLQHTSINGKAINQGNFSATMNGEDLDY 599  
QY 600 KTFRTVGTTFPSFLDVGOSTTIGAWNFSSGNEVVIDRIEFPVPEVVEYAEYDFEKAQEK 659  
DB 600 KTFRTVGTTFPSFLDVGOSTTIGAWNFSSGNEVVIDRIEFPVPEVVEYAEYDFEKAQEK 659  
QY 660 VTALFTSNPRLGKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
DB 660 VTALFTSNPRLGKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
  
RESULT 2  
Q6X181 PRELIMINARY; PRT; 719 AA.  
AC Q6X181;  
DT 05-JUL-2004 (TREMELrel. 27, Created)  
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)  
DE CryII.  
GN Name=cryII;  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AY262167; AAP86782.1; -;  
DR GO; GO:0005102; F-receptor binding; IEA.  
DR GO; GO:0006952; P-defense response; IEA.  
DR GO; GO:0009405; P-pathogenesis; IEA.  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR008979; Gal bind like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;  
  
Query Match 99.0%; Score 3724; DB 2; Length 719;  
Best Local Similarity 99.3%; Pred. No. 5.1e-252;  
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;  
  
QY 1 MCLKNQKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKMSEYENVEPVSASTI 60  
DB 1 MCLKNQKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKMSEYENVEPVSASTI 60  
  
QY 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
DB 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
  
QY 120 ARNKALTDLKGDLALAVYHDSLESWGNNRNTARSVRSQYIALELMFVKLPSPFVS 179  
DB 120 ARNKALTDLKGDLALAVYHDSLESWGNNRNTARSVRSQYIALELMFVKLPSPFVS 179  
  
QY 180 GEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSDHCVKWY 239  
DB 180 GEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSDHCVKWY 239



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QY 240 STGLNNLRGTNAESWRYNQFRDMLTLMVLDLVALFPSYDTQMPYPIKTTAQLTREYVYDA 299
DB 240 STGLNNLRGTNAESWRYNQFRDMLTLMVLDLVALFPSYDTQMPYPIKTTAQLTREYVYDA 299
QY 300 ICTVHPHPSFTSTTWNNAAPSFAEAAVVRNPHLLDLEQVTTIYSLSRNSNTQYMMN 359
DB 300 ICTVHPHPSFTSTTWNNAAPSFAEAAVVRNPHLLDLEQVTTIYSLSRNSNTQYMMN 359
QY 360 WGGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLFLTQPVNGVP 419
DB 360 WGGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLFLTQPVNGVP 419
QY 420 RVDHFWKFTVTHPIASDNFYYPGAGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLI 479
DB 420 RVDHFWKFTVTHPIASDNFYYPGAGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLI 479
QY 480 SASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539
DB 480 SASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539
QY 540 NTGTFGDIRVNINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDDLDY 599
DB 540 NTGTFGDIRVNINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDDLDY 599
QY 600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEK 659
DB 600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEK 659
QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFPIVKYAKQLHIERNM 719
DB 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFPIVKYAKQLHIERNM 719

RESULT 3
Q93NJ5 PRELIMINARY; PRT; 719 AA.
AC Q93NJ5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Crylla.
GN Name=crylla;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Song F., Zhang J., Gu A., Huang D., Li G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF373207; AAK66742.1; -.
DR HSSP; P02965; 1CIV.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;

Query Match 98.9%; Score 3719; DB 2; Length 719;
Best Local Similarity 99.2%; Pred. No. 1.1e-251;
Matches 714; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

QY 1 MKLNQDKHQSFSSNAKVKISTDSLKNETDIELQINHEDCLKMGEYENVEPFVGSASTI 60
DB 1 MKLNQDKHQSFSSNAKVKISTDSLKNETDIELQINHEDCLKMGEYENVEPFVGSASTI 60
QY 61 QTGIGIAGKILGTLPVFPAGQVASLYSIFLGBELPKGNQWEI - FMEHVEEINQKISTY 119
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DB 61 QTGIGIAGKILGTLPVFPAGQVASLYSIFLGBELPKGNQWEI - FMEHVEEINQKISTY 119
QY 120 ARNKALTDLKGGLDALAVYHDSLESGVGNRNTRARSVVRQVIALLELMFVKQLPSFAVS 179
DB 120 ARNKALTDLKGGLDALAVYHDSLESGVGNRNTRARSVVRQVIALLELMFVKQLPSFAVS 179
QY 180 GSEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSCHVKWY 239
DB 180 GSEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSCHVKWY 239
QY 240 STGLNNLRGTNAESWRYNQFRDMLTLMVLDLVALFPSYDTQMPYPIKTTAQLTREYVYDA 299
DB 240 STGLNNLRGTNAESWRYNQFRDMLTLMVLDLVALFPSYDTQMPYPIKTTAQLTREYVYDA 299
QY 300 ICTVHPHPSFTSTTWNNAAPSFAEAAVVRNPHLLDLEQVTTIYSLSRNSNTQYMMN 359
DB 300 ICTVHPHPSFTSTTWNNAAPSFAEAAVVRNPHLLDLEQVTTIYSLSRNSNTQYMMN 359
QY 360 WGGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLFLTQPVNGVP 419
DB 360 WGGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLFLTQPVNGVP 419
QY 420 RVDHFWKFTVTHPIASDNFYYPGAGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLI 479
DB 420 RVDHFWKFTVTHPIASDNFYYPGAGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLI 479
QY 480 SASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539
DB 480 SASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539
QY 540 NTGTFGDIRVNINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDDLDY 599
DB 540 NTGTFGDIRVNINPPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDDLDY 599
QY 600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEK 659
DB 600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEK 659
QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFPIVKYAKQLHIERNM 719
DB 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFPIVKYAKQLHIERNM 719

RESULT 4
O85796 PRELIMINARY; PRT; 719 AA.
AC O85796;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Insecticidal protein.
GN Name=crv101;
OS Bacillus thuringiensis (subsp. kurstaki).
OC Plasmid large plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S101;
RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076953; AAC26910.1; -.
DR HSSP; P02965; 1CIV.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.

|||||
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Tue Feb 15 10:07:56 2005

us-10-019-823b-58.rup

KW Plasmid. 719 AA; 81230 MW; 42746D478359BBA7 CRC64;  
SQ SEQUENCE  
Query Match 98.9%; Score 3718; DB 2; Length 719;  
Best Local Similarity 99.2%; Pred. No. 1.3e-251;  
Matches 714; Conservative 2; Mismatches 2; Indels 2; Gaps 2;  
QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60  
D b 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60  
QY 61 Q T G I G I A G K I L G T L G V P F A G V A S L Y S F I L G E L W P K G N Q W E I L F M E H V E E - I N Q I S T Y 119  
D b 61 Q T G I G I A G K I L G T L G V P F A G V A S L Y S F I L G E L W P K G N Q W E I - F M E H V E E I I N Q I S T Y 119  
QY 120 A R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A R S V V R S Q Y I A L E L M F V Q K L P S F A V S 179  
D b 120 A R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A R S V V R S Q Y I A L E L M F V Q K L P S F A V S 179  
QY 180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q V R A G D Y S D H C V K W Y 239  
D b 180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q V R A G D Y S D H C V K W Y 239  
QY 240 S T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T O M P I K T T A Q L T R E V Y T D A 299  
D b 240 S T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T O M P I K T T A Q L T R E V Y T D A 299  
QY 300 I G T V H P H P S F T S T T W Y N N N A P S F A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T O Y M N M 359  
D b 300 I G T V H P H P S F T S T T W Y N N N A P S F A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T O Y M N M 359  
QY 360 W G H K L E F R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P 419  
D b 360 W G H K L E F R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P 419  
QY 420 R V D F H K F V T H P I A S D N F Y P G A G I G T Q L Q D S E N E L P P E A T G P N Y E S Y S H R L S H I G L I 479  
D b 420 R V D F H K F V T H P I A S D N F Y P G A G I G T Q L Q D S E N E L P P E A T G P N Y E S Y S H R L S H I G L I 479  
QY 480 S A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G D I L R R T 539  
D b 480 S A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G D I L R R T 539  
QY 540 N T G T F G D I R V N I N P P P A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M R G E D L D Y 599  
D b 540 N T G T F G D I R V N I N P P P A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M R G E D L D Y 599  
QY 600 K T F R T V G T T P P S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659  
D b 600 K T F R T V G T T P P S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659  
QY 660 V T A L F T S T N P R G L K T D V K Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719  
D b 660 V T A L F T S T N P R G L K T D V K Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719

RESULT 5  
Q8KY61 ID Q8KY61 PRELIMINARY; PRT; 719 AA.  
AC Q8KY61;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Cry.  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
ON NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Porcar M., Martinez C., Caballero P.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF278797; AA073516.1; -.  
DR PIR; B42459; B42459.

HSSP; P02965; 1CIY.  
GO; GO:0005102; F:receptor binding; IEA.  
GO; GO:0006952; P:defense response; IEA.  
GO; GO:0009405; P:pathogenesis; IEA.  
InterPro; IPR001178; Endotoxin.  
InterPro; IPR005638; endotoxin C.  
InterPro; IPR005639; endotoxin N.  
InterPro; IPR008979; Gal\_bind\_Like.  
Pfam; PF03944; Endotoxin\_C; 1.  
Pfam; PF00555; Endotoxin\_M; 1.  
Pfam; PF03945; Endotoxin\_N; 1.  
SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;  
Query Match 95.4%; Score 3589; DB 2; Length 719;  
Best Local Similarity 95.6%; Pred. No. 1.5e-242;  
Matches 688; Conservative 14; Mismatches 16; Indels 2; Gaps 2;  
QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N V E P F V S A S T I 60  
D b 1 M K L K N P D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K I S E Y N V E P F V S A S T I 60  
QY 61 Q T G I G I A G K I L G T L G V P F A G V A S L Y S F I L G E L W P K G N Q W E I L F M E H V E E - I N Q I S T Y 119  
D b 61 Q T G I S I A G K I L G T L G V P F A G V A S L Y S F I L G E L W P K G N Q W E I - P M E H V E E I I N Q I S T Y 119  
QY 120 A R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A R S V V R S Q Y I A L E L M F V Q K L P S F A V S 179  
D b 120 A R N K A L T D L K G L D A L A V V H E S L E S W G N R K N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S 179  
QY 180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q V R A G D Y S D H C V K W Y 239  
D b 180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q V R A G D Y S D H C V K W Y 239  
QY 240 S T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T O M P I K T T A Q L T R E V Y T D A 299  
D b 240 S T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T L V Y P I K T T S Q L T R E V Y T D A 299  
QY 300 I G T V H P H P S F T S T T W Y N N N A P S F A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T O Y M N M 359  
D b 300 I G T V H P N A S F A S T T W Y N N N A P S F T I E S A V V R N P H L L D F L E Q V T I Y S L L S R W S N T O Y M N M 359  
QY 360 W G H K L E F R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P 419  
D b 360 W G H R L E F R T I G G L M T S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P 419  
QY 420 R V D F H K F V T H P I A S D N F Y P G A G I G T Q L Q D S E N E L P P E A T G P N Y E S Y S H R L S H I G L I 479  
D b 420 R V D F H K F V T H P I A S D N F Y P G A G I G T Q L Q D S E N E L P P E T T G P N Y E S Y S H R L S H I G L I 479  
QY 480 S A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G D I L R R T 539  
D b 480 S A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G D I L R R T 539  
QY 540 N T G T F G D I R V N I N P P P A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M R G E D L D Y 599  
D b 540 N T G T F G D I R V N I N P P P A Q R Y R V R I R Y A S T T D I Q F H T S I N G K A I N Q G N F S A T M R G E D L D Y 599  
QY 600 K T F R T V G T T P P S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659  
D b 600 K T F R T V G T T P P S F S D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659  
QY 660 V T A L F T S T N P R G L K T D V K Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719  
D b 660 V T A L F T S T N P G L K T N T V E H I D Q V S N L V E S L S N E F Y L D E K R E L F E I V K Y A K Q L H T G R N M 719

RESULT 6  
Q9F0P8 ID Q9F0P8 PRELIMINARY; PRT; 719 AA.  
AC Q9F0P8;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

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DE GN Name=cryII;
OS Bacillus thuringiensis.
OC Plasmid pBTC19.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BTC007;
RX DOI=10.1128/AEM.69.9.5207-5211.2003;
RA Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,
Hu Y., Li G., Huang D.;
RT "Identification of cryII-type genes from Bacillus thuringiensis
RT strains and characterization of a novel cryII-type gene.";
RL Appl. Environ. Microbiol. 69:5207-5211(2003).
DR EMBL; AF211190; AAG43526.1; -.
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF03945; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Plasmid.
KW SEQUENCE 719 AA; 81024 MW; 7E17481922C435E6 CRC64;
SQ
Query Match 93.5%; Score 3517; DB 2; Length 719;
Best Local Similarity 93.1%; Pred. No. 1.6e-237;
Matches 670; Conservative 27; Mismatches 21; Indels 2; Gaps 2;
QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFVSASTI 60
QY 61 QTGIGTAGKILGTLGVPFAGQVSLYFILGELWPKGKQWELFMEHVVEE-INQKISTY 119
DB 61 QTGIGTAGKILGTLGVPFAGQVSLYFILGELWPKGKQWEL-FMEHVVEELIDKISTY 119
QY 120 ARNKALTDLKGDLALAVYHDSLESVGNRNTRRSVVRQYIALLELMFVQKLPFSAYS 179
DB 120 ARNKALTDLKGDLALAVYHDSLESVGNRNTRRSVVRQYIALLELMFVQKLPFSAYS 179
QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDDHCWKY 239
DB 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDDHCWKY 239
QY 240 STGLNNLRGTNAESWRYNQFRDMLTMDLVALPVSVDYDQWYPIKTTAQLTREVVTDA 299
DB 240 STGLNNLRGTNAESWRYNQFRDMLTMDLVALPVSVDYDQWYPIKTTAQLTREVVTDA 299
QY 300 IGVTHPHSPSTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMM 359
DB 300 IGVTHPHSPSTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMM 359
QY 360 WGGHKLFEFTTIGTGLNISQGSNTSINPVTLPTGTRDVRVYRTSLAGLNLFLTQPVNGVP 419
DB 360 WGGHKLFEFTTIGTGLNISQGSNTSINPVTLPTGTRDVRVYRTSLAGLNLFLTQPVNGVP 419
QY 420 RVDPHKKEVTHPTASDNFYYPGAGIGTQDSENELPPEATGQPNYESVSHRLSHIGLI 479
DB 420 RVDPHKKEVTHPTASDNFYYPGAGIGTQDSENELPPEATGQPNYESVSHRLSHIGLI 479
QY 480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
DB 480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
QY 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGSDLOY 599
DB 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGSDLOY 599
CryII.
DB 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGSDLOY 599
QY 600 KTFRTVGFTTPTPSFLDVQSTFTIGAWNFGSGNEVYIDRIEFVEVYEAEDFEKAQEK 659
DB 600 KTFRTVGFTTPTPSFLDVQSTFTIGAWNFGSGNEVYIDRIEFVEVYEAEDFEKAQEK 659
QY 660 VTALFTSTNPRGLKTDVDYHIDQVSNLVESLSDEFYLDKRELFKELFVYKYNELHIERNM 719
DB 660 VTALFTSTNPRGLKTDVDYHIDQVSNLVESLSDEFYLDKRELFKELFVYKYNELHIERNM 719
RESULT 7
CLIB_BACTE STANDARD; PRT; 719 AA.
AC Q45709;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIb (insecticidal delta-endotoxin
DE CryII(b)) (crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIIb; Synonyms=cryII(b), cryV, cryV465;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP465;
RX MEDLINE=95314293; PubMed=7793960;
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;
RT "Distribution of cryV-type insecticidal protein genes in Bacillus
RT thuringiensis and cloning of cryV-type genes from Bacillus
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
RT entomocidus.";
RL Appl. Environ. Microbiol. 61:2402-2407(1995).
CC -!- FUNCTION: Promotes colloidsomic lysis by binding to the midgut
CC epithelial cells of certain coleopteran and lepidopteran species.
CC Active on Plutella xylostella but not on Bombyx mori.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC
CC EMBL; U07642; AAA82114.1; -.
CC FIR; I40590; I40590.
CC HSSP; P02965; 1CIY.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC InterPro; IPR008979; Gal_bind_like.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81295 MW; E8210ABEA97688E CRC64;
Query Match 92.6%; Score 3484; DB 1; Length 719;
Best Local Similarity 92.2%; Pred. No. 3.3e-235;
Matches 664; Conservative 33; Mismatches 21; Indels 2; Gaps 2;
QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFVSASTI 60
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61 QTGIGIAGKILGTVFPAGQASLYSIFILGELMPKQKQWELFMEHVEE-INQKISTY 119  
 CC  
 61 QTGIGIAGKILGTVFPAGQASLYSIFILGELMPKQKQWELFMEHVEE-INQKISTY 119  
 CC  
 120 ARNKALTDLKGDLAVYHDSLESWGNRNTRRSVRSQYIALELMPVQKLPSFVS 179  
 CC  
 120 ARNKALSDRLGDLAVYHDSLESWGNRNTRRSVRSQYIALELMPVQKLPSFVS 179  
 CC  
 180 GEEVPLPIYAQAANLHLLLRDASIFGKEMWGLSSSEISTFYNRQVERAGDYSDHCVKWY 239  
 CC  
 180 GEEVPLPIYAQAANLHLLLRDASIFGKEMWGLSSSEISTFYNRQVERAGDYSDHCVKWY 239  
 CC  
 240 STGLNNLRGNAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLREVYTD 299  
 CC  
 240 NTGLNNLRGNAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLREVYTD 299  
 CC  
 300 IGTVHPHPSFTTWNNAAPSAIEAAVVRPHLLDFLEQVITYSLLSRWNTQYMMN 359  
 CC  
 300 IGTVHPHPSFTTWNNAAPSAIEAAVVRPHLLDFLEQVITYSLLSRWNTQYMMN 359  
 CC  
 360 WGGHKLFRFTIGTGLNISTOGSTNTSINPVTLPFTSRDVTYTESLAGLNLFLTPQVNGVP 419  
 CC  
 360 WGGHKLFRFTIGTGLNISTOGSTNTSINPVTLPFTSRDVTYTESLAGLNLFLTPQVNGVP 419  
 CC  
 420 RVDPHMKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLI 479  
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 420 RVDPHMKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLI 479  
 CC  
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 480 SASHVKALVSWTHRSADRNTNTPNSITQIPLVKAFLNLSGAAVVRGPGFTGDIILRR 539  
 CC  
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 600 KTFRTVGTFTPFSDVQSTFTIGAMFNSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
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 660 VTALFTSTNPRGLTKDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719  
 CC  
 660 VTALFTSTNPRGLTKDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719  
 CC

## RESULT 8

CLID\_BACTU STANDARD; PRT; 719 AA.  
 ID CLID\_BACTU STANDARD; PRT; 719 AA.  
 AC Q9XDL1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryII (Insecticidal delta-endotoxin  
 DE CryII(d)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryIId; Synonyms=cryII(d), NRCryV;  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RP STRAIN=BR30;  
 RX MEDLINE=20374042; PubMed=10919402;  
 RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;  
 RA "Cloning of a new Bacillus thuringiensis cryII-type crystal protein  
 RT gene.";  
 RL Curr. Microbiol. 41:65-69(2000).  
 CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut  
 CC epithelial cells of many lepidopteran larvae. Active on Plutella  
 CC xylostella and on Bombyx mori.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-

terminus.  
 -!- SIMILARITY: Belongs to the delta endotoxin family.  
 -----  
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 or send an email to license@isb-sib.ch).  
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 EMBL; AF047579; AAD44366.1; -;  
 HSP; P02965; 1C1Y.  
 InterPro: IPR001178; Endotoxin.  
 InterPro: IPR005638; endotoxin\_C.  
 InterPro: IPR005639; endotoxin\_N.  
 InterPro: IPR008979; Gal\_bind\_like.  
 Pfam: PF03944; Endotoxin\_C; 1.  
 Pfam: PF00555; Endotoxin\_M; 1.  
 Pfam: PF03945; Endotoxin\_N; 1.  
 Sporulation; Toxin.  
 SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;  
 Query Match 89.4%; Score 3363; DB 1; Length 719;  
 Best Local Similarity 89.3%; Pred. No. 9.8e-227;  
 Matches 643; Conservative 36; Mismatches 39; Indels 2; Gaps 2;

1 MKLKNQDKHQSFSNAKVDKISTSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60  
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 1 MKSKNQMTKFSNSATVDKSTFDPLEHNTMELQNSHEDCLKMEYESVEFPVSSTI 60  
 DB  
 61 QTGIGIAGKILGTVFPAGQASLYSIFILGELMPKQKQWELFMEHVEE-INQKISTY 119  
 QY  
 61 QTGIGIAGKILGTVFPAGQASLYSIFILGELMPKQKQWELFMEHVEE-INQKISTY 119  
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 120 ARNKALTDLKGDLAVYHDSLESWGNRNTRRSVRSQYIALELMPVQKLPSFVS 179  
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 180 GEEVPLPIYAQAANLHLLLRDASIFGKEMWGLSSSEISTFYNRQVERAGDYSDHCVKWY 239  
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 180 GEEVPLPIYAQAANLHLLLRDASIFGKEMWGLSSSEISTFYNRQVERAGDYSDHCVKWY 239  
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 240 STGLNNLRGNAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLREVYTD 299  
 QY  
 240 STGLNNLRGNAESWRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLREVYTD 299  
 DB  
 300 IGTVHPHPSFTTWNNAAPSAIEAAVVRPHLLDFLEQVITYSLLSRWNTQYMMN 359  
 QY  
 300 IGTVHPHPSFTTWNNAAPSAIEAAVVRPHLLDFLEQVITYSLLSRWNTQYMMN 359  
 DB  
 360 WGGHKLFRFTIGTGLNISTOGSTNTSINPVTLPFTSRDVTYTESLAGLNLFLTPQVNGVP 419  
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 360 WGGHKLFRFTIGTGLNISTOGSTNTSINPVTLPFTSRDVTYTESLAGLNLFLTPQVNGVP 419  
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 420 RVDPHMKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLI 479  
 QY  
 420 RVDPHMKFVTHPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLI 479  
 DB  
 480 SASHVKALVSWTHRSADRNTNTPNSITQIPLVKAFLNLSGAAVVRGPGFTGDIILRR 539  
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 480 SASHVKALVSWTHRSADRNTNTPNSITQIPLVKAFLNLSGAAVVRGPGFTGDIILRR 539  
 DB  
 540 NTGTFGDIRVNIINPPFAQRVRYRIRYASTTDLQPHTSINGKAINQGNFSATMNRGDL 599  
 QY  
 540 NTGTFGDIRVNIINPPFAQRVRYRIRYASTTDLQPHTSINGKAINQGNFSATMNRGDL 599  
 DB  
 600 KTFRTVGTFTPFSDVQSTFTIGAMFNSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
 QY  
 600 KTFRTVGTFTPFSDVQSTFTIGAMFNSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
 DB  
 660 VTALFTSTNPRGLTKDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719  
 QY  
 660 VTALFTSTNPRGLTKDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719  
 DB





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QY 542 GTFGDIRVNINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKT 601
D 540 GTFGDIRVNINPVSQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKT 601
QY 602 FRTVGTTPFSLDVQSTTIGANFSSGNEVYIDRIEFPVVEVYEAEDFEKAQKVT 661
D 600 FRTAGSTFPNLNAQSTTFLQAQSFN-OEVYIDRVEFVPAEVTFEAEYDLERAQKAVN 658
QY 662 ALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 719
D 659 ALFTSTNPRRLKTDVVDYHIDQVSNLVACLSDEFCLDEKRELFEKVYAKRLSDERNL 716

RESULT 12
Q93T75
ID C1BA BACTK STANDARD; PRT; 1228 AA.
AC P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Delta-endotoxin Cry1Ba2.
GN Name=cry1Ba2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAK51084.1; -.
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0003405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match 59.8%; Score 2250.5; DB 2; Length 1228;
Best Local Similarity 62.5%; Pred. No. 1.8e-148;
Matches 448; Conservative 78; Mismatches 164; Indels 27; Gaps 8;

QY 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEFPFVSASTIQTGIGIAGKI 70
D 2 TSNRKNENIINAVSNHSAQMDLLDPARTEDSLCIAEGNIDPFVSASTVQTGINIAGRI 61
QY 71 LGTLGVPPAGQVASYFLGELWPKGNKQWELFMEHVEE-INQISTYARKALTDLK 129
D 62 LGVLGVPPAGQVASYFLGELWPKGRDQWEI-FLEHVEQLNQIQTINARNALRLQ 120
QY 130 GLGDALAVYHDSLESWGNRNTRASVVRISOVIALELMFVKLPSPFVSGVEVPLPT 189
D 121 GLGDSFRAVQOQSLDWLENRDARVSLHTQVIALELDFLAMPFAIRNQEVPFLMWY 180
QY 190 AQAAHLHLLLRDASIFGKWSLSSEISTFYNRQVERAGDSDHCVKWYSTGLNNLRGT 249
D 181 AQAAHLHLLLRDASIFGSEFGLTSQEIQRKYERQVERTRDYSYDCEWYNTGLNSLROT 240
QY 250 NAEWRYNRQFRDMLWLDLVALPPSYDTQMPYKTTAQLTREYTTDAITGVHPHPSF 309
D 241 NAEWRYNRQFRDMLWLDLVALPPSYDTQMPYKTTAQLTREYTTDAITGVHPHPSF 309
QY 310 TSTTWNNAFSAEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYMMWGWGHKLEPT 369
D 299 ASWNTWNNAPFSAEAAAIRSPHLLDFLEQVTIYSLLSRWNSNTQYMMWGWGHKLEPT 358
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DR	InterPro; IPR001178; Endotoxin.
DR	InterPro; IPR005638; endotoxin_C.
DR	InterPro; IPR005639; endotoxin_N.
DR	InterPro; IPR008979; Gal bind_Like.
DR	Pfam; PF03944; Endotoxin_C_1.
DR	Pfam; PF00555; Endotoxin_M_1.
DR	Pfam; PF03945; Endotoxin_N_1.
KW	Sporulation; Toxin.
FT	VARIANT 150 150 Y -> H (in strain HD-110).
SQ	SEQUENCE 1228 AA; 139647 MW; C8E3A19FB5D98575 CRC64;
	Query Match 59.8%; Score 2248.5; DB 1; Length 1228;
	Best Local Similarity 62.5%; Pred. No. 2.5e-148;
	Matches 448; Conservative 78; Mismatches 164; Indels 27; Gaps 8;
Qy	23 TDSLKNETDIELQNINH-----EDCLAKMSEVENVEPFSASTIQTGIGIAGKI 70
Dd	2 TSNRKNNEINAVNSHAQMLLPDARIEDSLCIAEGNNIDPFVASTVTGTGINIAGRI 61
Qy	71 LGTLGVFPAGVASLYSFILGELMPKGKNQWEILFMEHVEE-INQIKISTYARNKALTDLK 129
Dd	62 LGLVLGVFPAGQLASFYSFLVGELWPGRGDQWEI-FLEHVEQLINQQITENARTALARLQ 120
Qy	130 GLGDALAVYHDSLSBSWGVRNNTARSVVRRQYIALELMFVKQLPSFAVSSEEVPPLPIY 189
Dd	121 GLGDSFRAYQQSLSDWLENRDDARTSRVLYTQYIALELDLFNAMPLFAIRNQEVPELLMVY 180
Qy	190 AQAAHLHLLLRDAISIFCKEWGLASSETSTFYNRQVERAGYSDHCVKWYSTGLNNLRGT 249
Dd	181 AQAAHLHLLLRDASLGFSEFGLTSQEIQRTYERQVETRDYSDICVWYNITGLNSLRGT 240
Qy	250 NAEWSRVYRNPQRDMWTMLVDLVALFPSYDTQMYPKITTAQLTREVVYDAICTGVHPSPS 309
Dd	241 NAASWRYVQPRFDLTGLVDLVALFPSYDTRTPINTSAQLTREVVYDAIGAT--GYNM 298
Qy	310 TSTTWYNNAPSFSAIEAAVVRNPHLLDFLBQVTIYLSLLSWNSTQYNNMGCHKLERTP 369
Dd	299 ASMNWYNNAPSFSAIEAAAIRSPLLDFLBQLTIIFSASSRWNSNRHTMYRGHTIQSRP 358
Qy	370 IGGTLNISTQGSTNTSINPVTLPTSRDYRTESLAGNLNF--LTQPVGNGPRVDPFWKFE 427
Dd	359 IGGGLNTSTHGATNTSINPVTLRFASRDYRTESYAGVLLMGIIYLEPIHGVTYRFP-- 416
Qy	428 VTHP-----IASDNFYPYGVAGIGTQLODSENELPEPATGPNYESYSHRLSHIGLIAS 482
Dd	417 -TNQNISDRGTANYSQP-YESPGIQLDSETELPETTERPNYESYSHRLSHIGLIQS 474
Qy	483 HVKALVYSWTHRSADRTNTIPNSITQIPLKAFNLSSGAAVVRPGFTGGDILRRWTG 542
Dd	475 RVNVFVYSWTHRSADRTNTIGPNRITQIPMKASELPQGITTVVRGFGFTGGDILRRWTG 534
Qy	543 TFGDIRVINPPFAQRVRYRYASTDLQHFTSINGKAINGNFSATNMRCGEDLDYKTF 602
Dd	535 GFGPRIRVTWNGPLTQRYRIGFRYASTVDFPFVSRGGTTVNFRFRTWNSGDELUKNF 594
Qy	603 RTVGFTTPFSFLDVOSTFTIGAWNFSNGNEVVIDRIEFVPVMTVEAEYDFEKAEKVTA 662
Dd	595 VRRATFTTFTTQIODIRTSIQGLSGNGEVVIDKIEIIPVTATFEAEYDLERAQEAUNA 654
Qy	663 LFTSTNPRGLTKDVXKHIDIQVSNLVESIISDFYLDEKKRELPEIVKYIANELHIERNM 719
Dd	655 LFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKKRELLKVKYAKRLSDERNL 711
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ID Q93NM5	
AC Q93NM5	
DT 01-DEC-2001	(TrEMBLrel. 19, Created)
DT 01-DEC-2001	(TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004	(TrEMBLrel. 26, Last annotation update)
DE Cry1Ba	
GN Name=crv1Ba;	



Search completed: February 14, 2005, 20:40:33  
Job time : 84.1112 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:32:21 ; Search time 16.5835 seconds  
(without alignments)  
4171.616 Million cell updates/sec

Title: US-10-019-823B-58  
Perfect score: 3761  
Sequence: 1 MKLKNQDKHQSFSNAKVDK.....KRELFEIVKYANELHIERNM 719  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3724	99.0	719	2 I39814	insecticidal prote
2	3724	99.0	719	2 I39815	insecticidal prote
3	3715	98.8	719	2 S25383	parasporal crystal
4	3484	92.6	719	2 I40590	cryV465 protein -
5	2248.5	59.8	1228	2 S00873	parasporal crystal
6	1872	49.8	380	2 B42459	hypothetical prote
7	1466	39.0	1157	1 S49247	parasporal crystal
8	1458.5	38.8	1166	2 S32645	parasporal crystal
9	1450	38.6	1155	2 A26513	parasporal crystal
10	1449	38.5	1174	2 S32649	parasporal crystal
11	1443	38.4	1155	2 JD00012	parasporal crystal
12	1443	38.4	1156	2 A29125	parasporal crystal
13	1434	38.1	1155	2 I39838	parasporal crystal
14	1430.5	38.0	934	2 A22798	parasporal crystal
15	1429.5	38.0	1176	2 JT0241	parasporal crystal
16	1426	37.9	1155	2 S02134	parasporal crystal
17	1425.5	37.9	1181	2 A41052	parasporal crystal
18	1423.5	37.8	1176	2 JC2219	parasporal crystal
19	1419.5	37.7	1176	2 A22617	parasporal crystal
20	1419.5	37.7	1176	2 S02215	parasporal crystal
21	1338	35.6	1174	2 A42459	parasporal crystal
22	1334	35.2	1138	2 A48944	parasporal crystal
23	1315.5	35.0	1156	2 A29838	parasporal crystal
24	1304.5	34.7	823	2 S04181	parasporal crystal
25	1295.5	34.4	1189	2 S00944	parasporal crystal
26	1281	34.1	1154	2 S39536	parasporal crystal
27	1248	33.2	1171	2 I40572	parasporal crystal
28	1248	33.2	1171	2 A37829	parasporal crystal
29	1235	32.8	1176	2 A48970	parasporal crystal

30	1208	32.1	1160	2 S32647	parasporal crystal
31	1193.5	31.7	1165	2 S11446	parasporal crystal
32	1188.5	31.6	655	2 JC7140	procoxin - Bacillu
33	1172	31.2	1172	2 S32689	parasporal crystal
34	1154	30.7	1160	2 I40589	parasporal crystal
35	1139.5	30.3	1178	1 USBSXH	parasporal crystal
36	1139	30.3	1177	2 A49785	parasporal crystal
37	1137	30.2	652	2 A27323	parasporal crystal
38	1113	29.6	659	2 S10228	parasporal crystal
39	1080.5	28.7	652	2 I39811	parasporal crystal
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41	917	24.4	618	2 S11445	parasporal crystal
42	881	23.4	1156	2 S19306	parasporal crystal
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45	645	17.1	1180	2 I39870	parasporal crystal

RESULT 1  
I39814  
insecticidal protein cryV1 - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 26-Aug-1999  
C:Accession: I39814  
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis  
tomocidus.  
A:Reference number: I39814; MUID:95314293; PMID:7793960  
A:Accession: I39814  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:Cross-references: GB:L36338; NID:9540281; PIDN:AAC36999.1; PID:9540282  
C:Genetics:  
A:Gene: cryV1  
C:Superfamily: parasporal crystal protein

ALIGNMENTS

Query Match	99.0%;	Score 3724;	DB 2;	Length 719;
Best Local Similarity	99.4%;	Pred. No. 2.4e-254;		
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Db	1	MKLKNQDKHQSFSNAKVDKISTDSLKNETDLEQININHEDECLKNSEYENVEPVSASTI	60	
Qy	61	QTGIGIAGKILGTGVPPAGQVASYLSFTLGBELWPKGNQWEILFMEHVEE-INQKISTY	119	
Db	61	QTGIGIAGKILGTGVPPAGQVASYLSFTLGBELWPKGNQWEI-FMEHVEEINQKISTY	119	
Qy	120	ARNKALTDLKGIDALAVYHDSLESWGVGNRNTRARSVRSQYIALELMFVKQLPSFAVS	179	
Db	120	ARNKALTDLKGIDALAVYHDSLESWGVGNRNTRARSVRSQYIALELMFVKQLPSFAVS	179	
Qy	180	GREVPLLPYIAAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSYHCVKMY	239	
Db	180	GREVPLLPYIAAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSYHCVKMY	239	
Qy	240	STGLNLRGTAESWVRYNQFRDMTLMVLIDLVALFPSTQYPIKTTAQLTREYVYTD	299	
Db	240	STGLNLRGTAESWVRYNQFRDMTLMVLIDLVALFPSTQYPIKTTAQLTREYVYTD	299	
Qy	300	IGTVPHPSFTTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRNSNTQYNNM	359	
Db	300	IGTVPHPSFTTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRNSNTQYNNM	359	
Qy	360	WGSHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVP	419	
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QY	420	RVDPHKFEVTHPIASDNFFYPGYAGIGTQLODSENELPPBPAATQPNYESYSHRLSHIGLI	479
DB	420	RVDPHKFEVTHPIASDNFFYPGYAGIGTQLODSENELPPBPAATQPNYESYSHRLSHIGLI	479
QY	480	SASHVKALVYSWTHRSADRNTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT	539
DB	480	SASHVKALVYSWTHRSADRNTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT	539
QY	540	NTGTFGDIRVNNPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSAATMNRGDLDY	599
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QY	600	KTFRTVGTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK	659
DB	600	KTFRTVGTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK	659
QY	660	VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM	719
DB	660	VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM	719
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139815			
insecticidal protein cryV - Bacillus thuringiensis			
C:Species: Bacillus thuringiensis			
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004			
C:Accession: I39815			
R:Gleave, A.P.; Williams, R.; Hedges, R.J.			
Appl. Environ. Microbiol. 59, 1683-1687, 1993			
A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for			
iensis subsp. kurstaki			
A:Reference number: I39815; MUID:93298009; PMID:8517758			
A:Accession: I39815			
A>Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: DNA			
A:Residues: 1-719 <RES>			
A:Cross-references: UNIPROT:Q45752; GB:M98544; NID:g142767; PID:AAA22354.1; PID:g142766			
C:Genetics:			
A:Gene: cryV			
C:Superfamily: parasporal crystal protein			
Query Match' 99.0%; Score 3724; DB 2; Length 719;			
Best Local Similarity 99.3%; Pred. No. 2.4e-254;			
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;			
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DB	1	MLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCCLKMSEYENVEPFSASTI	60
QY	61	QTGIGIAGKILGTLGVPPAGQVASYLFGELWPKGNQWEILFMEHVEE-INQKISTY	119
DB	61	QTGIGIAGKILGTLGVPPAGQVASYLFGELWPKGNQWEI-FMEHVEEIIINQKISTY	119
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DB	120	ARNKALTDLKLGDALAVYHDSLESWGNRNNTARSVRSQYIALELMFVKQLPSFAVS	179
QY	180	GEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNROVERAGDYSCHVKWY	239
DB	180	GEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNROVERAGDYSCHVKWY	239
QY	240	STGLNNLRGTNAESWRYNQFRDWTLMVLVDLVALPFSYDTQMPYIKTTAQLTREYVTD	299
DB	240	STGLNNLRGTNAESWRYNQFRDWTLMVLVDLVALPFSYDTQMPYIKTTAQLTREYVTD	299
QY	300	IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNM	359
DB	300	IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNM	359
QY	360	WGGHKLFRITGGTINISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVP	419
DB	360	WGGHKLFRITGGTINISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVP	419

QY	420	RVDPHKFEVTHPIASDNFFYPGYAGIGTQLODSENELPPBPAATQPNYESYSHRLSHIGLI	479
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QY	480	SASHVKALVYSWTHRSADRNTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT	539
DB	480	SASHVKALVYSWTHRSADRNTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT	539
QY	540	NTGTFGDIRVNNPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSAATMNRGDLDY	599
DB	540	NTGTFGDIRVNNPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSAATMNRGDLDY	599
QY	600	KTFRTVGTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK	659
DB	600	KTFRTVGTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK	659
QY	660	VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM	719
DB	660	VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM	719
RESULT 3			
S25383			
parasporal crystal protein cryIIa1 - Bacillus thuringiensis			
N:Alternate names: delta-endotoxin; parasporal crystal protein cryV			
C:Species: Bacillus thuringiensis			
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004			
C:Accession: S25383			
R:Tailor, R.; Tippett, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.			
Mol. Microbiol. 6, 1211-1217, 1992			
A:Title: Identification and characterization of a novel Bacillus thuringiensis delta-end			
A:Reference number: S25383; MUID:92269582; PMID:1588820			
A:Accession: S25383			
A:Molecule type: DNA			
A:Residues: 1-719 <TAI>			
A:Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:g40289; PID:CAA44633.1; PID:g40290			
C:Genetics:			
A:Gene: cryV			
C:Superfamily: parasporal crystal protein			
C:Keywords: delta-endotoxin			
Query Match 98.8%; Score 3715; DB 2; Length 719;			
Best Local Similarity 99.2%; Pred. No. 1.1e-253;			
Matches 714; Conservative 2; Mismatches 2; Indels 2; Gaps 2;			
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QY	61	QTGIGIAGKILGTLGVPPAGQVASYLFGELWPKGNQWEILFMEHVEE-INQKISTY	119
DB	61	QTGIGIAGKILGTLGVPPAGQVASYLFGELWPKGNQWEI-FMEHVEEIIINQKISTY	119
QY	120	ARNKALTDLKLGDALAVYHDSLESWGNRNNTARSVRSQYIALELMFVKQLPSFAVS	179
DB	120	ARNKALTDLKLGDALAVYHDSLESWGNRNNTARSVRSQYIALELMFVKQLPSFAVS	179
QY	180	GEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNROVERAGDYSCHVKWY	239
DB	180	GEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNROVERAGDYSCHVKWY	239
QY	240	STGLNNLRGTNAESWRYNQFRDWTLMVLVDLVALPFSYDTQMPYIKTTAQLTREYVTD	299
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QY	300	IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNM	359
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QY 480 SASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539  
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QY 660 VTALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDRYLDEKRELFEIVKYANLHIERNM 719  
DB 660 VTALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDRYLDEKRELFEIVKYANLHIERNM 719

RESULT 4  
I40590  
cryV465 protein - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: I40590  
R.Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis  
tomocidus.  
A:Reference number: I39814; MUID:95314293; PMID:7793960  
A:Accession: I40590  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:G467234; PIDN:AAA82114.1; PID:G4672  
C:Gene: cryV465  
C:Superfamily: parasporal crystal protein

Query Match 92.8%; Score 3484; DB 2; Length 719;  
Best Local Similarity 92.2%; Pred. No. 2e-237;  
Matches 664; Conservative 33; Mismatches 21; Indels 2; Gaps 2;  
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DB 120 ARNKALSDRLGIDALAVHDSLESWGNRNTRARSVRSQVIALELMFVKQLPSFAVS 179  
QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQYERAGDYSCHCVKXY 239  
DB 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQYERTRDYSCHICKY 239  
QY 240 STGLNNLRGTNAESWRYNQFRDMLTLMVLDLVALPSPYDTQMPYIKTTAQLTREYVYTD 299  
DB 240 NTGLNNLRGTNAESWRYNQFRDMLTLMVLDLVALPSPYDTLYPKTTSQLTREYVYTD 299  
QY 300 IGVTHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMM 359  
DB 300 IGVTHPQAFSTWYNNAPSAIEAAVIRPHLLDFLEKVTIYSLSRWSNTQYMM 359  
QY 360 WGGHKLFEFTIGCTINISQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLTOPVNGVP 419  
DB 360 WGGHRLRESPIGGALNTSQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLTOPVNGVP 419

QY 420 RVDFAHFKVTHPIASDNFFYPGAGICTQLQDSENELPPEATGQPNYESYSHRLSHIGLI 479  
DB 420 RVDFAHFKVTHPIASDNFFYPGAGICTQLQDSENELPPEATGQPNYESYSHRLSHIGLI 479  
QY 480 SASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539  
DB 480 SASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539  
QY 540 NTGTGDIRVNINPPFAQRYRIRIYASTTDLQFHTSINGKAINQGNFSATWNRGDLDY 599  
DB 540 NTGTGDIRVNINPPFAQRYRIRIYASTTDLQFHTSINGKAINQGNFSATWNRGDLDY 599  
QY 600 KTFRTVGTPTPSFLDVQSTFTIGAWNFSNGEVYIDRIEFVPEVYVTEAEYDFFKAQEK 659  
DB 600 KTFRTVGTPTPSFLDVQSTFTIGAWNFSNGEVYIDRIEFVPEVYVTEAEYDFFKAQEK 659  
QY 660 VTALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDRYLDEKRELFEIVKYANLHIERNM 719  
DB 660 VTALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDRYLDEKRELFEIVKYANLHIERNM 719

RESULT 5  
S00873  
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis  
N:Alternate names: parasporal crystal protein cryA4  
C:Species: Bacillus thuringiensis subsp. thuringiensis  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C:Accession: S00873  
R.Brizzard, B.L.; Whiteley, H.R.  
Nucleic Acids Res. 16, 2723-2724, 1988  
A:Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus  
A:Reference number: S00873; MUID:88203216; PMID:3362680  
A:Accession: S00873  
A:Molecule type: DNA  
A:Residues: 1-1228 <BRI>  
A:Cross-references: UNIPROT:P05517; EMBL:X06711; NID:G40264; PIDN:CAA29898.1; PID:G58094  
C:Genetics:  
A:Gene: cryA4  
A:Start codon: TTG  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin  
Query Match 59.8%; Score 2248.5; DB 2; Length 1228;  
Best Local Similarity 62.5%; Pred. No. 5.7e-150;  
Matches 448; Conservative 78; Mismatches 164; Indels 27; Gaps 8;  
QY 23 TDSLKNETDIELQINHH-----EDCLKSEYENVRPFVSASTIQTGIGIAGKI 70  
DB 2 TSNRKNENSIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQGTINAGRI 61  
QY 71 LGTLGVPPFAGQVASYLSFILGELWPKGKQWEILFMEHVEE-INQKISTYARNKALTDLK 129  
DB 62 LGVLGVPPFAGQASLYSFILGELWPRGRDQWEI-FLEHVEQLINQOITENARNALARLQ 120  
QY 130 GLGDALAVHDSLESWGNRNTRARSVRSQVIALELMFVKQLPSFAVSGEEVPLPIY 189  
DB 121 GLGDSFRAYQOQSLDQWLENRDDARTSRVLYTQVIALELFLNAMPFLAIRNQEVPLIMVY 180  
QY 190 AQAAHLHLLLRDASIFGKEWGLSSSEISTFFYNQYERAGDYSCHCVKXYSGTGLNNLRGT 249  
DB 181 AQAAHLHLLLRDASLFGSEFGLTQSEIQRYERQYERTRDYSYCVWYNTGLNLRGT 240  
QY 250 NAESWRYNQFRDMLTLMVLDLVALPSPYDTQMPYIKTTAQLTREYVYTDVGVTHPHPSF 309  
DB 241 NAASWRYNQFRDMLTLMVLDLVALPSPYDTTYPTINTSAQLTREYVYTDVGVTHPHPSF 298  
QY 310 TSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMWGGHKLFEFT 359  
DB 299 ASMWYNNAPSAIEAAVIRPHLLDFLEQVTIYSLSRWSNTQYMMWGGHKLFEFT 358  
QY 370 IGTGLNISQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLTOPVNGVPRVDHFWKF 427  
DB 359 IGGGLNTSTHGATNTSINPVTLPFTSRDVRVRESYAGVLLWGLYLEPIHGVPTVRNF-- 416



Db 708 QYGHDKKMLLEAVRAAKRLSRERNL 732

RESULT 8  
S32645  
parasporal crystal protein crylGal - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S32645  
R:Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A:Reference number: S32645  
A:Accession: S32645  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1166 <LAMB>  
A:Cross-references: UNIPROT:Q45746; EMBL:Z22510; NID:g295861; PIDN:CAA80233.1; PID:g2958  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 38.8%; Score 1458.5; DB 2; Length 1166;  
Best Local Similarity 46.2%; Pred. No. 2.5e-94;  
Matches 326; Conservative 97; Mismatches 206; Indels 77; Gaps 19;

QY 41 DCLMSEYE-----NVPPFVSASTIQGIGIAGKILGTGLGVPPAGQVASLYSFTILGELWPK 96  
Db 13 NCLNPESEIFNARNNGFLVSVSSGL---TRFLLEAAVPEAGFALGLFDIIWGAL--- 66

QY 97 GKQWEILFMEHVEE--INQKISTYARKKALTDLKGLGDALAVYHDSLESWGNRRAR 155  
Db 67 GVDQWS-LFRLQIEQIROEITELERNRATILTGSSSYNLVYEAALREWENDPNPASQ 125

QY 156 SVRSOYIALEMFVOKLPSFAVSGBEVPLPIYAQAANLHLLLRDASIFGKEMGLSS 215  
Db 126 ERVTRFRLTDDAIVTGLPLAIRNLEVNLSVYTOANLHLSLRDADVFERWGLTQA 185

QY 216 EISTFYNRQVERAGDYSDHCKWYSYGLNNLRGTNAESWRYNQFRDRTMLMVLVDIALVP 275  
Db 186 NIEDLYTRLTNITQEYSDHCAWYNOCLNEIGISR---RYLDFORDLTISVLVDIALVP 241

QY 276 PSYDTQWYPIKTTAQLTREYVTDAL--GTVHPHPSFTSTTWNNNAPSFAIEAAVRNP 333  
Db 242 PNYDIIRTPYPTQSTQREIYTPVVGNI-----NFGLSIANVLRAP 284

QY 334 HLIDFLEQVITYSLLSRWSNTQYMMWGGHKLFRITIG-GLTN-----ISTQGSTNT 384  
Db 285 HLMDFIDRIVYNSVR--STPY--WAGEHVISRKTGOGQNEIRPPLYGAANAEPV 339

QY 385 SINPVTLPFTSRDVRYES-----LAGNLFLTQPVNGVPRVDFHWKFTVTHPIASDNFY 438  
Db 340 TIRPTGFTDEQRQWYRARSRVSVFRSSGQDFSLVDVAVG-----FLT-IFSAVSIV 388

QY 439 YPGYAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLISAS-----HVKALVSWTH 493  
Db 389 RNGF-GFNT---DTIDEIPIEGTDP--FTGYSHRLCHVGFLASSPFIQYARAPIESWTH 442

QY 494 RSADRTNTTIPNSITQIPLVKAFNLSSGAAVRPGFTGGDILRRNTGTGFDIRVNI 553  
Db 443 RSATLNTWTAPDVITQIPLVKAFNLHSGATVKGPGFTGGDILRRNTVSGFGDMRNI 502

QY 554 PFAQRVVRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGTFTPPFP 613  
Db 503 PLSQRVVRIRYASTTDLQFYTNINGTTINIGNFSSTMSDGDLDLQGRFVRVAGFTTPTTF 562

QY 614 LDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVITYEAEYDEFAKAEKVLTALFTSTNPR 673  
Db 563 SDANSTFTIGAFGSPNNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNALFTSSNOIGLK 622

QY 674 TDVKDYHIDQVSNLVESLSDYFLDEKRELFEIVKYVANELHIERNM 719  
Db 623 TDVTDYHIDQVSNLVESLSDYFLDEKRELFEIVKYVANELHIERNM 668

RESULT 9  
A26513  
parasporal crystal protein - Bacillus thuringiensis (strain aizawai)  
C:Species: Bacillus thuringiensis  
C:Date: 11-Mar-1988 #sequence\_revision 11-Mar-1988 #text\_change 09-Jul-2004  
C:Accession: A26513  
R:Oeda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H.  
Gene 53, 113-119, 1987  
A:Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis  
A:Reference number: A26513; MUID:87248103; PMID:3297927  
A:Accession: A26513  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1155 <OED>  
A:Cross-references: UNIPROT:P06578; GB:M16463; NID:g143098; PIDN:AAA22551.1; PID:g143099  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 38.6%; Score 1450; DB 2; Length 1155;  
Best Local Similarity 44.1%; Pred. No. 9.8e-94;  
Matches 313; Conservative 110; Mismatches 232; Indels 54; Gaps 12;

QY 36 NINHEDCLKMSYENVE-PFVSASTIQG-----IGIAGKILGTGLGVPPAGQVASLYS 87  
Db 4 NNINIECPYNCLSNPEVEVLGGERIETGYTIDISLSTQTLLEF-VPGAGFVLGLVD 62

QY 88 FTILGELWPKGKQWEILFMEHVEEINQKISTYARKKALTDLKGLGDALAVYHDSLESWVG 147  
Db 63 ILWGIYF---GPSQWDAFLVQIEQLNQRLEEERARQAIISRLSGLSNLYQIYAESPREMEA 119

QY 148 NNNTRARSVRSQYIALEMFVOKLPSPAVSGEVEPLPIYAQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREEMRIQDNMNSALTTPAIPAVQNYQVPLLSVYVQAANLHLSVLRDVSVEG 179

QY 208 KEMGLSSSEISTFYNRQVERAGDYSDHCKWYSTGLNNLRGTNAESWRYNQFRDRTMLM 267  
Db 180 QRWGDEAATINRYNDLTRLIGNYDDHAVRNTYGLERVMGPDSDRWIRYNFRRELTLT 239

QY 268 VLIDLVALPSTQWYPIKTTAQLTREYVTDALGTVHPHPSFTSTTWNNNAPSFAIEA 327  
Db 240 VLDIVSLFENYDSRYPIRTVSQLTIREIYNFV-----LENFSGSPRALAQ 285

QY 328 AV---VRNPHLLDFLEQVITYSLLSR-----WNTQYMMN---WGGHKLFRITIGTLNIS 377  
Db 286 GIEGSIKSHPLMDILNSITITDAHREYYSWGHQIMASPVGSGPEFTPLYGTMGNA 345

QY 378 TQGSTNTSINPVTLPFTSRDVRYESLAGNLFLTQPVNGVPRVDFHWKFTVTHPIASDNF 437  
Db 346 POORIVAQGGQGVYRTLSSTLYRRPFNIGIN---NQQLSVLDGTGEFAYG-----TSSNL 396

QY 438 YYPGVAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLI-----SASHVKALVYS 490  
Db 397 PSAVYKSGT--VDSLDEIPQNNVPPRQGSRLSHLSVMSFRSGFSNSVSIIRAPMS 454

QY 491 WTHRSADRTNTTIPNSITQIPLVKAFNLSSGAAVRPGFTGGDILRRNTGTGFDIRVN 550  
Db 455 WTHRSAEFNIIIPSSQITQIPLTKSTNLGSGTSVVKPGFTGGDILRRTSPOGI 514

QY 551 INPPFAQRVVRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGTFTTP 610  
Db 515 ITAPLSQRVVRIRYASTTDLQPHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGTFTTP 574

QY 611 PSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVITYEAEYDEFAKAEKVLTALFTSTNPR 670  
Db 575 PNFSGSSVFTLSAHVFNSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQI 634

QY 671 GLKTDVYHIDQVSNLVESLSDYFLDEKRELFEIVKYVANELHIERNM 719  
Db 635 GLKTDVYHIDQVSNLVESLSDYFLDEKRELFEIVKYVANELHIERNM 683

RESULT 10  
S32649

paraesporal crystal protein cryIFa3 - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S32649  
R:Jambert, B.  
Submitted to the EMBL Data Library, April 1993  
A:Reference number: S32645  
A:Accession: S32649  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1174 <LAM>  
A:Cross-references: UNIPROT:Q45749; EMBL:Z22512; NID:G295865; PIDN:CAA80235.1; PID:G29586  
C:Superfamily: paraesporal crystal protein  
C:Keywords: delta-endotoxin

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Query Match      38.5%; Score 1449; DB 2; Length 1174;
Best Local Similarity 44.5%; Pred. No. 1.2e-93;
Matches 323; Conservative 100; Mismatches 207; Indels 96; Gaps 17;

QY 36 NINHE---DCLKMEYENVEPFVSASTIQTGIGIA-GKILGTGLGVPPAGQVASLYSFIL 90
Db 4 NIQCVPVNCLSNEPEVILSEERSTGRPLDLSLSTRFLLSFPVPGVGVAFLGLI 63

QY 91 GELWPKGNQKQWEILFMEHVEEINQKISTYARNKALTDLKGDLALVYHDSLSWGNRN 150
Db 64 GFITP---SEWSLFLQIEQRIETLERNAITTLRGLADSVYVLEALREWEENPN 120

QY 151 NTRARSVRSOYIALELMFVKLPFAVSGEVPLPIYAQAANLHLLLRDASIFGKEW 210
Db 121 NAQLREDVIRFANTDDALITAINFTLTSFEIPLLSVYQAANLHLLSLDVAVSFGQW 180

QY 211 GLSSEISTFYNRQVERAGDSDHCVKWYSTGLNLRGTNAESVWRVNRQFRDMLVLD 270
Db 181 GLDIATVNNRLINLHRTVTEHCLDYNQGLENLRTNTRQWRFNRQFRELTLVLD 240

QY 271 LVALPSPDVTOMPKITTAQITREYVTDATGVHPHSFTTWNWNNAPS-PSAIAAV 329
Db 241 IVALLFPNDARAYPIQTSQLTREIYTSV--IEDSP-----VSANIPNGFNRAEFG- 290

QY 330 VRNPHLLDFLEQVITYISLSRWSNTQVMNMGHKLERTTIGTTLNISTQGSTNTSNPV 389
Db 291 VRPHLMDPMN-----SLFVTAETVRSQTWNGHLV-----SSRTAGNPI 331

QY 390 TLPF-----TSRDVYRTESLAGNLFLTQPVNGVPRVDFHMKFVTHPIAS 434
Db 332 NFPIYGIENPGGAIWADEDPFPVFT-----LSDPV-----FVRGGFGN 371

QY 435 DNFIYPGAGTGTQLQ-----DSENLPEATGQPNYESYSHRLSHI----- 476
Db 372 PH-VYLGURGVAFOQTGNHTRTFRNSGTIDSLDEIPQDNSGAPWNDYSHVLNHTVFR 430

QY 477 --GLISASHV-KALVYSWTHRSADRTNIEPNSITQPLVKAFLNSGAAVVRGPGTGG 533
Db 431 WPGELAGSDSWRAPMFSWTHRSADRTNIEPNSITQPLVKAFLNHSGSTVVRGPGTGG 490

QY 534 DILARTNTGTTGDIRVNIIPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNR 593
Db 491 DLLARTNTGTADIRVNIITGLSQRYRIRYASTTDLQFTRINGTSVNGNFORTMNR 550

QY 594 GEDLDYKTRFVGTTPPSFLDVOSTFTTIGAWNSSGNEVYIDRIEFVPEVTVTEAYDF 653
Db 551 GGNLESNGFRFAGSTPPSFNSAOSTFTLGTQAFSN-OEVYIDRIEFVPAEVTPEASDL 609

QY 654 EKAQEKVYALTSTNPRGLKTDVVDYHIDQVSNLVSLSDFYLDKRELFVEIKVYANEL 713
Db 610 ERAQKAVNALFTSTSQLGKTNVTGYHLDQVSNLVACLSDFCFLDKRELSSEKVKHAKRL 669

QY 714 HIERNM 719
Db 670 SDRKRL 675
```

RESULT 11

JD00002  
paraesporal crystal protein cryIAb3 - Bacillus thuringiensis  
N:Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal protein  
C:Species: Bacillus thuringiensis  
C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 09-Jul-2004  
C:Accession: A90025; A91560; A90955; S14555; A24172; A29043; JD00002  
R:Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.  
Agric. Biol. Chem. 51, 455-463, 1987  
A:Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from  
A:Reference number: A90025  
A:Accession: A90025  
A:Molecule type: mRNA  
A:Residues: 1-1155 <KON>  
A:Cross-references: UNIPROT:P06578  
A:Experimental source: subsp. kurstaki  
R:Geiser, M.; Schweitzer, S.; Grimm, C.  
Gene 48, 109-118, 1986  
A:Title: The hypervariable region in the genes coding for entomopathogenic crystal proteins  
A:Reference number: A91560; MUID:87163505; PMID:3557124  
A:Accession: A91560  
A:Molecule type: DNA  
A:Residues: 1-1155 <GEI>  
A:Cross-references: GB:M15271; NID:G143123; PIDN:AAA22561.1; PID:G143124  
A:Experimental source: subsp. kurstaki  
R:Mabiko, H.; Raymond, K.C.; Bulla Jr., L.A.  
DNA 5, 305-314, 1986  
A:Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product analysis  
A:Reference number: A90955; MUID:86300092; PMID:3743328  
A:Accession: A90955  
A:Molecule type: DNA  
A:Residues: 1-1155 <WAB>  
A:Cross-references: GB:M13898; NID:G142719; PIDN:AAA22330.1; PID:G142720  
A:Experimental source: subsp. berliner  
R:Chak, K.P.; Jen, J.C.  
submitted to the EMBL Data Library, October 1990  
A:Description: Complete nucleotide sequence and expression in Escherichia coli of a cry  
A:Reference number: S14555  
A:Accession: S14555  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1155 <CHA>  
A:Cross-references: EMBL:X54939; NID:G40272; PIDN:CAA38701.1; PID:G40273  
R:Hofte, H.; de Greve, H.; Seurinck, J.; Janssens, S.; Mahillon, J.; Ampe, C.; Vandekerckh  
Eur. J. Biochem. 161, 273-280, 1986  
A:Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thur  
A:Reference number: A26461; MUID:87054026; PMID:3023091  
A:Accession: A26461  
A:Molecule type: DNA  
A:Residues: 1-730, 'L', 732-784, 'R', 786-1155 <HOF>  
A:Cross-references: GB:X04698; NID:G40254; PIDN:CAA28405.1; PID:G40255  
A:Experimental source: strain berliner 1715  
C:Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.  
C:Genetics:  
A:Gene: cry-1-2; bt2  
C:Superfamily: paraesporal crystal protein  
C:Keywords: delta-endotoxin  
F:82-586/Product: toxic peptide #status predicted <TXP>  
F:82-300/Region: toxic #status predicted  
F:300-586/Region: insecticidal #status predicted  
Query Match 38.4%; Score 1443; DB 2; Length 1155;  
Best Local Similarity 44.2%; Pred. No. 3.1e-93;  
Matches 314; Conservative 109; Mismatches 231; Indels 56; Gaps 13;  
QY 36 NINHECLKMEYENVE-PFVSASTIQTG-----IGIAGKILGTGLGVPPAGQVASLYS 87  
Db 4 NPINECIPVNCLSNPEVEVLGGERIETGYTPIDISLSTQFLSEF-VPGAGFVLGLVD 62  
QY 88 FILGELWPKGNQWEILFMEHVEEINQKISTYARNKALTDLKGDLALVYHDSLSWVG 147  
Db 63 IIWGIF--GPSQWDAFLVQIEQLINQRIEFPARNQAISRLGSLNLYQIYAESFREWEA 119  
QY 148 NRNNTARSVRSOYIALELMFVKLPFAVSGEVPLPIYAQAANLHLLLRDASIFG 207



Db 120 DPTNPALREEMRIQFNDMSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFG 179  
Qy 208 KEWGLSSSEISTFYNRQVRAGDYSCHVKWYKSTGLNNLRGTNAESWVRYNQPRRDTLM 267  
Db 180 QRWGFDAATINSYNDLTRLIGNYTDHVRWYNTGLERWGPDSRDWRYNQPRRELTIT 239  
Qy 268 VLDLVALPSPYDTOMYPIKTAQTLREVYTDAGTGVHPHPSFTSTTWYNNAPSP-----S 323  
Db 240 VLDIVSLFPNYSRTYPIRTVSQLTREIYNTPV-----LENFDGSPRGSQAQ 285  
Qy 324 AIEAAVVRNPHLLDFLEQVTIYSLLSR-----WSNTQYMMN---WGHKLEFRTIGTGLNI 376  
Db 286 GIEGS-IRSPHLMIDLINSITITDAHRGEYVWSGHQIMASPVGFSGPBETFPFLYGTMGNA 344  
Qy 377 STQGSTNTSINPVTLPFTSRDVRYESLAGNLFLTPQVNGVPRVDFHMKFVTHPIASDN 436  
Db 345 APOORIVAQLGGQVYRTLSLTYRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSN 395  
Qy 437 FYYPGAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI-----SASHVKALVY 489  
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMF 453  
Qy 490 SWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGTGDIRV 549  
Db 454 SWTHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKPGFTGGDILRRTSPQISTLRV 513  
Qy 550 NINPPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDBLDYKTPRTVGF 609  
Db 514 NITAPLSQRVVRIRYASTTNLQFHTSIDGRPINQGNFSAATMSSGNLQSGSPRTVGF 573  
Qy 610 PFSFLDVQSTFTTICANFSSGNEVYIDRIEFVPEVYEAEDYFEKAQEKVATLFTSTNP 669  
Db 574 PFNFSNGSVFTLSAHVFNSEVYIDRIEFVPAEVTFEAEYDLERAQAVNELFTSSNQ 633  
Qy 670 RGLKTDVKDHYHDQVNLVESLDEFLDKRELFEIVKYANLHIERNM 719  
Db 634 IGLKTDVTDYHIDQVNLVECLSDPECLDEKSELSEKVKHAKLSDERNL 683

RESULT 12  
A29125  
parasporal crystal protein Bt2 - Bacillus thuringiensis subsp. kurstaki (strain HD-1)  
C;Species: Bacillus thuringiensis  
C;Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 09-Jul-2004  
C;Accession: A29125  
R;Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederm  
Bio/Technology 5, 807-813, 1987  
A;Title: Insect tolerant transgenic tomato plants.  
A;Reference number: A29125  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-1156 <PIS>  
A;Cross-references: UNIPROT:Q9P296; UNIPROT:Q93T21  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 38.4%; Score 1443; DB 2; Length 1156;  
Best Local Similarity 44.2%; Pred. No. 3.1e-93;  
Matches 314; Conservative 109; Mismatches 231; Indels 56; Gaps 13;  
Qy 36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTIGVFPAGQVSLYS 87  
Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGVTPTIDISLSLTQFLSEP-VPGAFVGLVD 62  
Qy 88 FILGELMPKGNQWEILFMHEVBEINQKISTYARNKALTDKGLGDALAYHYHDSLSWVG 147  
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFARNQAIISLEGLSNLYQIYAESFREW 119  
Qy 148 NNNTRARSVVRQYIALEMLFVQKLPSPAVSGEEVPLLPYIAQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFG 179

Qy 208 KEWGLSSSEISTFYNRQVRAGDYSCHVKWYKSTGLNNLRGTNAESWVRYNQPRRDTLM 267  
Db 180 QRWGFDAATINSYNDLTRLIGNYTDHVRWYNTGLERWGPDSRDWRYNQPRRELTIT 239  
Qy 268 VLDLVALPSPYDTOMYPIKTAQTLREVYTDAGTGVHPHPSFTSTTWYNNAPSP-----S 323  
Db 240 VLDIVSLFPNYSRTYPIRTVSQLTREIYNTPV-----LENFDGSPRGSQAQ 285  
Qy 324 AIEAAVVRNPHLLDFLEQVTIYSLLSR-----WSNTQYMMN---WGHKLEFRTIGTGLNI 376  
Db 286 GIEGS-IRSPHLMIDLINSITITDAHRGEYVWSGHQIMASPVGFSGPBETFPFLYGTMGNA 344  
Qy 377 STQGSTNTSINPVTLPFTSRDVRYESLAGNLFLTPQVNGVPRVDFHMKFVTHPIASON 436  
Db 345 APOORIVAQLGGQVYRTLSLTYRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSN 395  
Qy 437 FYYPGAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI-----SASHVKALVY 489  
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMF 453  
Qy 490 SWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGTGDIRV 549  
Db 454 SWTHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKPGFTGGDILRRTSPQISTLRV 513  
Qy 550 NINPPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDBLDYKTPRTVGF 609  
Db 514 NITAPLSQRVVRIRYASTTNLQFHTSIDGRPINQGNFSAATMSSGNLQSGSPRTVGF 573  
Qy 610 PFSFLDVQSTFTTICANFSSGNEVYIDRIEFVPEVYEAEDYFEKAQEKVATLFTSTNP 669  
Db 574 PFNFSNGSVFTLSAHVFNSEVYIDRIEFVPAEVTFEAEYDLERAQAVNELFTSSNQ 633  
Qy 670 RGLKTDVKDHYHDQVNLVESLDEFLDKRELFEIVKYANLHIERNM 719  
Db 634 IGLKTDVTDYHIDQVNLVECLSDPECLDEKSELSEKVKHAKLSDERNL 683

RESULT 13  
I39838  
parasporal crystal protein - Bacillus thuringiensis  
C;Species: Bacillus thuringiensis  
C;Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I39838  
R;Hefford, M.A.; Brousseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J.A.; Lau, P.C.K.  
J. Biotechnol. 6, 307-322, 1987  
A;Title: Sequence of a lepidopteran toxin gene of Bacillus thuringiensis subsp kurstaki  
A;Reference number: I39838  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1155 <RES>  
A;Cross-references: UNIPROT:P06578; GB:M37263; NID:g142885; PIDN:AAA22420.1; PID:g142886  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 38.1%; Score 1434; DB 2; Length 1155;  
Best Local Similarity 44.1%; Pred. No. 1.3e-92;  
Matches 313; Conservative 109; Mismatches 232; Indels 56; Gaps 13;  
Qy 36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTIGVFPAGQVSLYS 87  
Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGVTPTIDISLSLTQFLSEP-VPGAFVGLVD 62  
Qy 88 FILGELMPKGNQWEILFMHEVBEINQKISTYARNKALTDKGLGDALAYHYHDSLSWVG 147  
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFARNQAIISLEGLSNLYQIYAESFREW 119  
Qy 148 NNNTRARSVVRQYIALEMLFVQKLPSPAVSGEEVPLLPYIAQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFG 179  
Qy 208 KEWGLSSSEISTFYNRQVRAGDYSCHVKWYKSTGLNNLRGTNAESWVRYNQPRRDTLM 267

Db 180 QRWGFDATINSRYNDLTRIGNYTDHVAWYNTGLERWGPDSRDWIRYNQFRELTLT 239  
Qy 268 VLDLVALFPSTQMYPIKTAQLTREVYTDAGTGVHPHPSFTTTWNNAPSFAIEA 327  
Db 240 VLDLVALFSYDSSRRPIRTVSQLTREIYNPV-----LENFDSFRGMAQ 285  
Qy 328 AV---VRNPHLLDFLEQVITYSLLSRWSNTQYNNMGGHKLFRRTIGGT---LNISSQS 381  
Db 286 RIEQNIRQPHLMDILNRIITYTDVHRG-----FNYWSGHQITASPVGSGPEFAFLFGN 340  
Qy 382 TMTSIMPVTLPTFSRDVYTESL-----AGLNLFTQPVNGVPRVDVPHKVFTHPI 432  
Db 341 AGNAAPVLSLGLGIFRTLSPLRYRILGSGPN---NQELFVLDGTGFSASLTNLT 397  
Qy 433 ASDNFYYPGAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISAS-----HYKAL 487  
Db 398 PSTIYRQRTV-----DSLVDIIPQDNSVPPRAGFSHLSHVMTLSQAAGAVYTLRAP 450  
Qy 488 VYSWTHRSADRTWTIPNSITQIPLVKAFNLSSGAAVRGPFTGGDIILRTNTGTFGDIRV 549  
Db 451 TFSWQHRSABFNIIIPSSQITQIPLTKSTNLGSGTSVVKGPFTGGDIILRTSPGQISTL 510  
Qy 548 RVNINPPFAQRYRIRYASTTDLQPHSTINGKAINQGNFSAATMNGEDLDYKTRTVGF 607  
Db 511 RVNITAPLSQRYRIRYASTTDLQPHSTIDGRPINQGNFSAATMNGEDLDYKTRTVGF 570  
Qy 608 TTPFSLDVQSTTIGAWNFSSGNEVYIDRIEFPVPEVTEYAEYDFEKAQKVYALFTST 667  
Db 571 TTPFNSGSSVFTLSAHVNSGNEVYIDRIEFPVPAEVTFAEYDLERAKAVNELFTSS 630  
Qy 668 NPGLKTDVYHIDQVSNLVECLSDFECLDEKELSEKVKHAKRLSDERNL 719  
Db 631 NQGLKTDVYHIDQVSNLVECLSDFECLDEKELSEKVKHAKRLSDERNL 682

## RESULT 15

JT0241

parasporal crystal protein - *Bacillus thuringiensis* (strain aizawai IPL7)  
N;Alternate names: 135K insecticidal protein

C;Species: *Bacillus thuringiensis*

C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004

C;Accession: JT0241

R;Shimizu, M.; Ohie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.

Agricult. Biol. Chem. 52, 1563-1573, 1988

A;Title: Cloning and expression in *Escherichia coli* of the 135-kDa insecticidal protein

A;Reference number: JT0241

A;Accession: JT0241

A;Molecule type: DNA

A;Residues: 1-1176 &lt;SHI&gt;

A;Cross-references: UNIPROT:P02965

A;Note: *B. thuringiensis* aizawai IPL7 produces similar 130K and 135K insecticidal proteinC;Comment: The 135K protein has insecticidal activity against *Plutella xylostella* larvae

C;Superfamily: parasporal crystal protein

C;Keywords: delta-endotoxin

Query Match 38.0%; Score 1430.5; DB 2; Length 934;  
Best Local Similarity 43.3%; Pred. No. 1.7e-92;  
Matches 308; Conservative 116; Mismatches 227; Indels 61; Gaps 12;

Qy 36 NINHECLKMEYENVE-PFVSASTIQTG-----IGIAGKILGTLGVPPAGOVASLYS 87  
Db 4 NPNINECPYCNLSNPEVEVIGGERIETGYTPIDISLSTQFLUSEP-VPGAGFVLGLVD 62  
Qy 88 FILGELMPKGNQWEILFMEHVEEINQKISTYARNKALTDLKLGDALAVYHDSLSWVG 147  
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFAFNQALSRLEGLSNLYQIYAESFREWEA 119  
Qy 148 NRNNTRARSVRSQVIALELMFVKQLPSFAVSGEVEPLLPYIAQAANHLILLDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMNSALTTPALPLFAVQNYQVPLLSVYVQAANHLISLVDRDSVFG 179  
Qy 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNLRCTNAESWVRYNQFRRDWTLM 267  
Db 180 QRWGFDATINSRYNDLTRIGNYTDHVAWYNTGLERWGPDSRDWIRYNQFRELTLT 239

## RESULT 14

A22798

parasporal crystal protein - *Bacillus thuringiensis*C;Species: *Bacillus thuringiensis*

C;Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 09-Jul-2004

C;Accession: A22798

R;Shibano, Y.; Yamagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, M.

Gene 34, 243-251, 1985

A;Title: Nucleotide sequence coding for the insecticidal fragment of the *Bacillus thuringiensis* delta-endotoxin

A;Reference number: A22798; MUID:85232070; PMID:2989108

A;Accession: A22798

A;Molecule type: DNA

A;Residues: 1-934 &lt;SHI&gt;

A;Cross-references: UNIPROT:Q98SV8; GB:M10917; NID:g143100; PIDN:AAA22552.1; PID:g551713

C;Comment: The authors translated the codon ACA for residue 264 as Ser.

C;Superfamily: parasporal crystal protein

C;Keywords: delta-endotoxin



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2005, 20:22:09 ; Search time 60.0945 Seconds  
(without alignments)  
3909.384 Million cell updates/sec

Title: US-10-019-823B-58  
Perfect score: 3761  
Sequence: 1 MKLKNQDKHQSPSSNAKVDK.....KRELFEIVKYANELHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA.\*
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  - 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
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  - 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
  - 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3724	99.0	719	16	US-10-782-020-10
2	3724	99.0	719	16	US-10-782-141-8
3	3442.5	91.5	710	15	US-10-428-961-42
4	2250.5	59.8	1228	16	US-10-809-953-10
5	2236.5	59.5	1207	10	US-09-988-462-7
6	2157.5	57.4	1227	15	US-10-428-961-63
7	2142.5	57.0	1186	9	US-09-826-660-23
8	2087	55.5	1228	15	US-10-428-961-38
9	2087	55.5	1228	15	US-10-614-524-2
10	1909.5	50.8	643	9	US-09-826-660-25
11	1694.5	45.1	1167	14	US-10-089-678-1
12	1658.5	44.1	653	15	US-10-428-961-6
13	1643.5	43.7	1157	16	US-10-782-141-16

14	1485	39.5	1206	13	US-10-032-717-2	Sequence 2, Appli
15	1485	39.5	1206	14	US-10-414-637-2	Sequence 2, Appli
16	1485	39.5	1206	15	US-10-606-320-2	Sequence 2, Appli
17	1469	39.1	1210	13	US-10-032-717-4	Sequence 4, Appli
18	1469	39.1	1210	14	US-10-414-637-4	Sequence 4, Appli
19	1469	39.1	1210	15	US-10-606-320-4	Sequence 4, Appli
20	1459.5	38.8	1156	14	US-10-099-285-72	Sequence 72, Appli
21	1459.5	38.8	1156	15	US-10-428-961-28	Sequence 28, Appli
22	1443	38.4	1155	9	US-09-756-643-2	Sequence 2, Appli
23	1443	38.4	1155	10	US-09-988-462-9	Sequence 9, Appli
24	1443	38.4	1155	15	US-10-136-988A-2	Sequence 2, Appli
25	1443	38.4	1177	14	US-10-035-060-6	Sequence 6, Appli
26	1443	38.4	1181	10	US-09-988-462-11	Sequence 11, Appli
27	1443	38.4	1181	10	US-09-988-462-13	Sequence 13, Appli
28	1443	38.4	1181	10	US-09-988-462-15	Sequence 15, Appli
29	1443	38.4	1181	10	US-09-988-462-17	Sequence 17, Appli
30	1443	38.4	1181	10	US-09-988-462-28	Sequence 28, Appli
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32	1443	38.4	1181	15	US-10-136-988A-8	Sequence 8, Appli
33	1443	38.4	1181	15	US-10-136-988A-10	Sequence 10, Appli
34	1443	38.4	1181	15	US-10-136-988A-12	Sequence 12, Appli
35	1438	38.2	1177	14	US-10-035-060-2	Sequence 2, Appli
36	1436	38.2	1177	14	US-10-035-060-8	Sequence 8, Appli
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38	1419.5	37.7	1176	16	US-10-782-141-6	Sequence 6, Appli
39	1407.5	37.4	1176	11	US-09-837-961-2	Sequence 2, Appli
40	1407.5	37.4	1176	16	US-10-825-751-2	Sequence 2, Appli
41	1376	36.6	1167	15	US-10-428-961-40	Sequence 40, Appli
42	1355	36.0	1177	9	US-09-873-873-26	Sequence 26, Appli
43	1355	36.0	1177	10	US-09-916-956A-26	Sequence 26, Appli
44	1355	36.0	1177	10	US-09-997-914-26	Sequence 26, Appli
45	1355	36.0	1177	14	US-10-365-645-26	Sequence 26, Appli

ALIGNMENTS

RESULT 1  
US-10-782-020-10  
; Sequence 10, Application US/10782020  
; Publication No. US20040197916A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and  
; FILE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274139  
; CURRENT APPLICATION NUMBER: US/10/782,020  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,810  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-020-10

Query Match	99.0%	Score 3724;	DB 16;	Length 719;
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Qy	1	MKLKNQDKHQSPSSNAKVDKISTDSLKNQETDIQLQNHEDCLKNSEYENVPFVSASTI 60		
Db	1	MKLKNQDKHQSPSSNAKVDKISTDSLKNQETDIQLQNHEDCLKNSEYENVPFVSASTI 60		
Qy	61	QTGIGIAGKILGTGVPFAGQVASYLSFILGLWPKGNQWILFMEHVEE-INQIKISTY 119		
Db	61	QTGIGIAGKILGTGVPFAGQVASYLSFILGLWPKGNQWILFMEHVEE-INQIKISTY 119		

QY	120	ARNKALTDLKGGLDALAVYHDSLESWGNRNTRRSVVRQYIALELMFVQKLPSPFAVS	179
Db	120	ARNKALTDLKGGLDALAVYHDSLESWGNRNTRRSVVRQYIALELMFVQKLPSPFAVS	179
QY	180	GEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISFYNRQVERAGDYSCHCVKWY	239
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QY	240	STGLNNLKGTAESWVRNQFRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREVVYDA	299
Db	240	STGLNNLKGTAESWVRNQFRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREVVYDA	299
QY	300	IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSTQYMMN	359
Db	300	IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLLSRWSTQYMMN	359
QY	360	WGHKLEPRTIGGTINISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVP	419
Db	360	WGHKLEPRTIGGTINISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVP	419
QY	420	RVDHFWKVTHTPIASDNFYFGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI	479
Db	420	RVDHFWKVTHTPIASDNFYFGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI	479
QY	480	SASHVKALVYSWTHRSADRTNTEPNSITQIPLKAFNLSSGAAVVRGPGFTGGDILRRT	539
Db	480	SASHVKALVYSWTHRSADRTNTEPNSITQIPLKAFNLSSGAAVVRGPGFTGGDILRRT	539
QY	540	NTGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY	599
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Db	600	KTFRTVGTTPPSFLDVQSTFTIGAMNFSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK	659
QY	660	VTALFTSTNPRGLKTDVKDHYIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM	719
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; Sequence 8, Application US/10782141			
; Publication No. US20040197917A1			
; GENERAL INFORMATION:			
; APPLICANT: Carozzi, Nadine			
; APPLICANT: Hargiss, Tracy			
; APPLICANT: Koziel, Michael G.			
; APPLICANT: Duck, Nicholas B.			
; APPLICANT: Carr, Brian			
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and			
; TITLE OF INVENTION: Methods for Its Use			
; FILE REFERENCE: 045600/274143			
; CURRENT APPLICATION NUMBER: US/10/782,141			
; CURRENT FILING DATE: 2004-02-20			
; PRIOR FILING DATE: 2004-02-20			
; PRIOR FILING DATE: 2003-02-20			
; NUMBER OF SEQ ID NOS: 23			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 8			
; LENGTH: 719			
; TYPE: PRT			
; ORGANISM: Bacillus thuringiensis			
US-10-782-141-8			
Query Match 99.0%; Score 3724; DB 16; Length 719;			
Best Local Similarity 99.3%; Pred. No. 1.9e-306;			
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;			
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NAME/KEY: misc feature  
LOCATION: (200)..(200)  
OTHER INFORMATION: The 'xaa' at location 200 stands for any naturally occurring amino acid  
US-10-428-961-42

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Matches 662; Conservative 16; Mismatches 31; Indels 11; Gaps 3;

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DB 1 MKSKQNMHQSLSNNAITVDKFTGSLNNTNTELOQNFH-----EGIEPFFVSSTI 51

QY 61 QTGIGIAGKILGTLGPPAGQVASYSLFILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
DB 52 QTGIGIAGKILGNLGPAGQVASYSLFILGELWPKGNQWEI-FMEHVEELINQKISTY 110

QY 120 ARNKALTDLKGGLDALAVYHDSLESVGNRNTRARSVRSQYIALELMFVQKLPSPAYS 179  
DB 111 ARNKALADLKGGLDALAVYHDSLESVGNRNTRARSVRSQYIALELMFVQKLPSPAYS 170

QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCKVY 239  
DB 171 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCKVY 230

QY 240 STGLNNLRGTNAESWRYNQFRDMLTLMVLDLVALPSPYDTQMPYIKTTAQLTREYVYDA 299  
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DB 291 IGTVHPHPSFTSTWYNNAPSFSAEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMM 350

QY 360 WGGHKLFTTIGTLNISTQSTNTSINPVTLPFTSRDVRVRESLAGNLFLETPQVNGVP 419  
DB 351 WGGHKLFTTIGTLNISTQSTNTSINPVTLPFTSRDVRVRESLAGNLFLETPQVNGVP 410

QY 420 RVDPHKVFTHPIASDNFYYPGAGIGTQLQDSNELPPEATQPNYESYSHRSLSHIGLI 479  
DB 411 RVDPHKVFTHPIASDNFYYPGAGIGTQLQDSNELPPEATQPNYESYSHRSLSHIGLI 470

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DB 471 SASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 530

QY 540 NTGTFGDIRVNIWPPAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATWNRGDLDY 599  
DB 531 NTGTFGDIRVNIWPPAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATWNRGDLDY 590

QY 600 KTFRTVGTTPPSFLDVQSTFTTIGAWNFSGNEVYIDRIEFVPEVYTYEAEDYDPEKAEK 659  
DB 591 KTFRTVGTTPPSFLDVQSTFTTIGAWNFSGNEVYIDRIEFVPEVYTYEAEDYDPEKAEK 650

QY 660 VTALFTSTNPRGLKTDVQYHIDQVSNLVESLSDKFYLDKRELFEIVKYANLHIERNM 719  
DB 651 VTALFTSTNPRGLKTDVQYHIDQVSNLVESLSDKFYLDKRELFEIVKYANLHIERNM 710

RESULT 4  
US-10-809-953-10  
Sequence 10, Application US/10809953  
Publication No. US2004018125A1  
GENERAL INFORMATION:  
APPLICANT: Botterman, Johan  
APPLICANT: Van Mellaert, Herman  
APPLICANT: Van Rie, Jeroen  
TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTICIDAL PROTEINS  
FILE REFERENCE: 021565-078  
CURRENT APPLICATION NUMBER: US/10/809,953  
CURRENT FILING DATE: 2004-03-26  
PRIOR APPLICATION NUMBER: US/09/661,016

PRIOR FILING DATE: 2000-09-13  
PRIOR APPLICATION NUMBER: PCT/EP90/00905  
PRIOR FILING DATE: 1990-05-30  
PRIOR APPLICATION NUMBER: GB 89401499.2  
PRIOR FILING DATE: 1989-05-31  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 10  
LENGTH: 1228  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis  
US-10-809-953-10

Query Match 59.8%; Score 2250.5; DB 16; Length 1228;  
Best Local Similarity 62.5%; Pred. No. 3.9e-181;  
Matches 448; Conservative 78; Mismatches 164; Indels 27; Gaps 8;

QY 23 TDSLNKNETDIELQINNH-----EDCLKMEYENVEPVSASTIQTGIGTAGKI 70  
DB 2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61

QY 71 LGTLGVPAGQVASYSLFILGELWPKGNQWEILFMEHVEE-INQKISTYARKALTDLK 129  
DB 62 LGVLGVPAGQVASYSLFILGELWPKGNQWEI-FLEHVEQLINQOITENARTALARIQ 120

QY 130 GLGDALAVYHDSLESVGNRNTRARSVRSQYIALELMFVQKLPSPAYSGBEVPPLPIY 189  
DB 121 GLGDSFRAYQQSLEDWLENRDDARTSVLHTQYIALELDLFLNAMPFLFAIRNQEVPPLMYY 180

QY 190 AQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCKVYSLGLNNLRGT 249  
DB 181 AQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCKVYSLGLNNLRGT 240

QY 250 NAESWRYNQFRDMLTLMVLDLVALPSPYDTQMPYIKTTAQLTREYVYDAIGTVHPHPSF 309  
DB 241 NAESWRYNQFRDMLTLMVLDLVALPSPYDTQMPYIKTTAQLTREYVYDAIGTVHPHPSF 308

QY 310 TSTTWNNNAPSFSAEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMMWGGHKLFT 369  
DB 299 ASMNWYNNAPSFSAEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMMWGGHKLFT 358

QY 370 IGTNINISTQSTNTSINPVTLPFTSRDVRVRESLAGNLF--LTQPVNGVPRVDFHWKF 427  
DB 359 IGGGLNTSTHGATNTSINPVTLPFTSRDVRVRESLAGNLF--LTQPVNGVPRVDFHWKF 416

QY 428 VTHP-----IASDNFYYPGAGIGTQLQDSNELPPEATQPNYESYSHRSLSHIGLISAS 482  
DB 417 -TNPNISDRGTANTYQSP-YESFGLQKDSSETLPETTERPNYESYSHRSLSHIGLISAS 474

QY 483 HYKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTNTG 542  
DB 475 RVNVPVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTNTG 534

QY 543 TFGDIRVNIWPPAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATWNRGDLDYKTF 602  
DB 535 TFGDIRVNIWPPAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATWNRGDLDYKTF 594

QY 603 RTVGTFTTPPSFLDVQSTFTTIGAWNFSGNEVYIDRIEFVPEVYTYEAEDYDPEKAEK 662  
DB 595 VRRAFVTTPTFTQIQDIIRTSIQGLSGNEVYIDRIEFVPEVYTYEAEDYDPEKAEK 654

QY 663 LFTSTNPRGLKTDVQYHIDQVSNLVESLSDKFYLDKRELFEIVKYANLHIERNM 719  
DB 655 LFTSTNPRGLKTDVQYHIDQVSNLVESLSDKFYLDKRELFEIVKYANLHIERNM 711

RESULT 5  
US-09-988-462-7  
Sequence 7, Application US/09988462  
Publication No. US20030046726A1  
GENERAL INFORMATION:  
APPLICANT: Kozziel, Michael G.  
APPLICANT: Desai, Nalini M.

Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Lauais, Karen L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462

FILING DATE: 20-NO. US20030046726A1-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-188051

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1207 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7

Query Match 59.5%; Score 2236.5; DB 10; Length 1207;  
Best Local Similarity 64.1%; Pred. No. 5.8e-180;  
Matches 441; Conservative 76; Mismatches 156; Indels 15; Gaps 7;

QY 40 EDLKMSEYENVEPVFVSASTIQTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGN 99  
DB 10 EDSLCAEGNNIDPFVSASTVGTGINIAGRIILGVLPAGQVASYLSFILGELWPKGRD 69  
QY 100 QWEILFMEHVEE-INQKISTYARNKALTDLKGGLDALAVYHDSLESWGVNNTFARSVV 158  
DB 70 QWEI-FLEHVEQLINQITENARNTALRQLGDSFRAYQQSLDLENRDARTSVL 128  
QY 159 RSQYTALELMFVKQLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSRIS 218  
DB 129 YTYQTALELDLFLNAPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSFGLTQSIO 188  
QY 219 TFYNROVERAGDYSCHVCWKYSTGLNLRAGTNAESWRYNQPRRDMTLMVLDLVALFP 278  
DB 189 RYERQVERTRDYSYDVCWYNTGLNSLRAGTNAESWRYNQPRRDLTLGLVDLVALFP 248  
QY 279 DTQMPYIKTAQLTREYVTDALGTVHPHPSFTSTWYNNNAPFSAIEAAVVRNPHLLDF 338

DB 249 DTRTPINTSAQLTREYVTDALGT--GYNMASNMWYNNNAPFSAIEAAIRSPHLLDF 306  
QY 339 LEQVTYISLLSEWSNTQYNNMGHKLERTTIGTGLNISTOGSTNTSINPVTLPFTSRDV 398  
DB 307 LEQLTIFSASSRWSNTRHMYWRGHTIOSRPIGGGLNTSHGATNTSINPVTLPFTSRDV 366  
QY 399 YRTESLAGLNLF--LTQPVNGVPRVDFHWKVFTHP-----IASDNFYYPGYAGIGTQLOD 451  
DB 367 YRTESYAGVLLNGIYLEPIHGVTYRNF--TNQNISDRGTANYSQP--YESPGQLQKD 422  
QY 452 SNEULPPEATGQPNVESYSHRLSHIGLISASHVKALVSWTHRSADRTNTTIPNSITQIP 511  
DB 423 SETELPPETTERPNVESYSHRLSHIGLILQSRVNPVYSWTHRSADRTNTTIPNRITQIP 482  
QY 512 LVKAFNLSSGAAVRGPFTGGDILRRNTGTGFDIRVNINPFPFAQVRYRIRYASTTDL 571  
DB 483 MKVASELPQGTTVVRGFTGGDILRRNTGTGFGPGRVTVNGPLQRYRIGFYASTVDF 542  
QY 572 QFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGTTPFSLDVQSTFTTIGAWNFSSGN 631  
DB 543 DPFVSRGGTTVNNFRRLTMNSGDELKYGNFVRRATFTPTFTQIQDIIRTSIQGLSGNG 602  
QY 632 EVIDRIEFVPEVVEYAEYDEKAEKVTALFTSNPRGLKTDVYKHIDOVSNLVESEI 691  
DB 603 EVIDKIEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVLAC 662  
QY 692 SDEFYLDKRELFEIVKYANELHIERNM 719  
DB 663 SDEFCLDEKRELLEKVKYAKRLSDERNL 690

## RESULT 6

US-10-428-961-63  
; Sequence 63 Application US/10428961  
; Publication NO. US20030237111A1  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Rupa, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
; FILE REFERENCES: MECO201--1  
; CURRENT APPLICATION NUMBER: US/10/428,961  
; CURRENT FILING DATE: 2003-05-02  
; PRIOR FILING DATE: 2000-09-13  
; PRIOR FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 63  
; LENGTH: 1227  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-428-961-63

Query Match 57.4%; Score 2157.5; DB 15; Length 1227;  
Best Local Similarity 59.0%; Pred. No. 3e-173;  
Matches 422; Conservative 103; Mismatches 175; Indels 15; Gaps 5;

QY 13 SSNAKVDKISTDSLKN-----ETDIELQINIHEDCLKMSVENVEPVFVSASTIQTGIG 65  
DB 7 NENEIINALSTPAVSNHSAQMNLSLDARI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61  
QY 66 IAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTYARNKA 124  
DB 62 IAGRIILGVLPAGQVASYLSFILGELWPKGRDQWEI-FLEHVEHLIRQVIENTDRTA 120  
QY 125 LTDLKGLGDALAVYHDSLESWGVNNTNTRARSVRSQYIALELMFVKQLPSFAVSGBEVP 184





Query Match 55.5%; Score 2087; DB 15; Length 1228;  
Best Local Similarity 59.2%; Pred. No. 2.8e-167;  
Matches 423; Conservative 96; Mismatches 183; Indels 12; Gaps 9;

QY 13 SNAKVDKISTDSLNK-ETDIELQ-NINHEDCLKMEYENVEPVFVSGASTIQTGIGIAGKI 70  
DB 7 NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66

QY 71 LGTGVFPAGQVASYLFILOELWPKGNOWEILFMEHVEE-INOKISTYARNKALTDLK 129  
DB 67 LGVLGVFPAGQIASFYSLVGLWELNPRGRDQWEI-FLEHVEQLINQOITENARTALARQ 125

QY 130 GLGDALAVYHDSLESVGNRNNTARSVRSOYIALELMFVKLPSPFAVSGEVPPLPIY 189  
DB 126 GLGDSFRAYQOSLEDWLENRDDARTSRVLYTOYIALELDLFLNAMPLFAIRNQEVPLLMVY 185

QY 190 AQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGT 249  
DB 186 AQAANLHLLLRDASIFGSEFGLTSQEIQRYERQVEQTRDYSYCVIEWNTGLNSLRGT 245

QY 250 NAESWRYNQPRRDMTLMVLDFVALFPSYDTQMPYIKTTAQLTREVVYTDAGT--GVNM 303  
DB 246 NAASWRYNQPRRDLTLGLVDLVALFPSYDTRTPINTSAQLTREVVYTDAGT--GVNM 303

QY 310 TSTTWNNAAPSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMMWGGHKLFRPT 369  
DB 304 ASMWYNNAPSAIEATAVIRSPHLLDFLEQLTIFSTSRWSATRHMTYWRGHTIQSRP 363

QY 370 IGGTLNSTQGSTNTSINPVLPTSRDVRVYTESLAGLNF--LTOPVNGVPRVDPHWKF 427  
DB 364 IGGGLNSTHGSTNTSINPVLSPFSDRVYTESYAGVLLWGIYLEPIHGVPVTRFNRN 423

QY 428 V--THPIASDNFYPGYAGICTQODSENELPPEATGQPNYESYSHRLSHIGLISASHVK 485  
DB 424 PONTFERGTANYSQP--YESPGLQKDSLETLPPTTERPNYESYSHRLSHIGLISQSRVH 482

QY 486 ALVYSWTHRSADRTNTIENSIQIPLVKAFNLSSGAAVRGPFGTGGDILRNTTGTG 545  
DB 483 VPVYSWTHRSADRTNTISSDSITQIPLVKSFNLSGTSVSGPGFTGGDIIRTNVNGSVL 542

QY 546 DIRVNNPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAITMNRGDLDTKTRTV 605  
DB 543 SMGLNFNTSLQRYRVRVRYAASQTMVLRVTVGSGTTFDQGFPTMSANESLTSQSRFA 602

QY 606 GFTTFPSFLDVQSTFTIGAMNFSNGEVYIDRIEFVPEVYEAEDYFEKAQKVTALFT 665  
DB 603 EFPVGISAGSQ--TAGISISNNAGROTFFDKIEFIPITATFEAYDLERAQEAVALFT 661

QY 666 STNPRGLKTDVKDHYHIDQVSNLVESLSEDFYLDKRELFEIVKYANELHIERNM 719  
DB 662 NTNPRRLKTDVTDYHIDQVSNLVACLSEDFCLDEKRELLEKVKYAKRLSDERNL 715

RESULT 9  
US-10-614-524-2  
; Sequence 2, Application US/10614524  
; Publication No. US20040016020A1  
; GENERAL INFORMATION:  
; APPLICANT: Arnaut, Greta  
; APPLICANT: Boets, Annemie  
; APPLICANT: Damme, Nicole  
; APPLICANT: Mathieu, Eva  
; APPLICANT: Vanneste, Stijn  
; APPLICANT: Van Rie, Jeroen  
; TITLE OF INVENTION: Insecticidal proteins from *Bacillus thuringiensis*.  
; FILE REFERENCE: NEWBISUS2  
; CURRENT APPLICATION NUMBER: US/10/614,524  
; PRIOR FILING DATE: 2003-07-08  
; PRIOR APPLICATION NUMBER: US/09/739,243  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/173387  
; PRIOR FILING DATE: 1999-12-28

; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1228  
; TYPE: PRT  
; ORGANISM: *Bacillus thuringiensis*  
US-10-614-524-2

Query Match 55.5%; Score 2087; DB 15; Length 1228;  
Best Local Similarity 59.2%; Pred. No. 2.8e-167;  
Matches 423; Conservative 96; Mismatches 183; Indels 12; Gaps 9;

QY 13 SNAKVDKISTDSLNK-ETDIELQ-NINHEDCLKMEYENVEPVFVSGASTIQTGIGIAGKI 70  
DB 7 NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66

QY 71 LGTGVFPAGQVASYLFILOELWPKGNOWEILFMEHVEE-INOKISTYARNKALTDLK 129  
DB 67 LGVLGVFPAGQIASFYSLVGLWELNPRGRDQWEI-FLEHVEQLINQOITENARTALARQ 125

QY 130 GLGDALAVYHDSLESVGNRNNTARSVRSOYIALELMFVKLPSPFAVSGEVPPLPIY 189  
DB 126 GLGDSFRAYQOSLEDWLENRDDARTSRVLYTOYIALELDLFLNAMPLFAIRNQEVPLLMVY 185

QY 190 AQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGT 249  
DB 186 AQAANLHLLLRDASIFGSEFGLTSQEIQRYERQVEQTRDYSYCVIEWNTGLNSLRGT 245

QY 250 NAESWRYNQPRRDMTLMVLDFVALFPSYDTQMPYIKTTAQLTREVVYTDAGT--GVNM 309  
DB 246 NAASWRYNQPRRDLTLGLVDLVALFPSYDTRTPINTSAQLTREVVYTDAGT--GVNM 303

QY 310 TSTTWNNAAPSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMMWGGHKLFRPT 369  
DB 304 ASMWYNNAPSAIEATAVIRSPHLLDFLEQLTIFSTSRWSATRHMTYWRGHTIQSRP 363

QY 370 IGGTLNSTQGSTNTSINPVLPTSRDVRVYTESLAGLNF--LTOPVNGVPRVDPHWKF 427  
DB 364 IGGGLNSTHGSTNTSINPVLSPFSDRVYTESYAGVLLWGIYLEPIHGVPVTRFNRN 423

QY 428 V--THPIASDNFYPGYAGICTQODSENELPPEATGQPNYESYSHRLSHIGLISASHVK 485  
DB 424 PONTFERGTANYSQP--YESPGLQKDSLETLPPTTERPNYESYSHRLSHIGLISQSRVH 482

QY 486 ALVYSWTHRSADRTNTIENSIQIPLVKAFNLSSGAAVRGPFGTGGDILRNTTGTG 545  
DB 483 VPVYSWTHRSADRTNTISSDSITQIPLVKSFNLSGTSVSGPGFTGGDIIRTNVNGSVL 542

QY 546 DIRVNNPPAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAITMNRGDLDTKTRTV 605  
DB 543 SMGLNFNTSLQRYRVRVRYAASQTMVLRVTVGSGTTFDQGFPTMSANESLTSQSRFA 602

QY 606 GFTTFPSFLDVQSTFTIGAMNFSNGEVYIDRIEFVPEVYEAEDYFEKAQKVTALFT 665  
DB 603 EFPVGISAGSQ--TAGISISNNAGROTFFDKIEFIPITATFEAYDLERAQEAVALFT 661

QY 666 STNPRGLKTDVKDHYHIDQVSNLVESLSEDFYLDKRELFEIVKYANELHIERNM 719  
DB 662 NTNPRRLKTDVTDYHIDQVSNLVACLSEDFCLDEKRELLEKVKYAKRLSDERNL 715

RESULT 10  
US-09-826-660-25  
; Sequence 25, Application US/09826660  
; Patent No. US20010026940A1  
; GENERAL INFORMATION:  
; APPLICANT: Cardineau, Guy A.  
; APPLICANT: Stelman, Steven J.  
; APPLICANT: Narva, Kenneth E.  
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins  
; FILE REFERENCE: MA-714XC2D1  
; CURRENT APPLICATION NUMBER: US/09/826,660  
; CURRENT FILING DATE: 2001-04-05





Db 521 IYSDKITQIPAVKDMLYLGGSVVQPGFTGGDILKRTNPSILGTFAVTVNGSLSQRYV 580  
QY 562 RIRYASTTDLQFTSINGKAINOCNFSATNMGEDLDYKTFRTVGTFTTTPSFDFLDVOSTFT 621  
Db 581 RIRYASTTDFEF-TLYLGDITIEKRNKTNMGASITETFFKASITITDFQFRETQDKIL 639  
QY 622 IGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQKVTALFTSNPRGLKTDVKKYHI 681  
Db 640 LSMGDFSSQGEVYIDRIEFIPVDETYEAEQDLAAKAVNALFTNTKD-GLRPGVTDYEV 698  
QY 682 DQVSNLVESLSDREYLDKRELFPEIVKYANELHIERNM 719  
Db 699 NQAAANLVECLSDLLYPNEKRLLPDAVREAKRUSGARNL 736

RESULT 14  
US-10-032-717-2  
; Sequence 2, Application US/10032717  
; Publication No. US20020151709A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With  
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/032,717  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/242,838  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1206  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-032-717-2

Query Match 39.5%; Score 1485; DB 13; Length 1206;  
Best Local Similarity 44.3%; Pred. No. 3e-116;  
Matches 337; Conservative 127; Mismatches 231; Indels 66; Gaps 24;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDS----LKNETDIELQNHEDCLKM-----SEYE-N 50  
Db 1 MSPNNQNEYIIDATPST-SVSNDSNRYPPANEPTNALQNDYKYLKMSAGNASBYPGS 59  
QY 51 VEPFVSA-STIOTGIGIAGKILGTGVPFAGOVASLYSFTLGLBWPKG-KNOWEILFMEH 108  
Db 60 PEVLVSGQDAKAAIDIVGKLLSGLGVFPVPIVSLYTQLDILWPSGKSQNEI-FMEQ 118  
QY 109 VEE-INQKISTYARNKALTDLKGLGDALAVYHDSLESWGVRNNTNRRSVRSQYIALEL 167  
Db 119 VEELINQKIAEYARNKALSLEGLGNNYQLYLTALBEBEENPNGSRALRDVRNRFIELDS 178  
QY 168 MFVKQLPSPAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTYFNQVER 227  
Db 179 LFTQYMPSPFRVTNFEVPLFTVYAMAANLHLLLRDASIFGEEGWSTTTNNYDQMKL 238  
QY 228 AGDYSHCVKWYSTGLNLRGTNAESWVRNQFRDMLMVLVDLVALFSPYDQTPYIKT 287  
Db 239 TAYSCHVCWKYETGLAKLGTSAKQWVDYQFRREMTLAVLDVVALFPNDYRTYMET 298  
QY 288 TAQLTREVTYDAIGTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVITYSL 347  
Db 299 KAQLTREVTYDPLGAVNVUS---SIGSWY-DKAPSFVGISSVIRPPHFVYITGLTYTQ 354  
QY 348 LSRWSNTQYNNMGCHKLEFRITGGTINISQSGSTNTSINPV-TLPFTSRDVRTESLAG 406  
Db 355 SRGISARYIRHWAGHQSIVHRVSRGSLNQMYGTNQNLHSTSTDFDTNYDIYKTLSDKA 414

QY 407 LNLFTITQP-----VNGVPRVDFHMKPVTHPIASDN---FYYPGAGIGTQLODSENELEPP 458  
Db 415 VLLDVIYPGYTVIFFGMEVEF---FMVQLNTRKTLKYNPVSKDIIASTRDSLELEPP 471  
QY 459 EATGQPNYESYSHRLSHIGLISAS-HVKAL--VYSWTHESADRTNTEPNSITQIPLVKA 515  
Db 472 ETSQDPNYESYSHRLCHITSIFATGNTTGLVPVFWSTHRSADLNNTIYSDKITQIPAVKC 531  
QY 516 FNLSGAAVVRGPGFTGGDILR-RTNTGTGFGDI---RVNINPPFAQRYVRIRYASTTDL 571  
Db 532 WNLNLPVVPVKGPGHTGGDLLQYNRSTGSGVTLFLARYGLALEKAGKYRVLRYATDADI 591  
QY 572 QFHTSINGKAINQGNPSATNMGEDLDYKTFR-----TVGFTTTPSF------DVQS 618  
Db 592 VLH--VNDAAQI---QMPKTMNPGEDLTSKTFKVADAITTLNLATDSSLAKHNLGDPNS 646  
QY 619 TETIGANWFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQKVTALFTSNPRGLKTDVKK 678  
Db 647 TLS-----GIVYVDRIEFIPVDETYEAEQDLAAKAVNALFTNTKD-GLRPGVTD 696  
QY 679 YHIDOVSNLVESLSDREYLDKRELFPEIVKYANELHIERNM 719  
Db 697 YEVNQAAANLVECLSDLLYPNEKRLLPDAVREAKRUSGARNL 737

RESULT 15  
US-10-414-637-2  
; Sequence 2, Application US/10414637  
; Publication No. US20030177528A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With  
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/414,637  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: US/10/032,717  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/242,838  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1206  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-414-637-2

Query Match 39.5%; Score 1485; DB 14; Length 1206;  
Best Local Similarity 44.3%; Pred. No. 3e-116;  
Matches 337; Conservative 127; Mismatches 231; Indels 66; Gaps 24;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDS----LKNETDIELQNHEDCLKM-----SEYE-N 50  
Db 1 MSPNNQNEYIIDATPST-SVSNDSNRYPPANEPTNALQNDYKYLKMSAGNASBYPGS 59  
QY 51 VEPFVSA-STIOTGIGIAGKILGTGVPFAGOVASLYSFTLGLBWPKG-KNOWEILFMEH 108  
Db 60 PEVLVSGQDAKAAIDIVGKLLSGLGVFPVPIVSLYTQLDILWPSGKSQNEI-FMEQ 118  
QY 109 VEE-INQKISTYARNKALTDLKGLGDALAVYHDSLESWGVRNNTNRRSVRSQYIALEL 167  
Db 119 VEELINQKIAEYARNKALSLEGLGNNYQLYLTALBEBEENPNGSRALRDVRNRFIELDS 178  
QY 168 MFVKQLPSPAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTYFNQVER 227  
Db 179 LFTQYMPSPFRVTNFEVPLFTVYAMAANLHLLLRDASIFGEEGWSTTTNNYDQMKL 238



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:24:54 ; Search time 22.3302 Seconds  
(without alignments)  
2403.590 Million cell updates/sec

Title: US-10-019-823B-58

Perfect score: 3761

Sequence: 1 MKLKNQKHQSFSSNAKVDK.....KRELFEIVKYANELHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

1: /cgn2.6/prodata/1/iaa/5A COMB.pep.\*  
2: /cgn2.6/prodata/1/iaa/5B COMB.pep.\*  
3: /cgn2.6/prodata/1/iaa/6A COMB.pep.\*  
4: /cgn2.6/prodata/1/iaa/6B COMB.pep.\*  
5: /cgn2.6/prodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2.6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3720	98.9	719	3	US-08-286-870A-8
2	3442.5	91.5	710	4	US-09-661-322A-42
3	3370	89.6	648	3	US-08-286-870A-4
4	3341	88.8	719	2	US-09-003-217-2
5	3336	88.7	719	3	US-09-218-942-2
6	2776	73.8	535	3	US-08-286-870A-6
7	2417.5	64.3	1229	1	US-08-100-709-4
8	2417.5	64.3	1229	1	US-08-176-865-4
9	2417.5	64.3	1229	1	US-08-474-038-4
10	2417.5	64.3	1229	1	US-08-779-046-4
11	2417.5	64.3	1229	1	US-08-881-340-4
12	2318.5	61.6	488	1	US-08-448-170-10
13	2318.5	61.6	488	3	US-08-961-803-10
14	2236.5	59.5	1207	1	US-07-951-715A-7
15	2236.5	59.5	1207	1	US-08-459-448A-7
16	2236.5	59.5	1207	3	US-08-459-595A-7
17	2236.5	59.5	1207	3	US-08-459-504B-7
18	2236.5	59.5	1207	3	US-08-459-444-7
19	2236.5	59.5	1207	3	US-09-053-549-8
20	2236.5	59.5	1207	3	US-09-547-422-7
21	2236.5	59.5	1207	4	US-09-988-462-7
22	2236.5	59.4	1227	3	US-09-053-549-2
23	2166.5	57.6	1227	1	US-08-448-170-8
24	2166.5	57.6	1227	3	US-08-961-803-9
25	2157.5	57.4	1227	4	US-09-661-322A-63
26	2142.5	57.0	1186	3	US-09-178-252-23
27	2142.5	57.0	1186	4	US-09-826-660-23

28	2087	55.5	1228	4	US-09-661-322A-38	Sequence 38, Appl
29	1909.5	50.8	643	3	US-09-178-252-25	Sequence 25, Appl
30	1909.5	50.8	643	4	US-09-826-660-25	Sequence 25, Appl
31	1872	49.8	380	5	PCT-US91-02560-4	Sequence 4, Appl
32	1658.5	44.1	653	4	US-09-661-322A-6	Sequence 6, Appl
33	1643.5	43.7	1157	1	US-07-876-280-30	Sequence 30, Appl
34	1643.5	43.7	1157	1	US-07-812-180A-2	Sequence 2, Appl
35	1643.5	43.7	1157	1	US-08-315-468-2	Sequence 2, Appl
36	1643.5	43.7	1157	3	US-07-941-650A-2	Sequence 2, Appl
37	1481.5	39.4	1176	1	US-08-257-999-2	Sequence 5, Appl
38	1466	39.0	1157	2	US-08-532-547-5	Sequence 5, Appl
39	1466	39.0	1157	2	US-08-379-658B-5	Sequence 5, Appl
40	1466	39.0	1157	3	US-08-455-838-5	Sequence 5, Appl
41	1466	39.0	1157	3	US-09-019-809-5	Sequence 5, Appl
42	1466	39.0	1157	4	US-09-471-177-5	Sequence 5, Appl
43	1466	39.0	1157	4	US-09-220-806-5	Sequence 5, Appl
44	1461	38.8	1168	1	US-08-291-368-4	Sequence 4, Appl
45	1461	38.8	1168	2	US-08-962-190-4	Sequence 4, Appl

#### ALIGNMENTS

#### RESULT 1

US-08-286-870A-8  
; Sequence 8, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSES: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PAUL N. KOKULIS  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 70608/220720  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-286-870A-8

Query Match 98.9%; Score 3720; DB 3; Length 719;  
Best Local Similarity 99.2%; Pred. No. 0;  
Matches 714; Conservative 3; Mismatches 1; Indels 2; Gaps 2;  
QY 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P F V S A S T I 60  
Db 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P F V S A S T I 60  
QY 61 Q T G I G I A G K I L G T G V P F A G V A S L Y S F I L G E L W P K G K N Q W E I L F M E H V E E - I N Q I S T Y 119  
Db 61 Q T G I G I A G K I L G T G V P F A G V A S L Y S F I L G E L W P K G K N Q W E I - F M E H V E E I I N Q I S T Y 119  
QY 120 A R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A S V R S Q I A L E L M F V Q K L P S F A V S 179  
Db 120 A R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A S V R S Q I A L E L M F V Q K L P S F A V S 179  
QY 180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S D H C V K W Y 239  
Db 180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S D H C V K W Y 239  
QY 240 S T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T O M Y P I K T T A Q L T R E V Y T D A 299  
Db 240 S T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T O M Y P I K T T A Q L T R E V Y T D A 299  
QY 300 I G T V H P H S F T S T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M 359  
Db 300 I G T V H P H S F T S T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M 359  
QY 360 W G H K L E P T I G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P 419  
Db 360 W G H K L E P T I G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P 419  
QY 420 R V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I 479  
Db 420 R V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I 479  
QY 480 S A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G D I L R R T 539  
Db 480 S A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G D I L R R T 539  
QY 540 N T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T N R G E D L D Y 599  
Db 540 N T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T N R G E D L D Y 599  
QY 600 K T P R T V G T T P F S F L D V Q S T F T I G A M N F S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659  
Db 600 K T P R T V G T T P F S F L D V Q S T F T I G A M N F S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659  
QY 660 V T A L F T S T N P R G L K T D V K Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719  
Db 660 V T A L F T S T N P R G L K T D V K Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719

RESULT 2  
US-09-661-322A-42  
; Sequence 42, Application US/09661322A  
; Patent No. 6593293  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chin-Rel  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Rubar, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo  
; TITLE OF INVENTION: and Methods of Use  
; FILE REFERENCE: MECO201  
; CURRENT APPLICATION NUMBER: US/09/661,322A  
; CURRENT FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 42  
; LENGTH: 710  
; TYPE: PRT

ORGANISM: Bacillus thuringiensis  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (200)..(200)  
OTHER INFORMATION: No. 6593293-Coding  
US-09-661-322A-42  
Query Match 91.5%; Score 3442.5; DB 4; Length 710;  
Best Local Similarity 91.9%; Pred. No. 3.5e-304;  
Matches 662; Conservative 16; Mismatches 31; Indels 11; Gaps 3;  
QY 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P F V S A S T I 60  
Db 1 M K S K N Q N H Q S L S N A T V D K N F T G S L E N T N T L O N F N H ----- E G I E F F V S T I 51  
QY 61 Q T G I G I A G K I L G T G V P F A G V A S L Y S F I L G E L W P K G K N Q W E I L F M E H V E E - I N Q I S T Y 119  
Db 61 Q T G I G I A G K I L G T G V P F A G V A S L Y S F I L G E L W P K G K N Q W E I - F M E H V E E I I N Q I S T Y 119  
QY 120 A R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A S V R S Q I A L E L M F V Q K L P S F A V S 179  
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Db 180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S D H C V K W Y 239  
QY 240 S T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T O M Y P I K T T A Q L T R E V Y T D A 299  
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QY 300 I G T V H P H S F T S T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M 359  
Db 300 I G T V H P H S F T S T T W Y N N N A P S F S A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M 359  
QY 360 W G H K L E P T I G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P 419  
Db 360 W G H K L E P T I G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P 419  
QY 420 R V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I 479  
Db 420 R V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I 479  
QY 480 S A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G D I L R R T 539  
Db 480 S A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G D I L R R T 539  
QY 540 N T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T N R G E D L D Y 599  
Db 540 N T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T N R G E D L D Y 599  
QY 600 K T P R T V G T T P F S F L D V Q S T F T I G A M N F S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659  
Db 600 K T P R T V G T T P F S F L D V Q S T F T I G A M N F S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659  
QY 660 V T A L F T S T N P R G L K T D V K Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719  
Db 660 V T A L F T S T N P R G L K T D V K Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719

RESULT 3  
US-08-286-870A-4  
; Sequence 4, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: ELENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABY & CUSHMAN



ADDRESSEE: Intellectual Property Group of  
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/286,870A  
FILING DATE: 05-AUG-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520228  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8910624.9  
FILING DATE: 09-MAY-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: PAUL N. KOKULIS  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 70608/220720  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 648 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-286-870A-4

Query Match 89.6%; Score 3370; DB 3; Length 648;  
Best Local Similarity 99.5%; Pred. No. 1.2e-297;  
Matches 646; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLSKNETDIELQNHEDCLKMEYENVEPVASATI 60  
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLSKNETDIELQNHEDCLKMEYENVEPVASATI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKQWEILFMEHVVEE-INQIKISTY 119  
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKQWEILFMEHVVEE-INQIKISTY 119  
QY 120 ARNKALTDLKLGLDALAVYHDSLESVWGNRNTRARSVVRSQYIALELMFVQKLPFAVS 179  
DB 120 ARNKALTDLKLGLDALAVYHDSLESVWGNRNTRARSVVRSQYIALELMFVQKLPFAVS 179  
QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSCHCVKXY 239  
DB 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSCHCVKXY 239  
QY 240 STGLNLRGTNAESWRYNQFRDMLWLVDLVALPFSYDTQMPYIKTTAQLTREYVYTD 299  
DB 240 STGLNLRGTNAESWRYNQFRDMLWLVDLVALPFSYDTQMPYIKTTAQLTREYVYTD 299  
QY 300 IGTVPHPSTSTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYMMN 359  
DB 300 IGTVPHPSTSTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYMMN 359  
QY 360 WGGHKLKLEFRITIGTGLNISTGNTNTSINPVTLPTSRDVRTSLAGLNLFLTQPNVGP 419  
DB 360 WGGHKLKLEFRITIGTGLNISTGNTNTSINPVTLPTSRDVRTSLAGLNLFLTQPNVGP 419  
QY 420 RVDPHKFKVTHPTASDNFYYPGAGIGTQDSENELPPEATQPNYESYSHRLSHIGLI 479  
DB 420 RVDPHKFKVTHPTASDNFYYPGAGIGTQDSENELPPEATQPNYESYSHRLSHIGLI 479

QY 480 SASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGCDILRRT 539  
DB 480 SASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGCDILRRT 539  
QY 540 NTGTGDIIRVWNPPEAQRVVRIRYASTDLOFHTSINGKAINQGNESATMNRGDLDY 599  
DB 540 NTGTGDIIRVWNPPEAQRVVRIRYASTDLOFHTSINGKAINQGNESATMNRGDLDY 599  
QY 600 KTFRTVGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVYTYE 648  
DB 600 KTFRTVGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVYTYE 648

RESULT 4  
US-09-003-217-2  
Sequence 2, Application US/09003217  
Patent No. 5986177  
GENERAL INFORMATION:  
APPLICANT: Osman, Yehia A.  
APPLICANT: Madkour, Magdy A.  
APPLICANT: Bulla, Lee A.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH  
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)  
STREET: 3605 Glenwood Ave. Suite 310  
CITY: Raleigh  
STATE: NC  
COUNTRY: US  
ZIP: 27622  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/003,217  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: 5718-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919 420 2202  
TELEFAX: 919 881 3175  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 719 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-003-217-2

Query Match 88.8%; Score 3341; DB 2; Length 719;  
Best Local Similarity 89.2%; Pred. No. 6.1e-295;  
Matches 642; Conservative 35; Mismatches 41; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLSKNETDIELQNHEDCLKMEYENVEPVASATI 60  
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLSKNETDIELQNHEDCLKMEYENVEPVASATI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKQWEILFMEHVVEE-INQIKISTY 119  
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKQWEILFMEHVVEE-INQIKISTY 119  
QY 120 ARNKALTDLKLGLDALAVYHDSLESVWGNRNTRARSVVRSQYIALELMFVQKLPFAVS 179  
DB 120 ARNKALTDLKLGLDALAVYHDSLESVWGNRNTRARSVVRSQYIALELMFVQKLPFAVS 179  
QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSCHCVKXY 239  
DB 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSCHCVKXY 239

180 GEEVPLPIYAQAANLHLLLRDASIFPKNGGLSASEISTFYNRQVERTRDYSYHCWKVN 239  
 240 STGLNLRGNAESWRVYNQFRDMLTMDLVALPSPYDTOMYPIKTTAQLTRVYVYDA 299  
 240 NTGLNLRATNGOSWRVYNQFRDMLTMDLVALPSPYDTOMYPIKTTAQLTRVYVYDA 299  
 300 IGTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVITYSLSRWSNTQYMMN 359  
 300 IGTVDPNQALRSITWYNNAPSAIEAAVVRNPHLLDLEQVITYSLSRWSNTQYMMN 359  
 360 WGGHKLBERFTIGTNTSTQSTNTSINPVTLPFTSRDVRVTSAGLNLFLOPVGVP 419  
 360 WGGHKLBERFTIGTNTSTQSTNTSINPVTLPFTSRDVRVTSAGLNLFLOPVGVP 419  
 420 RVDHFWKFTPIASDNFYIYAGVGTQLODSENELPPEATGQPNVESYSHRSLHIGLI 479  
 420 RVDHFWKFTPIASDNFYIYAGVGTQLODSENELPPEATGQPNVESYSHRSLHIGLI 479  
 480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGCHILRT 539  
 480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGCHILRT 539  
 540 NTGTFGDIRVNIINPPFAQRYVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDY 599  
 540 KSGTFGHIRVNIINPPFAQRYVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDY 599  
 600 KTFRTVGTTPFSFSDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
 600 KTFRTVGTTPFSFSDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
 660 VTALFTSTNPRGLKTDVVDYHIDQVSNLVSDELYLDEKRELFEIVKYAKQIHIERNM 719  
 660 VTALFTSTNPRGLKTDVVDYHIDQVSNLVSDELYLDEKRELFEIVKYAKQIHIERNM 719

RESULT 5  
 US-09-218-942-2  
 ; Sequence 2, Application US/09218942  
 ; Patent No. 6232439  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Oman, Yehia  
 ; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum  
 ; FILE OF INVENTION: Activity  
 ; FILE REFERENCE: Crv11  
 ; CURRENT APPLICATION NUMBER: US/09/218,942  
 ; EARLIER FILING DATE: 1998-12-22  
 ; EARLIER APPLICATION NUMBER: 60/035,361  
 ; EARLIER FILING DATE: 1997-01-10  
 ; EARLIER APPLICATION NUMBER: 09/003,217  
 ; EARLIER FILING DATE: 1998-01-06  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: Patent in Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-09-218-942-2

Query Match 88.7%; Score 3336; DB 3; Length 719;  
 Best Local Similarity 89.2%; Pred. No. 1.7e-294;  
 Matches 642; Conservative 35; Mismatches 41; Indels 2; Gaps 2;

QY 1 MCLKNODKHOSFSSNAKVDKISTSLKNETDIELQINIBHDCMLKMSYENVRPFFVASTI 60  
 DB 1 MCLKNPKHQTLSSNAKVDKIATDSLKNETDIELKNNNEDYLRMSEHESIDPFVASTI 60  
 QY 61 QTGIGIAGKILGTGVFAGVASLYSFIIGELWPKGNQWELLFHEHVEE-INOKISY 119  
 DB 61 QTGIGIAGKILGTGVFAGVASLYSFIIGELWPKGNQWELLFHEHVEE-INOKISY 119  
 QY 120 ARNKALTDKLGDALAVYHDSLSWSVGNRRNTRARSVRSQVYALFELMFKVQLPSFAVS 179  
 DB 120 ARNKALTDKLGDALAVYHDSLSWSVGNRRNTRARSVRSQVYALFELMFKVQLPSFAVS 179

RESULT 6

US-08-286-870A-6  
 ; Sequence 6, Application US/08286870A  
 ; Patent No. 6063605  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ELY, S  
 ; APPLICANT: TAILOR, RH  
 ; APPLICANT: TIPPETT, JM  
 ; APPLICANT: BLENN, RG  
 ; TITLE OF INVENTION: BACTERIAL GENES  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CUSHMAN DABBY & CUSHMAN  
 ; ADDRESSEE: Intellectual Property Group of  
 ; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
 ; STREET: 1100 New York Avenue, N.W.  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005-3918  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/286,870A  
 ; FILING DATE: 05-AUG-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/520228  
 ; FILING DATE: 09-MAY-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 8910624.9  
 ; FILING DATE: 09-MAY-1989

```
/ ATTORNEY/AGENT INFORMATION:
/ NAME: PAUL N. KOKULIS
/ REGISTRATION NUMBER: 16,773
/ REFERENCE/DOCKET NUMBER: 70608/220720
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 861-3000
/ TELEFAX: (202) 822-0944
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 535 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-286-870A-6

Query Match 73.8%; Score 2776; DB 3; Length 535;
Best Local Similarity 99.4%; Pred. No. 1e-243; 0; Indels 2; Gaps 2;
Matches 533; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHHEDCLMKSEYENVEPFVSASTI 60
Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHHEDCLMKSEYENVEPFVSASTI 60
QY 61 QTGIGIAGKILGTLGVPPFAGQVASYLFIKELWPKGKNQWEILFMEHVVEE-INQKISTY 119
Db 61 QTGIGIAGKILGTLGVPPFAGQVASYLFIKELWPKGKNQWEILFMEHVVEE-INQKISTY 119
QY 120 ARNKALTDLKGDLAVHDSLESVGNRNTRARSVVRISOVIALELMFVQKLPSPFVS 179
Db 120 ARNKALTDLKGDLAVHDSLESVGNRNTRARSVVRISOVIALELMFVQKLPSPFVS 179
QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSCHVKWY 239
Db 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSCHVKWY 239
QY 240 STGLNNLRGNAESWRYNQFRDMLTMDLVALPSPDYQWPIKTTAQLTREVYTD 299
Db 240 STGLNNLRGNAESWRYNQFRDMLTMDLVALPSPDYQWPIKTTAQLTREVYTD 299
QY 300 IGTVVHPSPSTTWNNNAPSFAEAAVVRNPHLLDFLEQVTIYSLLSRWNTQVMNM 359
Db 300 IGTVVHPSPSTTWNNNAPSFAEAAVVRNPHLLDFLEQVTIYSLLSRWNTQVMNM 359
QY 360 WGGHKLFEFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVP 419
Db 360 WGGHKLFEFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVP 419
QY 420 RVDHFKFVTHPIASDNFYYPGAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLI 479
Db 420 RVDHFKFVTHPIASDNFYYPGAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLI 479
QY 480 SASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535
Db 480 SASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
/ Sequence 4, Application US/08100709
/ Patent No. 5322687
/ GENERAL INFORMATION:
/ APPLICANT: Donovan, William P.
/ APPLICANT: Tan, Yiping
/ APPLICANT: Jany, Christine S.
/ APPLICANT: Gonzalez Jr., Jose M.
/ TITLE OF INVENTION: BACILLUS THURINGIENSIS clyE4 AND clyE5
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Panich Schwarze Jacobs & Nadel c/o A.S.
/ ADDRESSEE: Nadel
/ STREET: 1601 Market Street, 36th Floor
/ CITY: Philadelphia
```

```
/ STATE: Pennsylvania
/ COUNTRY: U.S.A.
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/100,709
/ FILING DATE: 19930729
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Egolf, Christopher
/ REGISTRATION NUMBER: 27633
/ REFERENCE/DOCKET NUMBER: 7205-49
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-757-1590
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1229 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-100-709-4

Query Match 64.3%; Score 2417.5; DB 1; Length 1229;
Best Local Similarity 65.3%; Pred. No. 1.7e-210;
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

QY 13 SSNAKVDKISTDLKN-ETDIELQ-NINHHEDCLMKSEYENVEPFVSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTOMNLSDPARTIEDSLCAEVNNDIPFVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPFAGQVASYLFIKELWPKGKNQWEILFMEHVVEE-INQKISTYARKNALTDLK 129
Db 67 LGVLGVPPFAGQVASYLFIKELWPKGKNQWEILFMEHVVEE-INQKISTYARKNALTDLK 129
QY 130 GLGDALAVHDSLESVGNRNTRARSVVRISOVIALELMFVQKLPSPFVSAGEVPLPIY 189
Db 126 GLGGRVSRVQQALETWLDNRNDARSIIILERVVALELDITTAIPLFRINNEEVPLLMVY 185
QY 190 AQAAHLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSCHVKWYSTGLNNLRGT 249
Db 186 AQAAHLHLLLRDASIFGSEWGLSSSEISTFFYNQVERAGDYSCHVKWYSTGLNNLRGT 245
QY 250 NAESWRYNQFRDMLTMDLVALPSPDYQWPIKTTAQLTREVYTDIAGTVHHPSPF 309
Db 246 NAESWRYNQFRDMLTMDLVALPSPDYQWPIKTTAQLTREVYTDIAGTVHHPSPF 305
QY 310 TSTTWNNNAPSFAEAAVVRNPHLLDFLEQVTIYSLLSRWNTQVMNMWGGHKLFEFT 369
Db 306 ASTWNNNAPSFAEAAVVRNPHLLDFLEQVTIYSLLSRWNTQVMNMWGGHKLFEFT 365
QY 370 IGTGLNISTQGST-NTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPRVDFHFKFV 428
Db 366 IGTGLNISTQGST-NTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPRVDFHFKFV 422
QY 429 THPIASDNFYYPG-----YAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLI 481
Db 423 ---INPQTYERGATYSPQYQGVQGLDFDSELPETTERPNYESYSHRLSHIGLI 479
QY 482 SHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDIARNTNT 541
Db 480 NTLRAPVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDIARNTNT 539
QY 542 GTFGDIRVNINPPFAQRYVRIRYASTTDLQPHSTINGKAINQGNFSATNRGDEDLYKT 601
Db 540 GTFGDIRVNINPPFAQRYVRIRYASTTDLQPHSTINGKAINQGNFSATNRGDEDLYKT 599
QY 602 FRTVGTTPFSLDVOSTTIGANWSSNGNEVYIDRIEFPVPEVTEAEVDFEKAQKVT 661
Db 600 FRTAGFTFPFLNAQSTFTLGAQSFNS-OEVYIDRVEFPVPAEVTFEAEVDFEKAQKVT 658
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662 ALFTSTNPRGLKTDVYHIDQVSNLVESLSDFFYLDKRELFEIVKYANELHIERNM 719  
659 ALFTSTNPRGLKTDVYHIDQVSNLVESLSDFFYLDKRELFEIVKYANELHIERNM 716

RESULT 8  
US-08-176-865-4  
Sequence 4, Application US/08176865  
Patent No. 5616319  
GENERAL INFORMATION:  
APPLICANT: Donovan, William P.  
APPLICANT: Tan, Yiping  
APPLICANT: Jany, Christine S.  
APPLICANT: Gonzalez Jr., Jose M.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS cRYET4 AND cRYET5  
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
ADDRESS: Nadel  
STREET: 1601 Market Street, 36th Floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/176,865  
FILING DATE: 30-DEC-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/100,709  
FILING DATE: 29-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Egoif, Christopher  
REGISTRATION NUMBER: 27633  
REFERENCE/DOCKET NUMBER: 7205-49  
TELEPHONE: 215-757-1590  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1229 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-176-865-4

Query Match 64.3%; Score 2417.5; DB 1; Length 1229;  
Best Local Similarity 65.3%; Pred. No. 1.7e-210; Indels 19; Gaps 8;  
Matches 469; Conservative 90; Mismatches 140;

13 SSNAKVDKISLTKN-ETDIEIQ-NINHEDECKMSEYENVEFPVSASTIQTGIGIAKI 70  
7 NENEINALSIPVNSPSTQMNLSDPARIEDSLCAEVAENVIDPVSASTVQTGINAGRI 66  
71 LGTLGVFPAGQASLYSIFLIGELWPKGKQWELLFMEHVEE-INQKISTYAEKALTDLK 129  
67 LGVLGVFPAGQASLYSIFLIGELWPKGKQWELLFMEHVEE-INQKISTYAEKALTDLK 125  
130 GLGDALAVYHDSLESWGNNGNNTRARSVRSQYIALELMFVQKLPFSFVSGEVEPLLPY 189  
126 GLGGRYSYQOALETLWLDNRNDRSRIILERYVALELDITTAIFLFRIRNEEVEPLLMY 185  
190 AQAANLHLLLRDASIFGKEWGLSSSISFTYNNQVERAGDYSDHCKVYSGTLNLRGT 249  
186 AQAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYETYSNHCVCQWYNTGLNLRGT 245  
250 NAESWRYNQFRRLTLGLVLDLVALPFSYDTRTYPINTSAQLTREIYTDPIGRNAPSGF 305

246 NAESWLRNQFRRLTLGLVLDLVALPFSYDTRTYPINTSAQLTREIYTDPIGRNAPSGF 305  
310 TSTTWYNNAPSFAIAAUVNRPHLDLEFOVTIYSLLSRWNSQYMMWGGHKLFRFT 369  
306 ASTWNFNNAFSAIAEAAIFRPHLLDFPEQLTIYASASRWSTQHMYVWGHRLNFRP 365  
370 IGGTLNISTQGST-NTSINPVTLPTSRDVRVYRTSLAGLNLFLTPQVNGVPRVDFFHWKFV 428  
366 IGGTLNISTQGST-NTSINPVTLPTSRDVRVYRTSLAGLNLFLTPQVNGVPRVDFFHWKFV 422  
429 THPIASDNFYYPG-----YAGITQLODSNELPPEATGQPNVSVSHSLSHIGLISA 481  
423 ---INPQNIYERGATTYSQPYQGVGIQFDSSETLPPETTERPNYESVSHSLSHIGLII 479  
482 SHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSGAAVVRGPGFTCGDILRRNT 541  
480 NTLRAPVSWTHRSADRNTTIGPNRITQIPLVKALNLSHGVTVVGGPGFTCGDILRRNT 539  
542 GTFGDIRVNINPFPFAQRYRIRYASTTDLQPHTSINGKAINOGNFSATMNGEDLDYKT 601  
540 GTFGDIRVNINPFPFAQRYRIRYASTTDLQPHTSINGKAINOGNFSATMNGEDLDYKT 599  
602 FRTVGFTTPESELDVQSTFTIGAMNFSNGEVYIDRIEFVPEVETYEAYDPEKAQKVT 661  
600 FRTAGFSTPFNFNAQSTFTLGAQFSN-QEVYIDRIEFVPEVETYEAYDPEKAQKAVN 658  
662 ALFTSTNPRGLKTDVYHIDQVSNLVESLSDFFYLDKRELFEIVKYANELHIERNM 719  
659 ALFTSTNPRGLKTDVYHIDQVSNLVESLSDFFYLDKRELFEIVKYANELHIERNM 716

RESULT 9  
US-08-474-038-4  
Sequence 4, Application US/08474038  
Patent No. 5679343  
GENERAL INFORMATION:  
APPLICANT: Donovan, William P.  
APPLICANT: Tan, Yiping  
APPLICANT: Jany, Christine S.  
APPLICANT: Gonzalez Jr., Jose M.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS cRYET4 AND cRYET5  
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
ADDRESS: Nadel  
STREET: 1601 Market Street, 36th Floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,038  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/176,865  
FILING DATE: 30-DEC-1993  
APPLICATION NUMBER: US 08/100,709  
FILING DATE: 29-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Egoif, Christopher  
REGISTRATION NUMBER: 27633  
REFERENCE/DOCKET NUMBER: 7205-49  
TELEPHONE: 215-757-1590  
INFORMATION FOR SEQ ID NO: 4:

## SEQUENCE CHARACTERISTICS:

LENGTH: 1229 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-474-038-4

Query Match 64.3%; Score 2417.5; DB 1; Length 1229;

Best Local Similarity 65.3%; Pred. No. 1.7e-210;

Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

```
QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLKMSEYENVPFVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPTVSNPSTQMNLSPDARIEDSLCAEVANNIDPFVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWELFMHEVVEE-INQKISTYARKKALTDLK 129
DB 67 LGVLGVPPAGQVASYLSFILGELWPKGNQWELFMHEVVEE-INQKISTYARKKALTDLK 125
QY 130 GLGDALAVYHDSLESWGNRNTRARSVRSQVIALELMFVQKLPFAVSGEVPPLPIY 189
DB 126 GLGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPLFRIRNEEVPPLMWY 185
QY 190 AQAAHLHLRLDASIFGKMWGLSSSEISTFYNRQVERAGDYSCHVCWKYSTGLNLRGT 249
DB 186 AQAAHLHLRLDASIFGKMWGLSSSEISTFYNRQVERAGDYSCHVCWKYSTGLNLRGT 245
QY 250 NAESWVRNQFRDMLTLMVLVALPSPYDTOMYPIKTTAQLTREYVTDATGTVHPHPSF 309
DB 246 NAESWVRNQFRDMLTLMVLVALPSPYDTOMYPIKTTAQLTREYVTDATGTVHPHPSF 305
QY 310 TSTTWNNAFSAIEAAVVRNPHLLDFLEQVITYSLLSRMSNTQYMMNMGHKLFRPT 369
DB 306 ASTNWFNNAPSAIEAAVVRNPHLLDFLEQVITYSLLSRMSNTQYMMNMGHKLFRPT 365
QY 370 IGGTLNISTQGST-NTSINPVTLPFTSRDVRYESLAGNLFELTOPVNGVPRVDFHKEV 428
DB 366 IGGTLNISTQGST-NTSINPVTLPFTSRDVRYESLAGNLFELTOPVNGVPRVDFHKEV 422
QY 429 THPIASDNFPYPG-----YAGIGTQLODSNEIPLPEATGQPNYESYSHRSLHIGLISA 481
DB 423 ---INPQNIYERGATTYSQYQGVQLFDSSETLPPETTERPNYESYSHRSLHIGLII 479
QY 482 SHVKALVSWTHRSADRTNITPNSITQIPVKAFNLSSGAAVVRGPGTGGDILARTNT 541
DB 480 NTLRAPVSWTHRSADRTNITPNSITQIPVKAFNLSSGAAVVRGPGTGGDILARTNT 539
QY 542 GTFGDIRVINPFAQRYVRIRYASTTDLQFTSINGKAINQCNFSATWNGEDLDYKT 601
DB 540 GTFGDIRVINPFAQRYVRIRYASTTDLQFTSINGKAINQCNFSATWNGEDLDYKT 599
QY 602 FRTVGFTTTPFDVQSTFTIGAWNFSSGNEVVIDRIFVPVVTVEAEYDPEKAQKYT 661
DB 600 FRTAGSTFNFNAQSTTTLGQSFN-QEVVIDRIFVPVVTVEAEYDPEKAQKAVN 658
QY 662 ALFTSTNPRGLKTDVXDYHIDQVSNLSLSDSEFYLDKRELPEIVKYANELHIERNM 719
DB 659 ALFTSTNPRGLKTDVXDYHIDQVSNLSLSDSEFYLDKRELPEIVKYAKRLSDREL 716
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## RESULT 10

US-08-779-046-4

Sequence 4, Application US/08779046

Patent No. 5854053

GENERAL INFORMATION:

APPLICANT: Donovan, William P.

APPLICANT: Tan, Yuxing

APPLICANT: Jany, Christine S.

APPLICANT: Gonzalez Jr., Jose M.

TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYETS

TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Panitch Schwarze Jacobs &amp; Nadel c/o A.S.

ADDRESSEE: Nadel

STREET: 1601 Market Street, 36th Floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/779,046

FILING DATE: 06-JAN-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/100,709

FILING DATE: 29-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Egolf, Christopher

REGISTRATION NUMBER: 27633

REFERENCE/DOCKET NUMBER: 7205-49

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-757-1590

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1229 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-779-046-4

Query Match 64.3%; Score 2417.5; DB 2; Length 1229;

Best Local Similarity 65.3%; Pred. No. 1.7e-210;

Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

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QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCLKMSEYENVPFVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPTVSNPSTQMNLSPDARIEDSLCAEVANNIDPFVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWELFMHEVVEE-INQKISTYARKKALTDLK 129
DB 67 LGVLGVPPAGQVASYLSFILGELWPKGNQWELFMHEVVEE-INQKISTYARKKALTDLK 125
QY 130 GLGDALAVYHDSLESWGNRNTRARSVRSQVIALELMFVQKLPFAVSGEVPPLPIY 189
DB 126 GLGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPLFRIRNEEVPPLMWY 185
QY 190 AQAAHLHLRLDASIFGKMWGLSSSEISTFYNRQVERAGDYSCHVCWKYSTGLNLRGT 249
DB 186 AQAAHLHLRLDASIFGKMWGLSSSEISTFYNRQVERAGDYSCHVCWKYSTGLNLRGT 245
QY 250 NAESWVRNQFRDMLTLMVLVALPSPYDTOMYPIKTTAQLTREYVTDATGTVHPHPSF 309
DB 246 NAESWVRNQFRDMLTLMVLVALPSPYDTOMYPIKTTAQLTREYVTDATGTVHPHPSF 305
QY 310 TSTTWNNAFSAIEAAVVRNPHLLDFLEQVITYSLLSRMSNTQYMMNMGHKLFRPT 369
DB 306 ASTNWFNNAPSAIEAAVVRNPHLLDFLEQVITYSLLSRMSNTQYMMNMGHKLFRPT 365
QY 370 IGGTLNISTQGST-NTSINPVTLPFTSRDVRYESLAGNLFELTOPVNGVPRVDFHKEV 428
DB 366 IGGTLNISTQGST-NTSINPVTLPFTSRDVRYESLAGNLFELTOPVNGVPRVDFHKEV 422
QY 429 THPIASDNFPYPG-----YAGIGTQLODSNEIPLPEATGQPNYESYSHRSLHIGLISA 481
DB 423 ---INPQNIYERGATTYSQYQGVQLFDSSETLPPETTERPNYESYSHRSLHIGLII 479
QY 482 SHVKALVSWTHRSADRTNITPNSITQIPVKAFNLSSGAAVVRGPGTGGDILARTNT 541
DB 480 NTLRAPVSWTHRSADRTNITPNSITQIPVKAFNLSSGAAVVRGPGTGGDILARTNT 539
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 372-5800
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-448-170-10

Query Match 61.6%; Score 2318.5; DB 1; Length 488;
Best Local Similarity 89.4%; Pred. No. 3.8e-202;
Matches 445; Conservative 13; Mismatches 29; Indels 11; Gaps 3;

QY 1 MKLKQDKHQSPSSNAKVDKISTDSLKNETDIELQINHHEDCLKMSEYENVPFVSASTI 60
DB 1 MRSKQNMHQSLSNATVDKNFTGSLNNTNTLQNFH-----EGIEPFVSASTI 51
QY 61 QTGIGIAGKILGTLPVPFAGQVASYLSTFGLGELWPKGKQWEILFMEHVEE-INQIKISTY 119
DB 52 QTGIGIVGKILGNLGVPPAGQVASYLSTFGLGELWPKGKQWEI-FMEHVEELINQIKISTY 110
QY 120 ARNKALTDLKGDLALAVYHDSLESVGNRNNTARSVRSQYIALELMFVQKLPSPFAYS 179
DB 111 ARNKALADLKGDLALAVYHDSLESVGNRNNTARSVRSQYITILELMFVQSLPSFAYS 170
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKQWGLSDSEISTFTYNRQVERAGDYSCHVKWY 239
DB 171 GEEVPLLPPIYAQAANLHLLLRDASIFGKQWGLSDSEISTFTYNRQSGKSKSEYSDHCVKY 230
QY 240 STGLANLRGTNAESWVRYNQFRDMLVLDLVALFPSTDTQMPYIKTTAQLTREVYTTA 299
DB 231 NTGLNRLMGNAESWVRYNQFRDMLVLDLVALFPSTDTQMPYIKTTAQLTREVYTTA 290
QY 300 ICTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMMN 359
DB 291 ICTVHPHPSFTSTTWYNNAPSFSTIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMMN 350

; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,170
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: M/S 102DCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 372-8100
; TELEFAX: (352) 375-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-961-803-10

Query Match 61.6%; Score 2318.5; DB 3; Length 488;
Best Local Similarity 89.4%; Pred. No. 3.8e-202;
Matches 445; Conservative 13; Mismatches 29; Indels 11; Gaps 3;

QY 1 MKLKQDKHQSPSSNAKVDKISTDSLKNETDIELQINHHEDCLKMSEYENVPFVSASTI 60
DB 1 MRSKQNMHQSLSNATVDKNFTGSLNNTNTLQNFH-----EGIEPFVSASTI 51
QY 61 QTGIGIAGKILGTLPVPFAGQVASYLSTFGLGELWPKGKQWEILFMEHVEE-INQIKISTY 119
DB 52 QTGIGIVGKILGNLGVPPAGQVASYLSTFGLGELWPKGKQWEI-FMEHVEELINQIKISTY 110
QY 120 ARNKALTDLKGDLALAVYHDSLESVGNRNNTARSVRSQYIALELMFVQKLPSPFAYS 179
DB 111 ARNKALADLKGDLALAVYHDSLESVGNRNNTARSVRSQYITILELMFVQSLPSFAYS 170
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKQWGLSDSEISTFTYNRQVERAGDYSCHVKWY 239
DB 171 GEEVPLLPPIYAQAANLHLLLRDASIFGKQWGLSDSEISTFTYNRQSGKSKSEYSDHCVKY 230
QY 240 STGLANLRGTNAESWVRYNQFRDMLVLDLVALFPSTDTQMPYIKTTAQLTREVYTTA 299
DB 231 NTGLNRLMGNAESWVRYNQFRDMLVLDLVALFPSTDTQMPYIKTTAQLTREVYTTA 290
QY 300 ICTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMMN 359
DB 291 ICTVHPHPSFTSTTWYNNAPSFSTIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMMN 350

; TITLE OF INVENTION: Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PSI58C2, Active Against Lepidopteran Pests, and Genes
```

Tue Feb 15 10:07:55 2005

Qy 360 WGGHKLFRITGGTNTSTOGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVP 419  
Db 351 WGGHKLFRITGGTNTSTOGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVP 410  
Qy 420 RVDPHMKFVTHPTIASDNFFYPGVAGIGTQDSENELPPEATQPNYESYSHRLSHIGLI 479  
Db 411 RVDPHMKFVTHPTIASDNFFYPGVAGIGTQDSENELPPEATQPNYESYSHRLSHIGLI 470  
Qy 480 SASHVKALVSWTHRSAD 497  
Db 471 SASHVKALVSWTHRSAD 488

RESULT 14  
US-07-951-715A-7  
; Sequence 7, Application US/07951715A  
; Patent No. 5625136

GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
APPLICANT: Desai, Nalini M.  
APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/951,715A  
FILING DATE: 25-SEP-1992  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8615  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 7:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-07-951-715A-7  
Query Match 59.5%; Score 2236.5; DB 1; Length 1207;

Best Local Similarity 64.1%; Pred. No. 5e-194;  
Matches 441; Conservative 76; Mismatches 156; Indels 15; Gaps 7;  
Qy 40 EDCLMGSEYENVEPVSASTIOTIGTAGILGTGVPFAGOVASLYSFTILGELWPKGN 99  
Db 10 EDSLCIAEGNNIDPVSASTVQTGINIAGRILGVLGVPFAGQASLYSFTILGELWPKGRD 69  
Qy 100 QWEILFWEHVEE-INOKISTVARNKALTDLKGDLALAVHDSLESVWGNRNNTARSV 158  
Db 70 QWEI-FLEHVEQLINQITENARNATALRQGLGDSFRAYQOSLEDWLENRDDARTARSVL 128  
Qy 159 RSQYIALELMFVQKLPSPAVSGEEVPLPIYQAANLHLLLRDASIFGKENGWLSSEIS 218  
Db 129 YTOYIALELDPLNAPLFAIRNQEVPLIMVYQAANLHLLLRDASLFGSEFGTSQEIQ 188  
Qy 219 TFYNQVERAGDYSCHCVKWTSTGLNNLRGTNAESWRYNQFRDMLTLMVLVLPF 278  
Db 189 RYERQVERTRDYSYCVWEYNTGLNSLRGTNAESWRYNQFRDMLTLMVLVLPF 248  
Qy 279 DTOMYPIKTTAQLTREVTDAIGTVHPHPSFTSTTWYNNAPSPSAIAEAAVVRPHLLDF 338  
Db 249 DTRTPINTSAQLTREVTDAIGAT-GVNMAWMYNNAPSPSAIAEAAVVRPHLLDF 306  
Qy 339 LEQVTIYLLSRWSNTQYNNMGHKLFRITGGTNTSTOGSTNTSINPVTLPFTSRDV 398  
Db 307 LEQLTIFSASSRWSNRHTMYWRGHTIOSRPIGGLNTSTHGATNTSINPVTLPFTSRDV 366  
Qy 399 YRTESLAGLNLF-LTOPVNGVPRVDHFHVKFTHP-----IASDNFFYPGVAGIGTQLOD 451  
Db 367 YRTESVAGVLLGVIPLHGVPTVRNF--TFNQNISDRGTANYSQP-YESPGLQLKD 422  
Qy 452 SENELPPEATQPNYESYSHRLSHIGLISASHVKALVSWTHRSADRTNTEPNISITQIP 511  
Db 423 SETELPPTETTERPNYESYSHRLSHIGILOSARNVPVSWTHRSADRTNTEPNISITQIP 482  
Qy 512 LKAFNLSSGAAVVRGPGTGGDILRRNTGTGFDIRVNNINPFAQRYKVRIRYASTTDL 571  
Db 483 MTKASELPQSTTVVRGPGTGGDILRRNTGTGFDIRVNNINPFAQRYKVRIRYASTTDL 542  
Qy 572 QFHTSINGKAINQGNFSATMNGEDLDYKTFRTVGTFTTFFSFLDVQSTTIGAMNFSSGN 631  
Db 543 DFFVSRGGTTVANNFRFLRTMNSGDELKYGNFVRRATFTTFTTQODIIRTSIQGLSGNG 602  
Qy 632 EYVIDRIEFPVVEVTEAEYDEKAEKVTAFTSTNPRGLKTDVXDYHIDQVSNLVESL 691  
Db 603 EYVIDKIEIIPVTATFEAEYDLERAQEVNALTNTNPRRLKTDVTDYHIDQVSNLVACL 662  
Qy 692 SDEFYLDKEKELFEIVKYANLHIERNM 719  
Db 663 SDEFCLDEKELFEIVKYAKRLSDERNL 690

RESULT 15  
US-08-459-448A-7  
; Sequence 7, Application US/08459448A  
; Patent No. 5859336  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
APPLICANT: Desai, Nalini M.  
APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.



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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:20:21 ; Search time 98.3514 Seconds  
(without alignments)  
2827.419 Million cell updates/sec

Title: US-10-019-823B-58

Perfect score: 3761

Sequence: 1 MKLNQDKHQSFSSNAKVDK.....KRELFEIVKYANELHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Genesecp1980s:\*
- 2: Genesecp1990s:\*
- 3: Genesecp2000s:\*
- 4: Genesecp2001s:\*
- 5: Genesecp2002s:\*
- 6: Genesecp2003as:\*
- 7: Genesecp2003bs:\*
- 8: Genesecp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3736	99.3	719	4	AAB66911 Insectici
2	3736	99.3	719	6	Aae36275 B. thurin
3	3724	99.0	719	4	AAB66908 Insectici
4	3724	99.0	719	4	AAB66909 Insectici
5	3724	99.0	719	6	Aae36273 B. thurin
6	3724	99.0	719	6	Aae36272 B. thurin
7	3724	99.0	719	8	ADR89421 cryIIa. 1
8	3720	98.9	719	4	AAB66910 Insectici
9	3720	98.9	719	6	Aae36274 B. thurin
10	3715	98.8	719	4	Aau02095 Bacillus
11	3703	98.5	719	2	AAR08041 81 kd end
12	3692.5	98.2	718	6	Aae36271 B. thurin
13	3686.5	98.0	718	4	AAB66907 Insectici
14	3517	93.5	719	7	ADM74717 B. thurin
15	3484	92.6	719	6	AAB66912 Insectici
16	3484	92.6	719	6	Aae36276 B. thurin
17	3442.5	91.5	710	4	Aau02041 B. thurin
18	3363	89.4	719	3	ABB07073 Bacillus
19	3341	88.8	719	2	Aaw49089 Bacillus
20	3257	86.6	1217	4	Aau02092 Bacillus
21	2705	71.9	1208	8	Aau02093 Bacillus
22	2419	64.3	1230	8	ADK98484 B thuring
23	2419	64.3	1230	8	ADK98489 B thuring
24	2419	64.3	1230	8	ADK98481 B thuring
25	2419	64.3	1230	8	ADK98491 B thuring

ALIGNMENTS

RESULT 1

AAB66911  
ID AAB66911 standard; protein; 719 AA.

XX AC AAB66911;

XX DT 12-APR-2001 (first entry)

DE Insecticidal protein cryIIa5.

XX KW Insecticide; transgenic plant; insect-resistance.

XX OS Paecilomyces sp.

XX PN WO200100841-A1.

XX PD 04-JAN-2001.

XX PF 23-JUN-2000; 2000WO-GB002457.

XX PR 29-JUN-1999; 99GB-00015215.

XX PR 23-DEC-1999; 99GB-00030536.

XX (ZENE ) ZENECA LTD.

PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;

PI Vincent JL, Lee MD;

DR WPI; 2001-123015/13.

PT Novel insecticidal protein obtained from species of Paecilomyces for controlling insects, and for insect-resistant transgenic plant production.

XX Claim 14; Page 62-64; 72pp; English.

XX The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed

XX Sequence 719 AA;

Query Match 99.3%; Score 3736; DB 4; Length 719;

Best Local Similarity 99.7%; Pred. No. 1.2e-291;

Matches 718; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 MCLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQNHEDCLKMSYENVEPFFVSASTI 60  
DB 1 MCLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQNHEDCLKMSYENVEPFFVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASLYSFIIGELWPKGNQWELFMEHVEE-INQKISTY 119  
DB 61 QTGIGIAGKILGTGVPFAGQVASLYSFIIGELWPKGNQWELFMEHVEE-INQKISTY 119  
QY 120 ARNKALTDLKLGDALAVYHDSLESWGNNRNRARSVRSQYIALELMFVKLPSPFAYS 179  
DB 120 ARNKALTDLKLGDALAVYHDSLESWGNNRNRARSVRSQYIALELMFVKLPSPFAYS 179  
QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSISTFYNRQVERAGDYSCHVKWY 239  
DB 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSISTFYNRQVERAGDYSCHVKWY 239  
QY 240 STGLNLRGNTNAESWRYNQFRDMLVLDLVALPFSYDTQMPYIKTTAQLTREVYTD 299  
DB 240 STGLNLRGNTNAESWRYNQFRDMLVLDLVALPFSYDTQMPYIKTTAQLTREVYTD 299  
QY 300 IGVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMMN 359  
DB 300 IGVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMMN 359  
QY 360 WGGHKLFRITGGTLNISTQSGTNTSINPVTLPFTSRDVRVYTESLAGNLFLTQPVNGVP 419  
DB 360 WGGHKLFRITGGTLNISTQSGTNTSINPVTLPFTSRDVRVYTESLAGNLFLTQPVNGVP 419  
QY 420 RVDHFWKFTVTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
DB 420 RVDHFWKFTVTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQPLVKAFLNLSGAAVVRGPGTGGDILRRT 539  
DB 480 SASHVKALVYSWTHRSADRTNTEPNSITQPLVKAFLNLSGAAVVRGPGTGGDILRRT 539  
QY 540 NTGTFGDIRVNIINPPFAQRYRIRYASTTDLOPHTSINGKAINQGNFSATMNRGEDLDY 599  
DB 540 NTGTFGDIRVNIINPPFAQRYRIRYASTTDLOPHTSINGKAINQGNFSATMNRGEDLDY 599  
QY 600 KTFRTVGTFTPPSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVVPVETVEAEYDPEKAQEK 659  
DB 600 KTFRTVGTFTPPSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVVPVETVEAEYDPEKAQEK 659  
QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719  
DB 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719

## RESULT 2

AAE36275  
ID AAE36275 standard; protein; 719 AA.

AC AAE36275;

XX 26-JUN-2003 (first entry)

DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa5.

KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

OS Bacillus thuringiensis.

PN WO2002098911-A2.

XX 12-DEC-2002.

PF 30-MAY-2002; 2002WO-GB002666.

PR 07-JUN-2001; 2001GB-00013900.

PA (SYGN ) SYNGENTA LTD.

Vincent JL, Viner R;

WPI; 2003-175137/17.

New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

Claim 12; Page 53-56; 67pp; English.

The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insect. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

Sequence 719 AA;

Query Match 99.3%; Score 3736; DB 6; Length 719;

Best Local Similarity 99.7%; Pred. No. 1.2e-291;

Matches 718; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 MCLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQNHEDCLKMSYENVEPFFVSASTI 60  
DB 1 MCLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQNHEDCLKMSYENVEPFFVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASLYSFIIGELWPKGNQWELFMEHVEE-INQKISTY 119  
DB 61 QTGIGIAGKILGTGVPFAGQVASLYSFIIGELWPKGNQWELFMEHVEE-INQKISTY 119  
QY 120 ARNKALTDLKLGDALAVYHDSLESWGNNRNRARSVRSQYIALELMFVKLPSPFAYS 179  
DB 120 ARNKALTDLKLGDALAVYHDSLESWGNNRNRARSVRSQYIALELMFVKLPSPFAYS 179  
QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSISTFYNRQVERAGDYSCHVKWY 239  
DB 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSISTFYNRQVERAGDYSCHVKWY 239  
QY 240 STGLNLRGNTNAESWRYNQFRDMLVLDLVALPFSYDTQMPYIKTTAQLTREVYTD 299  
DB 240 STGLNLRGNTNAESWRYNQFRDMLVLDLVALPFSYDTQMPYIKTTAQLTREVYTD 299  
QY 300 IGVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMMN 359  
DB 300 IGVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMMN 359  
QY 360 WGGHKLFRITGGTLNISTQSGTNTSINPVTLPFTSRDVRVYTESLAGNLFLTQPVNGVP 419  
DB 360 WGGHKLFRITGGTLNISTQSGTNTSINPVTLPFTSRDVRVYTESLAGNLFLTQPVNGVP 419  
QY 420 RVDHFWKFTVTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
DB 420 RVDHFWKFTVTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQPLVKAFLNLSGAAVVRGPGTGGDILRRT 539  
DB 480 SASHVKALVYSWTHRSADRTNTEPNSITQPLVKAFLNLSGAAVVRGPGTGGDILRRT 539  
QY 540 NTGTFGDIRVNIINPPFAQRYRIRYASTTDLOPHTSINGKAINQGNFSATMNRGEDLDY 599  
DB 540 NTGTFGDIRVNIINPPFAQRYRIRYASTTDLOPHTSINGKAINQGNFSATMNRGEDLDY 599  
QY 600 KTFRTVGTFTPPSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVVPVETVEAEYDPEKAQEK 659  
DB 600 KTFRTVGTFTPPSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVVPVETVEAEYDPEKAQEK 659  
QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719  
DB 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719

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RESULT 3
AAB66908
ID AAB66908 standard; protein; 719 AA.
XX
AC AAB66908;
XX
DT 12-APR-2001 (first entry)
DE Insecticidal protein cryIIa2.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX
OS Paecilomyces sp.
XX
PN WO200100841-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-GB002457.
XX
PR 29-JUN-1999; 99GB-00015215.
PR 23-DEC-1999; 99GB-00030536.
XX
PA (ZENE ) ZENECA LTD.
XX
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX
DR WPI; 2001-123015/13.
XX
PT Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
XX
PS Claim 14; Page 55-57; 72pp; English.
XX
CC The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
XX
SQ Sequence 719 AA;

Query Match          99.0%; Score 3724; DB 4; Length 719;
Best Local Similarity 99.4%; Pred. No. 1.1e-290;
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEHDCMKSEYENVEPFFVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEHDCMKSEYENVEPFFVSASTI 60
QY 61 QTGIGIAGKILGTLGVPPFAGQVNASLYSPILGELMPKGNQWEILFMEHVEE-INQKISTY 119
DB 61 QTGIGIAGKILGTLGVPPFAGQVNASLYSPILGELMPKGNQWEI-FMEHVEEIIINQKISTY 119
QY 120 ARNKALTDLKLGDALAVHDSLESVWGNRNNTARSVRSQVIALELMFVOKLPSFAVS 179
DB 120 ARNKALTDLKLGDALAVHDSLESVWGNRNNTARSVRSQVIALELMFVOKLPSFAVS 179
QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNRQVERAGDYSCHVKWY 239
DB 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNRQVERAGDYSCHVKWY 239
QY 240 STGLNNLRGTNAESWRYNQFRDMLTLMVLDLVALPFSYDTQMPYIKTTAQLTREVYTTA 299
DB 240 STGLNNLRGTNAESWRYNQFRDMLTLMVLDLVALPFSYDTQMPYIKTTAQLTREVYTTA 299
QY 300 IGTVHPHPSFTSTWYNNNAPSFAEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMN 359
DB 300 IGTVHPHPSFTSTWYNNNAPSFAEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMN 359

RESULT 4
AAB66909
ID AAB66909 standard; protein; 719 AA.
XX
AC AAB66909;
XX
DT 12-APR-2001 (first entry)
DE Insecticidal protein cryIIa3.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX
OS Paecilomyces sp.
XX
PN WO200100841-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-GB002457.
XX
PR 29-JUN-1999; 99GB-00015215.
PR 23-DEC-1999; 99GB-00030536.
XX
PA (ZENE ) ZENECA LTD.
XX
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX
DR WPI; 2001-123015/13.
XX
PT Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
XX
PS Claim 14; Page 57-59; 72pp; English.
XX
CC The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
XX
SQ Sequence 719 AA;

Query Match          99.0%; Score 3724; DB 4; Length 719;
Best Local Similarity 99.4%; Pred. No. 1.1e-290;
Matches 716; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

QY 360 WGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVP 419
DB 360 WGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVP 419
QY 420 RVDFWKFWTHPIASDNFYYPGYAGTGTQLODSENELPPEATGQPNYESYSHLSHIGLI 479
DB 420 RVDFWKFWTHPIASDNFYYPGYAGTGTQLODSENELPPEATGQPNYESYSHLSHIGLI 479
QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGFGFTGGDLRLRT 539
DB 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGFGFTGGDLRLRT 539
QY 540 NTGTGDIRVNIINPPFAQRYRIRYASTTDIQLFHTSINGKAINQCNFSAATWNRGDDLY 599
DB 540 NTGTGDIRVNIINPPFAQRYRIRYASTTDIQLFHTSINGKAINQCNFSAATWNRGDDLY 599
QY 600 KTFRTVGTTPSFVLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659
DB 600 KTFRTVGTTPSFVLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659
QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKEKELFEIVKYAKQLHIERNM 719
DB 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKEKELFEIVKYAKQLHIERNM 719
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QY 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P F V S A S T I 60  
D B 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P F V S A S T I 60  
QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E - I N Q I S T Y 119  
D B 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I - F M E H V E E I I N Q I S T Y 119  
QY 120 A R N K A L T D L K G L D A L A V H D S L E S W G N R N N T R A S V V R S O Y I A L E M F V K L P S F A V S 179  
D B 120 A R N K A L T D L K G L D A L A V H D S L E S W G N R N N T R A S V V R S O Y I A L E M F V K L P S F A V S 179  
QY 180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q R V E R A G D Y S D H C V K W Y 239  
D B 180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q R V E R A G D Y S H C V K W Y 239  
QY 240 S T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A 299  
D B 240 S T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A 299  
QY 300 I G T V H P H S F T S T T W Y N N A P S F A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q M N M 359  
D B 300 I G T V H P H S F T S T T W Y N N A P S F A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q M N M 359  
QY 360 W G H K L E F R T I G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S I A G L N L F L T Q P V N G V P 419  
D B 360 W G H K L E F R T I G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S I A G L N L F L T Q P V N G V P 419  
QY 420 R V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I 479  
D B 420 R V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I 479  
QY 480 S A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G D I L R R T 539  
D B 480 S A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G D I L R R T 539  
QY 540 N T G T F G D I R V N I N P P F A Q R Y R I R Y A S T T D L O F H T S I N G K A I N Q G N F S A T M N R G E D L D Y 599  
D B 540 N T G T F G D I R V N I N P P F A Q R Y R I R Y A S T T D L O F H T S I N G K A I N Q G N F S A T M N R G E D L D Y 599  
QY 600 K T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659  
D B 600 K T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659  
QY 660 V T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719  
D B 660 V T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719

RESULT 5  
AAE36273 standard; protein; 719 AA.  
AC AAE36273;  
XX AAE36273;  
DT 26-JUN-2003 (first entry)  
XX B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.  
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.  
XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
XX Bacillus thuringiensis.  
OS Bacillus thuringiensis.  
XX WO200298911-A2.  
XX 12-DEC-2002.  
XX 30-MAY-2002; 2002WO-GB002666.  
XX 07-JUN-2001; 2001GB-00013900.  
XX (SYGN ) SYNGENTA LTD.

P I Vincent JL, Viner R;  
D R WPI; 2003-175137/17.  
X X New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
P T Claim 12; Page 47-50; 67pp; English.  
X X The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
X X Sequence 719 AA;

Query Match 99.0%; Score 3724; DB 6; Length 719;  
Best Local Similarity 99.4%; Pred. No. 1, le-290;  
Matches 716; Conservative 1; Mismatches 1; Indels 2; Gaps 2;  
QY 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P F V S A S T I 60  
D B 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V P F V S A S T I 60  
QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E - I N Q I S T Y 119  
D B 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I - F M E H V E E I I N Q I S T Y 119  
QY 120 A R N K A L T D L K G L D A L A V H D S L E S W G N R N N T R A S V V R S O Y I A L E M F V K L P S F A V S 179  
D B 120 A R N K A L T D L K G L D A L A V H D S L E S W G N R N N T R A S V V R S O Y I A L E M F V K L P S F A V S 179  
QY 180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q R V E R A G D Y S D H C V K W Y 239  
D B 180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q R V E R A G D Y S H C V K W Y 239  
QY 240 S T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A 299  
D B 240 S T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A 299  
QY 300 I G T V H P H S F T S T T W Y N N A P S F A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q M N M 359  
D B 300 I G T V H P H S F T S T T W Y N N A P S F A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q M N M 359  
QY 360 W G H K L E F R T I G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S I A G L N L F L T Q P V N G V P 419  
D B 360 W G H K L E F R T I G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S I A G L N L F L T Q P V N G V P 419  
QY 420 R V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I 479  
D B 420 R V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I 479  
QY 480 S A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G D I L R R T 539  
D B 480 S A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G D I L R R T 539  
QY 540 N T G T F G D I R V N I N P P F A Q R Y R I R Y A S T T D L O F H T S I N G K A I N Q G N F S A T M N R G E D L D Y 599  
D B 540 N T G T F G D I R V N I N P P F A Q R Y R I R Y A S T T D L O F H T S I N G K A I N Q G N F S A T M N R G E D L D Y 599  
QY 600 K T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659  
D B 600 K T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659  
QY 660 V T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719  
D B 660 V T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719

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RESULT 6
AAE36272
ID AAE36272 standard; protein; 719 AA.
XX
AC AAE36272;
XX
DT 26-JUN-2003 (first entry)
XX
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.
XX
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX
OS
XX
PN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN ) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-
PT terminus, useful as an active ingredient of a pesticide.
XX
PS Claim 12; Page 44-47; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine
CC motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC invention are useful for producing plants or plant parts that are
CC resistant to insects. The protein or synergistic combination is useful as
CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify
CC other proteins with insecticidal activity. The present sequence is
CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This
CC sequence is used in the invention
XX
SQ Sequence 719 AA;

Query Match          99.0%; Score 3724; DB 6; Length 719;
Best Local Similarity 99.3%; Pred. No. 1.le-290;
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCIKMSEYENVPFVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCIKMSEYENVPFVSASTI 60
QY 61 QTGIGIAGKILGTLGVFPAGQVASYLSFILGELWPKGKNQWEILFMHVEE-INQKISTY 119
DB 61 QTGIGIAGKILGTLGVFPAGQVASYLSFILGELWPKGKNQWEI-FMHVEEIIINQKISTY 119
QY 120 ARNKALTDLKGLDALAVVHDSLSVWGNRNTRARSVVRQYIALELMFVOKLPSFAYS 179
DB 120 ARNKALTDLKGLDALAVVHDSLSVWGNRNTRARSVVRQYIALELMFVOKLPSFAYS 179
QY 180 GBEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSDHCVKWY 239
DB 180 GBEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSDHCVKWY 239
QY 240 STGLNLRGNTAESWRYNQFRDWTLMVLDLVALPSPYDQNYPIKTTAQLTREYVYDA 299
DB 240 STGLNLRGNTAESWRYNQFRDWTLMVLDLVALPSPYDQNYPIKTTAQLTREYVYDA 299
QY 300 IGTVHPHPSFTSTWTNNNAPSFAEAAVVRNPHLLDFLEQVTIYSLSRNSNTQYMN 359
DB 300 IGTVHPHPSFTSTWTNNNAPSFAEAAVVRNPHLLDFLEQVTIYSLSRNSNTQYMN 359

360 WGGHKLPRRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRTTESLAGLNLFLTQPVNGVP 419
360 WGGHKLPRRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRTTESLAGLNLFLTQPVNGVP 419
420 RYDFHWKFWTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
420 RYDFHWKFWTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539
480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539
540 NTGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGSDLDY 599
540 NTGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGSDLDY 599
600 KTFRTVGFTTTPSFILDVQSTFTIGAWNFSSGNEVIDRIEFVVPVEVYEAEDYDFAQAEK 659
600 KTFRTVGFTTTPSFILDVQSTFTIGAWNFSSGNEVIDRIEFVVPVEVYEAEDYDFAQAEK 659
660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELPEIVKYANELHIERNM 719
660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELPEIVKYANELHIERNM 719

RESULT 7
ADR89421
ID ADR89421 standard; protein; 719 AA.
XX
AC ADR89421;
XX
DT 18-NOV-2004 (first entry)
XX
DE cryIIa.
XX
KW delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
XX
OS Bacillus thuringiensis.
XX
PN WO200407462-A2.
XX
PD 02-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005829.
XX
PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
XX
(ATHE-) ATHENIX CORP.
XX
Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
WPI; 2004-635574/61.
XX
New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
and polypeptides, useful for killing lepidopteran or coleopteran pests or
for producing organisms with pesticide resistance.
XX
Example 6; SEQ ID NO 33; 178pp; English.

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XX This sequence represents a delta-endotoxin crystal protein. This protein  
 CC was included in the scope of the invention as a comparison to the delta-  
 CC endotoxins of the invention. Some of the delta-endotoxin coding sequences  
 CC of the invention have alternative start codons, producing more than one  
 CC protein from a single open reading frame. The nucleic acid sequences of  
 CC the invention are useful in DNA constructs or expression cassettes for  
 CC transformation and expression in plants and bacteria. The nucleic acids  
 CC and corresponding polypeptides are useful for killing lepidopteran or  
 CC coleopteran pests. Compositions containing the delta-endotoxins of the  
 CC invention, and methods for their production, are useful for the  
 CC production of organisms with pesticide resistance, specifically bacteria  
 CC and plants. These organisms are useful for generating altered or improved  
 CC delta-endotoxin or delta-endotoxin-associated proteins that have  
 CC pesticidal activity, or for detecting the presence of delta-endotoxin or  
 CC delta-endotoxin-associated proteins or nucleic acids in products or  
 CC organisms.

XX SQ Sequence 719 AA;  
 Query Match 99.0%; Score 3724; DB 8; Length 719;  
 Best Local Similarity 99.3%; Pred. No. 1.1e-290;  
 Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;  
 QY 1 MKLKNQDKHQSNAKVDKISTSLKNETDIELQINHEHEDCLKMSYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSNAKVDKISTSLKNETDIELQINHEHEDCLKMSYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
 QY 120 ARNKALTDLKLGDALAVYHDSLESWGNRNTRARSVRSQYIALELMFVKLPSPFVS 179  
 DB 120 ARNKALTDLKLGDALAVYHDSLESWGNRNTRARSVRSQYIALELMFVKLPSPFVS 179  
 QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDSDHCVKMY 239  
 DB 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDSDHCVKMY 239  
 QY 240 STGLNNLRGTNAESWVRYNQFRDWTMLVLDLVALFPSTYDTOMYPKTTAQLTREVTDA 299  
 DB 240 STGLNNLRGTNAESWVRYNQFRDWTMLVLDLVALFPSTYDTOMYPKTTAQLTREVTDA 299  
 QY 300 IGVTHPHPSFTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNM 359  
 DB 300 IGVTHPHPSFTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNM 359  
 QY 360 WGGHKLFEFTIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGNLFUTQPVNGVP 419  
 DB 360 WGGHKLFEFTIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGNLFUTQPVNGVP 419  
 QY 420 RVDPHMKFVTHPIASDNFYYPGAGIGTQLDSENELPPEATGQPNYESYSHRLSHIGLI 479  
 DB 420 RVDPHMKFVTHPIASDNFYYPGAGIGTQLDSENELPPEATGQPNYESYSHRLSHIGLI 479  
 QY 480 SASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539  
 DB 480 SASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539  
 QY 540 NTGTFGDIRVNNPPFAQRVRIYASTTDLQFHTSINGKAINQGNFSAATNMRGDDLDY 599  
 DB 540 NTGTFGDIRVNNPPFAQRVRIYASTTDLQFHTSINGKAINQGNFSAATNMRGDDLDY 599  
 QY 600 KTFRTVGTFTTFFSLDVQSTFTICAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659  
 DB 600 KTFRTVGTFTTFFSLDVQSTFTICAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVKDHYDQVSNLVESLSEDEFYLDKRELFEIVKATNELHERNM 719  
 DB 660 VTALFTSTNPRGLKTDVKDHYDQVSNLVESLSEDEFYLDKRELFEIVKATNELHERNM 719

## RESULT 8

AAB66910 AAB66910 standard; protein; 719 AA.

XX AC AAB66910;

XX DT 12-APR-2001 (first entry)

XX DE Insecticidal protein cryIIa4.

XX KW Insecticide; transgenic plant; insect-resistance.

XX OS Paecilomyces sp.

XX PN WO200100841-A1.

XX PD 04-JAN-2001.

XX PF 23-JUN-2000; 2000WO-GB002457.

XX PR 29-JUN-1999; 99GB-00015215.

XX PR 23-DEC-1999; 99GB-00030536.

XX XX (ZENEC) ZENEC LTD.

XX PA Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;

XX PI Vincent JL, Lee MD;

XX XX WPI; 2001-123015/13.

XX DR Novel insecticidal protein obtained from species of Paecilomyces for

XX PT controlling insects, and for insect-resistant transgenic plant

XX PT production.

XX PS Claim 14; Page 60-62; 72pp; English.

XX CC The present invention relates to novel insecticidal proteins obtained

XX CC from Paecilomyces sp. (see AAB66910 and AAB66913). The

XX CC insecticidal proteins can be used to produce transgenic plants, which are

XX CC insect-resistant. Also, the insecticidal proteins are useful for

XX CC controlling insects by providing them at a locus where insects feed

XX SQ Sequence 719 AA;

Query Match 98.9%; Score 3720; DB 4; Length 719;

Best Local Similarity 99.2%; Pred. No. 2.3e-290;

Matches 714; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSNAKVDKISTSLKNETDIELQINHEHEDCLKMSYENVEPVSASTI 60

DB 1 MKLKNQDKHQSNAKVDKISTSLKNETDIELQINHEHEDCLKMSYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119

DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119

QY 120 ARNKALTDLKLGDALAVYHDSLESWGNRNTRARSVRSQYIALELMFVKLPSPFVS 179

DB 120 ARNKALTDLKLGDALAVYHDSLESWGNRNTRARSVRSQYIALELMFVKLPSPFVS 179

QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDSDHCVKMY 239

DB 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDSDHCVKMY 239

QY 240 STGLNNLRGTNAESWVRYNQFRDWTMLVLDLVALFPSTYDTOMYPKTTAQLTREVTDA 299

DB 240 STGLNNLRGTNAESWVRYNQFRDWTMLVLDLVALFPSTYDTOMYPKTTAQLTREVTDA 299

QY 300 IGVTHPHPSFTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNM 359

DB 300 IGVTHPHPSFTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNM 359

QY 360 WGGHKLFEFTIGTGLNISTQGSTNTSINPVTLPFTSRDYRTESLAGNLFUTQPVNGVP 419



Db 360 WGGHKLFEFTIGTGLNISTQSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVP 419  
Qy 420 RVDHFWKFTHTPIASDNFYYPGAGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLI 479  
Db 420 RVDHFWKFTHTPIASDNFYYPGAGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLI 479  
Qy 480 SASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSGGAUVVRGPGFTGGDILRRT 539  
Db 480 SASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSGGAUVVRGPGFTGGDILRRT 539  
Qy 540 NTGTFGDIRVNIWNPPEAQRVRIYASTDLOFHTSINGKAINQGNFSAATWNRGDDLDY 599  
Db 540 NTGTFGDIRVNIWNPPEAQRVRIYASTDLOFHTSINGKAINQGNFSAATWNRGDDLDY 599  
Qy 600 KTFRTVGTFTPSFLDVQSTFTIGAWNFSGNEVIIDRIEFVPEVVEYAEYDFEKAQEK 659  
Db 600 KTFRTVGTFTPSFLDVQSTFTIGAWNFSGNEVIIDRIEFVPEVVEYAEYDFEKAQEK 659  
Qy 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
Db 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 9  
AAE36274  
ID AAE36274 standard; protein; 719 AA.

XX AAE36274;  
DT 26-JUN-2003 (first entry)  
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.  
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

XX Bacillus thuringiensis.  
PN WO200298911-A2.  
XX 12-DEC-2002.  
XX 30-MAY-2002; 2002WO-GB002666.  
PR 07-JUN-2001; 2001GB-00013900.  
PA (SYGN ) SYNGENTA LTD.  
XX Vincent JL, Viner R;  
DR WPI; 2003-175137/17.

PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
XX Claim 12; Page 50-53; 67pp; English.

CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

XX Sequence 719 AA;  
SQ Query Match 98.9%; Score 3720; DB 6; Length 719;  
Best Local Similarity 99.2%; Pred. No. 2.3e-290;  
Matches 714; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

Qy 1 MKLKNQDKHQSFSSNAKVVDKISTDSLKNETDLELQININHEDCMKSEYENVEPFFVASTI 60  
Db 1 MKLKNQDKHQSFSSNAKVVDKISTDSLKNETDLELQININHEDCMKSEYENVEPFFVASTI 60  
Qy 61 QTGIGTAGKILGTGVPFAGQVASLYSFTLGBLWPKGNQWELFMHEHVEE-INQIKISTY 119  
Db 61 QTGIGTAGKILGTGVPFAGQVASLYSFTLGBLWPKGNQWELFMHEHVEE-INQIKISTY 119  
Qy 120 ARNKALTDLKGIGDALAVVYHDSLESWVGNNRNNTRARSVVRQVYALIELMFKVQLPSFAVS 179  
Db 120 ARNKALTDLKGIGDALAVVYHDSLESWVGNNRNNTRARSVVRQVYALIELMFKVQLPSFAVS 179  
Qy 180 GBEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFTYNRQVERAGDYSCHVKWY 239  
Db 180 GBEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFTYNRQVERAGDYSCHVKWY 239  
Qy 240 STGLANLRGTNAESWVRYNQFRDWTLMVLDLVALFPSPYDTOMYPIKTTAQLTREYVYTD 299  
Db 240 STGLANLRGTNAESWVRYNQFRDWTLMVLDLVALFPSPYDTOMYPIKTTAQLTREYVYTD 299  
Qy 300 ICTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYSLLSRWSTNTQYMMN 359  
Db 300 ICTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYSLLSRWSTNTQYMMN 359  
Qy 360 WGGHKLFEFTIGTGLNISTQSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVP 419  
Db 360 WGGHKLFEFTIGTGLNISTQSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVP 419  
Qy 420 RVDHFWKFTHTPIASDNFYYPGAGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLI 479  
Db 420 RVDHFWKFTHTPIASDNFYYPGAGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLI 479  
Qy 480 SASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSGGAUVVRGPGFTGGDILRRT 539  
Db 480 SASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSGGAUVVRGPGFTGGDILRRT 539  
Qy 540 NTGTFGDIRVNIWNPPEAQRVRIYASTDLOFHTSINGKAINQGNFSAATWNRGDDLDY 599  
Db 540 NTGTFGDIRVNIWNPPEAQRVRIYASTDLOFHTSINGKAINQGNFSAATWNRGDDLDY 599  
Qy 600 KTFRTVGTFTPSFLDVQSTFTIGAWNFSGNEVIIDRIEFVPEVVEYAEYDFEKAQEK 659  
Db 600 KTFRTVGTFTPSFLDVQSTFTIGAWNFSGNEVIIDRIEFVPEVVEYAEYDFEKAQEK 659  
Qy 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
Db 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 10  
AAU02095  
ID AAU02095 standard; protein; 719 AA.

XX AAU02095;  
AC AAU02095;  
XX 07-SEP-2001 (first entry)

DE Bacillus thuringiensis partial mutant CryIIa.  
XX Crystal protein; CryIIa; CryIIa; moth; butterfly; Colorado potato beetle; mutant; mutein.

XX Bacillus thuringiensis.  
XX Key Location/Qualifiers  
FT Peptide 1..19  
FT Protein /label= Signal\_peptide 20..719  
FT /label= Mature\_CryIIa

XX EP1099760-A1.  
XX 16-MAY-2001.



Db 180 GEEVPLPIYAQAANLHLLLRDASIFGKESWGLSSSEISTFYNRQVERAGDYSYHCVKY 239  
Qy 240 STGLNNLRGNAESWRYNQFRDMLVLDLVALPSPDYDTOMYPIKTTAQLTREVYTD 299  
Db 240 STGLNNLRGNAESWRYNQFRDMLVLDLVALPSPDYDTOMYPIKTTAQLTREVYTD 299  
Qy 300 IGTVPHPSPFTSTTWNNAAPSAIEAAVVRNPHLLDFLEQVTIYSLSRMSNTQYMM 359  
Db 300 IGTVPHPSPFTSTTWNNAAPSAIEAAVVRNPHLLDFLEQVTIYSLSRMSNTQYMM 359  
Qy 360 WGGHKLFPRTIGTTLNISTQSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVP 419  
Db 360 WGGHKLFPRTIGTTLNISTQSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVP 419  
Qy 420 RVDPHWKFTVTHPIASDNFYVPGYAGIGTQLODSENLPEATGQPNYESYSHRLSHIGLI 479  
Db 420 RVDPHWKFTVTHPIASDNFYVPGYAGIGTQLODSENLPEATGQPNYESYSHRLSHIGLI 479  
Qy 480 SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGGAAVVRGPGFTGGDILRRT 539  
Db 480 SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGGAAVVRGPGFTGGDILRRT 539  
Qy 540 NTGTFGDIRVNIINPPPAQRYRVRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDL 599  
Db 540 NTGTFGDIRVNIINPPPAQRYRVRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDL 599  
Qy 600 KTFRTVGTFTPSFLDVQSTFTIGAWNFSSGNEVIIDRIEFVPEVITYEAEDFEKAQEK 659  
Db 600 KTFRTVGTFTPSFLDVQSTFTIGAWNFSSGNEVIIDRIEFVPEVITYEAEDFEKAQEK 659  
Qy 660 VTALFTSTNPRGLKTDVQDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
Db 660 VTALFTSTNPRGLKTDVQDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 12  
AAE36271  
ID AAE36271 standard; protein; 718 AA.

XX AAE36271;  
AC AAE36271;  
XX AAE36271;  
DT 26-JUN-2003 (first entry)  
XX  
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa1.  
DE Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
Kw Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

OS Bacillus thuringiensis.  
XX WO200298911-A2.  
XX 12-DEC-2002.  
XX 30-MAY-2002; 2002WO-GB002666.  
XX 07-JUN-2001; 2001GB-00013900.  
XX (SYGN ) SYNGENTA LTD.  
XX Vincent J'L, Viner R;  
PI WPI; 2003-175137/17.  
XX  
XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

PT  
PT  
XX  
PS Claim 12; Page 42-44; 67pp; English.  
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as

CC an active ingredient of a pesticide or for controlling insects.  
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
XX  
SQ Sequence 718 AA;

Query Match 98.2%; Score 3692.5; DB 6; Length 718;  
Best Local Similarity 98.9%; Pred. No. 3.7e-288;  
Matches 712; Conservative 2; Mismatches 3; Indels 3; Gaps 3;

Qy 1 MKLKNQDQKHSFSSNAKVDKISTDSLNKNTDIELQINHEDECLKMSYENVEPFASTI 60  
Db 1 MKLKNQDQKHSFSSNAKVDKISTDSLNKNTDIELQINHEDECLKMSYENVEPFASTI 60  
Qy 61 OTGIGTAGKILGTGVPFAGQVASYFLGELMPKGNQWEILFMEHVEE-INOKISTY 119  
Db 61 OTGIGTAGKILGTGVPFAGQVASYFLGELMPKGNQWEILFMEHVEE-INOKISTY 119  
Qy 120 ARNKALTDLKGGLDALAVYHDSLESWVGNNRNTARSVVRQVIALLELMFVQKLPFAVS 179  
Db 120 ARNKALTDLKGGLDALAVYHDSLESWVGNNRNTARSVVRQVIALLELMFVQKLPFAVS 179  
Qy 180 GBEVPLLPITYAQAANLHLLLRDASIFGKESWGLSSSEISTFYNRQVERAGDYSYHCVKY 239  
Db 180 GBEVPLLPITYAQAANLHLLLRDASIFGKESWGLSSSEISTFYNRQVERAGDYSYHCVKY 239  
Qy 240 STGLNNLRGNAESWRYNQFRDMLVLDLVALPSPDYDTOMYPIKTTAQLTREVYTD 299  
Db 240 STGLNNLRGNAESWRYNQFRDMLVLDLVALPSPDYDTOMYPIKTTAQLTREVYTD 299  
Qy 300 IGTVPHPSPFTSTTWNNAAPSAIEAAVVRNPHLLDFLEQVTIYSLSRMSNTQYMM 359  
Db 300 IGTVPHPSPFTSTTWNNAAPSAIEAAVVRNPHLLDFLEQVTIYSLSRMSNTQYMM 359  
Qy 360 WGGHKLFPRTIGTTLNISTQSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVP 419  
Db 360 WGGHKLFPRTIGTTLNISTQSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVP 419  
Qy 420 RVDPHWKFTVTHPIASDNFYVPGYAGIGTQLODSENLPEATGQPNYESYSHRLSHIGLI 479  
Db 420 RVDPHWKFTVTHPIASDNFYVPGYAGIGTQLODSENLPEATGQPNYESYSHRLSHIGLI 479  
Qy 480 SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGGAAVVRGPGFTGGDILRRT 539  
Db 480 SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGGAAVVRGPGFTGGDILRRT 539  
Qy 540 NTGTFGDIRVNIINPPPAQRYRVRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDL 599  
Db 540 NTGTFGDIRVNIINPPPAQRYRVRIRYASTDLOFHTSINGKAINQGNFSAATMNRGDL 599  
Qy 600 KTFRTVGTFTPSFLDVQSTFTIGAWNFSSGNEVIIDRIEFVPEVITYEAEDFEKAQEK 659  
Db 600 KTFRTVGTFTPSFLDVQSTFTIGAWNFSSGNEVIIDRIEFVPEVITYEAEDFEKAQEK 659  
Qy 660 VTALFTSTNPRGLKTDVQDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
Db 660 VTALFTSTNPRGLKTDVQDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 13  
AAE66907  
ID AAE66907 standard; protein; 718 AA.  
XX AAE66907;  
AC AAE66907;  
XX  
DT 12-APR-2001 (first entry)  
XX  
XX Insecticidal protein cryIIa1.  
DE Insecticide; transgenic plant; insect-resistance.  
XX  
XX

OS Paecilomyces sp.  
XX WO200100841-A1.  
EN 04-JAN-2001.  
XX 23-JUN-2000; 2000WO-GB002457.  
XX 29-JUN-1999; 99GB-00015215.  
XX 23-DEC-1999; 99GB-00030536.  
XX (ZENE ) ZENECA LTD.  
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX WPI; 2001-123015/13.  
XX Novel insecticidal protein obtained from species of Paecilomyces for  
XX controlling insects, and for insect-resistant transgenic plant  
XX production.  
XX Claim 14; Page 53-55; 72pp; English.  
XX The present invention relates to novel insecticidal proteins obtained  
XX from Paecilomyces sp. (see AAB6699 to AAB6691 and AAB66913). The  
XX insecticidal proteins can be used to produce transgenic plants, which are  
XX insect-resistant. Also, the insecticidal proteins are useful for  
XX controlling insects by providing them at a locus where insects feed  
XX Sequence 718 AA;  
SQ

Query Match 98.0%; Score 3686.5; DB 4; Length 718;  
Best Local Similarity 98.8%; Pred. No. 1.1e-287;  
Matches 711; Conservative 2; Mismatches 4; Indels 3; Gaps 3;

QY 1 MKLNQDKHQSSNAKVDKISTDLKNETDIELQNHEDCLKMSYENVEPFVSASTI 60  
DB 1 MKLNQDKHQSSNAKVDKISTDLKNETDIELQNHEDCLKMSYENVEPFVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLFGELMFKGNQWEILFMEHVEE-INQIKISTY 119  
DB 61 QTGIGIAGKILGTGVPFAGQVASYLFGELMFKGNQWEILFMEHVEE-INQIKISTY 119  
QY 120 ARNKALTDLKGDLAVYHDSLESWGNRNTRARSVRSQYIALELMFVKQLPSFAVS 179  
DB 120 ARNKALTDLKGDLAVYHDSLESWGNRNTRARSVRSQYIALELMFVKQLPSFAVS 179  
QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKMY 239  
DB 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKMY 239  
QY 240 STGLNLRGNAESWRYNQFRDMLVLDLVALPSPYDTOMYPIKTAQLTREYVYDA 299  
DB 240 STGLNLRGNAESWRYNQFRDMLVLDLVALPSPYDTOMYPIKTAQLTREYVYDA 299  
QY 300 IGTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMN 359  
DB 300 IGTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMN 359  
QY 360 WGGHKLBFRTIGTGLNISTOGSNTSINPVTLPFTSRDYVYRTESLAGNLFLTOPVNGVP 419  
DB 360 WGGHKLBFRTIGTGLNISTOGSNTSINPVTLPFTSRDYVYRTESLAGNLFLTOPVNGVP 419  
QY 420 RVDPHKVFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI 479  
DB 419 RVDPHKVFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI 478  
QY 480 SASHVKALVYSWTHRSADRNTNTPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDTILRT 539  
DB 479 SASHVKALVYSWTHRSADRNTNTPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDTILRT 538  
QY 540 NTGTFGDIRVNINPPFAQRYVRIRYASTTDLQPHTSINGKAINQGNFSATMNRGDLDY 599

DB 539 NTGTFGDIRVNINPPFAQRYVRIRYASTTDLQPHTSINGKAINQGNFSATMNRGDLDY 598  
QY 600 KTFRTVGFTTTPFSLDVQSFTICAWNFSSGNEVYIDRIEFPVVEVYEAEDFEKAQEK 659  
DB 599 KTFRTVGFTTTPFSLDVQSFTICAWNFSSGNEVYIDRIEFPVVEVYEAEDFEKAQEK 658  
QY 660 VTALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFELFVKYANELHIERNM 719  
DB 659 VTALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFELFVKYANELHIERNM 718

RESULT 14  
ADM74717  
ID ADM74717 standard; protein; 719 AA.  
XX  
AC ADM74717;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE B. thuringiensis cryIIel SEQ ID NO:2.  
XX  
KW cryI; toxicity; lepidoptera; cryIaB; cryIa; coleoptera; diptera;  
KW cryIIel.  
XX  
OS Bacillus thuringiensis.  
XX  
PN CN1401772-A.  
XX  
PD 12-MAR-2003.  
XX  
XX 20-AUG-2001; 2001CN-00124163.  
XX  
PR 20-AUG-2001; 2001CN-00124163.  
XX  
PA (PLAN-) PLANT PROTECTION INST CHINESE ACAD AGRIC.  
XX  
PI Song F, Zhang J, Huang D;  
XX  
XX WPI; 2003-442339/42.  
XX  
DR N-PSDB; ADM74716.  
XX  
XX Bacillus thuringiensis cryI gene, expression vector, nucleotide sequence  
XX with high-toxicity to lepidoptera pests, encoded protein, primer  
XX sequences and the shuttle vector pSX422b, useful as a pesticide.  
XX  
PS Example 3; SEQ ID NO 2; 29pp; Chinese.  
XX  
CC The invention relates to a novel Bacillus thuringiensis cryI gene, gene  
CC combination, expression vector, nucleotide sequence of the B  
CC thuringiensis cryI gene with high-toxicity to lepidoptera pests and the  
CC amino acid sequence of the protein encoded by it, cooperative use of the  
CC cryI gene with the expression product of cryIaB or cryIa, primer  
CC sequences for expressing the genes, and the constructed shuttle vector  
CC pSX422b. The gene in combination with the cryIaB or cryIa genes  
CC displays high toxicity to the lepidoptera, coleoptera and diptera pests.  
CC The present sequence represents the cryIIel protein.  
XX  
SQ Sequence 719 AA;  
Query Match 93.5%; Score 3517; DB 7; Length 719;  
Best Local Similarity 93.1%; Pred. No. 5.1e-274;  
Matches 670; Conservative 27; Mismatches 21; Indels 2; Gaps 2;

QY 1 MKLNQDKHQSSNAKVDKISTDLKNETDIELQNHEDCLKMSYENVEPFVSASTI 60  
DB 1 MKLNQDKHQSSNAKVDKISTDLKNETDIELQNHEDCLKMSYENVEPFVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLFGELMFKGNQWEILFMEHVEE-INQIKISTY 119  
DB 61 QTGIGIAGKILGTGVPFAGQVASYLFGELMFKGNQWEILFMEHVEE-INQIKISTY 119  
QY 120 ARNKALTDLKGDLAVYHDSLESWGNRNTRARSVRSQYIALELMFVKQLPSFAVS 179

Db 120 ARNALADLGLDALAVYHESLESWKORNNARATSVVKSQVIALELLFVQKLPFAVS 179  
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSDDHCVKWY 239  
Db 180 GEEVPLLPPIYAQAANLHLLLRDASVFGKEWGLSNSQISTFYNQVERSDYSDHCVKWY 239  
QY 240 STGLNNLRGTNAESWRYNQFRDMTLMVLDLVALPFSYDQMYPIKTTAQLTREYVYTD 299  
Db 240 STGLNNLRGTNAESWRYNQFRDMTLMVLDLVALPFSYDQMYPIKTTAQLTREYVYTD 299  
QY 300 IGTVHPHPSFTTWNNNAPSATESAEEAVVRNPHLLDLEQVYIYSLSRMSNTQYMMN 359  
Db 300 IGTVHPNASFSTTWNNNAPSATESAVVRNPHLLDLEQVYIYSLSRMSNTQYMMN 359  
QY 360 WGGHLEPRTIGTGLNISQSTNTSINPVTLPFTSRDVRVRESLAGLNLFTQPVNGVP 419  
Db 360 WGGHLEPRTIGTGLNISQSTNTSINPVTLPFTSRDVRVRESLAGLNLFTQPVNGVP 419  
QY 420 RVDPHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRSLHIGLI 479  
Db 420 RVDPHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRSLHIGLI 479  
QY 480 SASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539  
Db 480 SASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539  
QY 540 NTGTFGDIRVNIWPPPAQRVYRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDDLDY 599  
Db 540 NTGTFGDIRVNIWPPPAQRVYRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDDLDY 599  
QY 600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDYFEKAQEK 659  
Db 600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDYFEKAQEK 659  
QY 660 VTALFTSTNPRGLKTDVYHIDQVSNLVESLSDDEFYLDKRELFEIVKYANELHIERNM 719  
Db 660 VTALFTSTNPRGLKTDVYHIDQVSNLVESLSDDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 15

AAB66912 standard; protein; 719 AA.

XX AAB66912;  
XX AAB66912;  
DT 12-APR-2001 (first entry)  
XX Insecticidal protein cry1bl.  
XX Insecticide; transgenic plant; insect-resistance.  
XX Paecilomyces sp.  
XX WO200100841-A1.  
XX 04-JAN-2001.  
XX 23-JUN-2000; 2000WO-GB002457.  
XX 29-JUN-1999; 99GB-00015215.  
XX 23-DEC-1999; 99GB-00030536.  
XX (ZENE ) ZENECA LTD.  
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX WPI; 2001-123015/13.  
XX Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PT production.

XX Claim 14; Page 64-66; 72pp; English.

XX The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed

XX Sequence 719 AA;

Query Match 92.6%; Score 3484; DB 4; Length 719;  
Best Local Similarity 92.2%; Pred. No. 2.3e-271;  
Matches 664; Conservative 33; Mismatches 21; Indels 2; Gaps 2;

QY 1 MCLKNQDKHQSFFSSNAKVDKISTDSLKNKTDTELQNIHEDCLKMEYENVEPFVSASTI 60  
Db 1 MCLKNPDKKQSSSSNAKVDKIATDSLKNKTDTELKMNEDYLRMSEHSIDPFVSASTI 60  
QY 61 QTGIGIAGKILGTGVFPAGQVAVSLYSFILGELMPKGNQWILFMEHVEE-INQKISTY 119  
Db 61 QTGIGIAGKILGTGVFPAGQVAVSLYSFILGELMPKGNQWILFMEHVEE-INQKISTY 119  
QY 120 ARNKALTDLGLGDALAVYHDSLESWGNRNNTARSVRSQVIALELMPVQKLPFAVS 179  
Db 120 ARNKALSDLRGLGDALAVYHDSLESWGNRNNTARSVRSQVIALELMPVQKLPFAVS 179  
QY 180 GREVPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSDDHCVKWY 239  
Db 180 GREVPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSDDHCVKWY 239  
QY 240 STGLNNLRGTNAESWRYNQFRDMTLMVLDLVALPFSYDQMYPIKTTAQLTREYVYTD 299  
Db 240 STGLNNLRGTNAESWRYNQFRDMTLMVLDLVALPFSYDQMYPIKTTAQLTREYVYTD 299  
QY 300 IGTVHPHPSFTTWNNNAPSATESAEEAVVRNPHLLDLEQVYIYSLSRMSNTQYMMN 359  
Db 300 IGTVHPNQAFTTWNNNAPSATESAEEAVVRNPHLLDLEQVYIYSLSRMSNTQYMMN 359  
QY 360 WGGHLEPRTIGTGLNISQSTNTSINPVTLPFTSRDVRVRESLAGLNLFTQPVNGVP 419  
Db 360 WGGHLEPRTIGTGLNISQSTNTSINPVTLPFTSRDVRVRESLAGLNLFTQPVNGVP 419  
QY 420 RVDPHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRSLHIGLI 479  
Db 420 RVDPHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRSLHIGLI 479  
QY 480 SASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539  
Db 480 SASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539  
QY 540 NTGTFGDIRVNIWPPPAQRVYRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDDLDY 599  
Db 540 NTGTFGDIRVNIWPPPAQRVYRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDDLDY 599  
QY 600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDYFEKAQEK 659  
Db 600 KTFRTVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDYFEKAQEK 659  
QY 660 VTALFTSTNPRGLKTDVYHIDQVSNLVESLSDDEFYLDKRELFEIVKYANELHIERNM 719  
Db 660 VTALFTSTNPRGLKTDVYHIDQVSNLVESLSDDEFYLDKRELFEIVKYANELHIERNM 719

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Job time : 101.351 secs

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OM protein - protein search, using sw model

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Title: US-10-019-823B-58

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Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 15: /cgn2\_6/ptodata/1/pubaa/US10C\_PUBCOMB.pep.\*
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- 20: /cgn2\_6/ptodata/1/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3724	99.0	719	16	US-10-782-020-10
2	3724	99.0	719	16	US-10-782-141-8
3	3442.5	91.5	710	15	US-10-428-961-42
4	2250.5	59.8	1228	16	US-10-809-953-10
5	2236.5	59.5	1207	10	US-09-988-462-7
6	2157.5	57.4	1227	15	US-10-428-961-63
7	2142.5	57.0	1186	9	US-09-826-660-23
8	2087	55.5	1228	15	US-10-428-961-38
9	2087	55.5	1228	15	US-10-614-524-2
10	1909.5	50.8	643	9	US-09-826-660-25
11	1694.5	45.1	1167	14	US-10-089-678-1
12	1656.5	44.1	653	15	US-10-428-961-6
13	1643.5	43.7	1157	16	US-10-782-141-16

14	1485	39.5	1206	13	US-10-032-717-2	Sequence 2, Appli
15	1485	39.5	1206	14	US-10-414-637-2	Sequence 2, Appli
16	1485	39.5	1206	15	US-10-606-320-2	Sequence 2, Appli
17	1469	39.1	1210	13	US-10-032-717-4	Sequence 4, Appli
18	1469	39.1	1210	14	US-10-414-637-4	Sequence 4, Appli
19	1469	39.1	1210	15	US-10-606-320-4	Sequence 4, Appli
20	1459.5	38.8	1156	14	US-10-099-285-72	Sequence 72, Appli
21	1459.5	38.8	1156	15	US-10-428-961-28	Sequence 28, Appli
22	1443	38.4	1155	9	US-09-756-643-2	Sequence 2, Appli
23	1443	38.4	1155	10	US-09-988-462-9	Sequence 9, Appli
24	1443	38.4	1155	15	US-10-136-998A-2	Sequence 6, Appli
25	1443	38.4	1177	14	US-10-035-060-6	Sequence 6, Appli
26	1443	38.4	1181	10	US-09-988-462-11	Sequence 11, Appli
27	1443	38.4	1181	10	US-09-988-462-13	Sequence 13, Appli
28	1443	38.4	1181	10	US-09-988-462-15	Sequence 15, Appli
29	1443	38.4	1181	10	US-09-988-462-17	Sequence 17, Appli
30	1443	38.4	1181	10	US-09-988-462-28	Sequence 28, Appli
31	1443	38.4	1181	15	US-10-136-998A-4	Sequence 4, Appli
32	1443	38.4	1181	15	US-10-136-998A-8	Sequence 8, Appli
33	1443	38.4	1181	15	US-10-136-998A-10	Sequence 10, Appli
34	1443	38.4	1181	15	US-10-136-998A-12	Sequence 12, Appli
35	1438	38.2	1177	14	US-10-035-060-2	Sequence 2, Appli
36	1436	38.2	1177	14	US-10-102-469-24	Sequence 24, Appli
37	1435	38.2	1177	14	US-10-102-469-24	Sequence 24, Appli
38	1419.5	37.7	1176	16	US-10-782-141-6	Sequence 6, Appli
39	1407.5	37.4	1176	11	US-09-837-961-2	Sequence 2, Appli
40	1407.5	37.4	1176	16	US-10-825-751-2	Sequence 2, Appli
41	1376	36.6	1167	15	US-10-428-961-40	Sequence 40, Appli
42	1355	36.0	1177	9	US-09-873-873-26	Sequence 26, Appli
43	1355	36.0	1177	10	US-09-916-956A-26	Sequence 26, Appli
44	1355	36.0	1177	10	US-09-997-914-26	Sequence 26, Appli
45	1355	36.0	1177	14	US-10-365-645-26	Sequence 26, Appli

#### ALIGNMENTS

#### RESULT 1

US-10-782-020-10  
; Sequence 10, Application US/10782020  
; Publication No. US20040197916A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for its Use  
; FILE REFERENCE: 045600/274139  
; CURRENT APPLICATION NUMBER: US/10/782.020  
; PRIOR FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,810  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
; US-10-782-020-10

Query Match 99.0%; Score 3724; DB 16; Length 719;  
Best Local Similarity 99.3%; Pred. No. 1.6e-306;  
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

Qy 1 MLLKNQKHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKMSYENVEPFSASTI 60

Db 1 MLLKNQKHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKMSYENVEPFSASTI 60

Qy 61 QTGTGIAGKILGTGVPPAGQVASYLSFILGELPKGNQWEILFMEHVEE-INOKISTY 119

Db 61 QTGTGIAGKILGTGVPPAGQVASYLSFILGELPKGNQWEILFMEHVEE-INOKISTY 119

QY 120 ARNKALTDLKGDLAVYHDSLESVWGNRNTRARSVRSOYIALELMFVQKLPFAVS 179  
DB 120 ARNKALTDLKGDLAVYHDSLESVWGNRNTRARSVRSOYIALELMFVQKLPFAVS 179  
QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFYNRQVERAGDYSCHVCWY 239  
DB 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFYNRQVERAGDYSCHVCWY 239  
QY 240 STGLNNLGTNAESWVRYNQPRDMLTMDLVALPESYDTQMPYPIKTTAQLTREVTDA 299  
DB 240 STGLNNLGTNAESWVRYNQPRDMLTMDLVALPESYDTQMPYPIKTTAQLTREVTDA 299  
QY 300 IGTVHPHPSFTTWNNAAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMN 359  
DB 300 IGTVHPHPSFTTWNNAAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMN 359  
QY 360 WGGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNFLTOPVNGVP 419  
DB 360 WGGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNFLTOPVNGVP 419  
QY 420 RVDFFHWKFVTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
DB 420 RVDFFHWKFVTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
DB 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
QY 540 NTGTFGDIRVNIWPPPAQRVRIYASTTDLOFHTSINGKAINOGNFSATMNRGEDLDY 599  
DB 540 NTGTFGDIRVNIWPPPAQRVRIYASTTDLOFHTSINGKAINOGNFSATMNRGEDLDY 599  
QY 600 KTRFTVGTTPSFELDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEK 659  
DB 600 KTRFTVGTTPSFELDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEK 659  
QY 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
DB 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 2  
US-10-782-141-8  
; Sequence 8, Application US/10782141  
; Publication No. US20040197917A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274143  
; CURRENT APPLICATION NUMBER: US/10782,141  
; CURRENT FILING DATE: 2004-02-20  
; PRIOR APPLICATION NUMBER: 60/448,632  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-141-8

Query Match 99.0%; Score 3724; DB 16; Length 719;  
Best Local Similarity 99.3%; Pred. No. 1.6e-306;  
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

QY 1 MCLKNQDKHQSFSNAKVDKISTDKNETDIELQINNHEDCLKMEYENVEPVFSASTI 60

DB 1 MCLKNQDKHQSFSNAKVDKISTDKNETDIELQINNHEDCLKMEYENVEPVFSASTI 60  
QY 61 QTGTGIAGKILGTGVFPAGQVSLFSLGELWPKGNQWEILFMEHVEE-INQKISTY 119  
DB 61 QTGTGIAGKILGTGVFPAGQVSLFSLGELWPKGNQWEILFMEHVEE-INQKISTY 119  
QY 120 ARNKALTDLKGDLAVYHDSLESVWGNRNTRARSVRSOYIALELMFVQKLPFAVS 179  
DB 120 ARNKALTDLKGDLAVYHDSLESVWGNRNTRARSVRSOYIALELMFVQKLPFAVS 179  
QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFYNRQVERAGDYSCHVCWY 239  
DB 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFYNRQVERAGDYSCHVCWY 239  
QY 240 STGLNNLGTNAESWVRYNQPRDMLTMDLVALPESYDTQMPYPIKTTAQLTREVTDA 299  
DB 240 STGLNNLGTNAESWVRYNQPRDMLTMDLVALPESYDTQMPYPIKTTAQLTREVTDA 299  
QY 300 IGTVHPHPSFTTWNNAAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMN 359  
DB 300 IGTVHPHPSFTTWNNAAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMN 359  
QY 360 WGGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNFLTOPVNGVP 419  
DB 360 WGGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNFLTOPVNGVP 419  
QY 420 RVDFFHWKFVTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
DB 420 RVDFFHWKFVTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
DB 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
QY 540 NTGTFGDIRVNIWPPPAQRVRIYASTTDLOFHTSINGKAINOGNFSATMNRGEDLDY 599  
DB 540 NTGTFGDIRVNIWPPPAQRVRIYASTTDLOFHTSINGKAINOGNFSATMNRGEDLDY 599  
QY 600 KTRFTVGTTPSFELDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEK 659  
DB 600 KTRFTVGTTPSFELDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEK 659  
QY 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
DB 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 3  
US-10-428-961-42  
; Sequence 42, Application US/10428961  
; Publication No. US2003023711A1  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rel  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Rugar, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)  
; FILE REFERENCE: MECO201--1  
; CURRENT APPLICATION NUMBER: US/10428,961  
; CURRENT FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: 09/661,322  
; PRIOR FILING DATE: 2000-09-13  
; PRIOR APPLICATION NUMBER: 60/153,995  
; PRIOR FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 42  
; LENGTH: 710  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
; FEATURE:



NAME/KEY: misc feature  
LOCATION: (200)..(200)  
OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid  
US-10-428-961-42

Query Match 91.5%; Score 3442.5; DB 15; Length 710;  
Best Local Similarity 91.9%; Pred. No. 1.2e-282; Mismatches 31; Indels 11; Gaps 3;  
Matches 662; Conservative 16;

Qy 1 MKLNQKHQFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSSEVENVEPFVASTI 60  
Db 1 MKSKNNQKHQSLNNATVDKNTGSLNNNTTELQNFH-----EGIEPFVSVSTI 51

Qy 61 QTGIGIAGKIIGTGVPPAGQVASYLSPILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
Db 52 QTGIGIAGKIIGLNLGVPAGQVASYLSPILGELWPKGNQWEI-FMEHVEELINQKISTY 110

Qy 120 ARNKALDGLGALAVYHDSLSWGNRNNTARSVVRQYIALELMFVKQLPSPAVS 179  
Db 111 ARNKALDGLGALAVYHDSLSWGNRNNTARSVVRQYIALELMFVKQLPSPAVS 170

Qy 180 GEEVPLPIYAQAANLHLLLRDASIFGKWLGLSSSEISTFYNQVERAGDYSDHCVKWY 239  
Db 171 GEEVPLPIYAQAANLHLLLRDASIFGKWLGLSSSEISTFYNQVERAGDYSDHCVKWY 230

Qy 240 STGLNNLRGTNAESWVRYNQRRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDA 299  
Db 231 NTGLNRLMGNAESWVRYNQRRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDA 290

Qy 300 IGTVHPHPSFTTWNNAEVSFAIEAARVNRPHLLDFLEQVITYSLSSWSNTQYNNM 359  
Db 291 IGTVHPHPSFTTWNNAEVSFAIEAARVNRPHLLDFLEQVITYSLSSWSNTQYNNM 350

Qy 360 WGGHKLFRPTIGTGLNTSTQGSTNTSINPVTLPFTSRDVTYTESLAGLNLFLTOPVNGVP 419  
Db 351 WGGHKLFRPTIGTGLNTSTQGSTNTSINPVTLPFTSRDVTYTESLAGLNLFLTOPVNGVP 410

Qy 420 RVDPHKFWTHPIASDNFYPYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
Db 411 RVDPHKFWTHPIASDNFYPYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 470

Qy 480 SASHVKALVSWTHRSADRNTIENPSTIQLPKAFNLSSGAAVVRGPGTGGDILRR 539  
Db 471 SASHVKALVSWTHRSADRNTIENPSTIQLPKAFNLSSGAAVVRGPGTGGDILRR 530

Qy 540 NTGTFGDIRVNINPPFAQRVRYRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599  
Db 531 NTGTFGDIRVNINPPFAQRVRYRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY 590

Qy 600 KTFRTVGFTTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEK 659  
Db 591 KTFRTVGFTTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEK 650

Qy 660 VTALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
Db 651 VTALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 710

RESULT 4  
US-10-809-953-10  
Sequence 10, Application US/10809953  
Publication No. US2004018125A1  
GENERAL INFORMATION:  
APPLICANT: Van Mellaert, Herman  
APPLICANT: Botterman, Johan  
APPLICANT: Van Rie, Jeroen  
APPLICANT: Joos, Henk  
TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTICIDAL PROTEINS  
FILE REFERENCE: 021565-078  
CURRENT APPLICATION NUMBER: US/10/809,953  
CURRENT FILING DATE: 2004-03-26  
PRIOR APPLICATION NUMBER: US/09/661,016

PRIOR FILING DATE: 2000-09-13  
PRIOR APPLICATION NUMBER: PCT/EP90/00905  
PRIOR FILING DATE: 1990-05-30  
PRIOR APPLICATION NUMBER: GB 89401499.2  
PRIOR FILING DATE: 1989-05-31  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 1228  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis  
US-10-809-953-10

Query Match 59.8%; Score 2250.5; DB 16; Length 1228;  
Best Local Similarity 62.5%; Pred. No. 3.4e-181;  
Matches 448; Conservative 78; Mismatches 164; Indels 27; Gaps 8;

Qy 23 TDSLKNETDIELQNH-----EDCLKMSSEVENVEPFVASTIOTGIGIAGKI 70  
Db 2 TSNKNEINEINAVNSHAQMDLLPDARIEDSLCIAEGNNDPPFVASTVQTGINIAGRI 61

Qy 71 LGTLGVPPAGQVASYLSPILGELWPKGNQWEILFMEHVEE-INQKISTYARNKALDGLK 129  
Db 62 LGVLGVPPAGQVASYLSPILGELWPKGNQWEI-FLEHVEQLINQITENARNTALARIQ 120

Qy 130 GLGALAVYHDSLSWGNRNNTARSVVRQYIALELMFVKQLPSPAVSSEVPLPIY 189  
Db 121 GLGDSFRAYQSLDLEWLENRDADRTRSVLHTQYIALELDPLNAMPFAIRNQEVPLLMVY 180

Qy 190 AQAANLHLLLRDASIFGKWLGLSSSEISTFYNQVERAGDYSDHCVKWYSTGLNLRGT 249  
Db 181 AQAANLHLLLRDASIFGSEFGLTSQEIQRVYQVTRDYSDYCVWEYNTGLNSLRGT 240

Qy 250 NAEWVRYNQRRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAIGTVHPHPSF 309  
Db 241 NAEWVRYNQRRDWTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAIGAT--GVNM 298

Qy 310 TSTTWNNAEVSFAIEAARVNRPHLLDFLEQVITYSLSSWSNTQYNNMGGHKLFRPT 369  
Db 299 ASMWYNNNAEVSFAIEAARVNRPHLLDFLEQVITYSLSSWSNTQYNNMGGHKLFRPT 358

Qy 370 IGTGLNTSTQGSTNTSINPVTLPFTSRDVTYTESLAGLNLFLTOPVNGVPVDFPHKFW 427  
Db 359 IGGGLNTSTHATNTSINPVTLPFTSRDVTYTESLAGLNLFLTOPVNGVPVDFPHKFW 416

Qy 428 VTHP-----TASDNFYPYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 482  
Db 417 -TNQNTSDRGTANYSQP-YESPGQLKDSSETLPETTERPNYESYSHRLSHIGLI 474

Qy 483 HVKALVSWTHRSADRNTIENPSTIQLPKAFNLSSGAAVVRGPGTGGDILRRNTG 542  
Db 475 RVNVPVSWTHRSADRNTIENPSTIQLPKAFNLSSGAAVVRGPGTGGDILRRNTG 534

Qy 543 TFGDIRVNINPPFAQRVRYRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTF 602  
Db 535 GFGDIRVNINPPFAQRVRYRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTF 594

Qy 603 RTVGFTTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKVTA 662  
Db 595 VRRFTTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKVTA 654

Qy 663 LFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
Db 655 LFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 711

RESULT 5  
US-09-988-462-7  
Sequence 7, Application US/09988462  
Publication No. US20030046726A1  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
APPLICANT: Desai, Nalini M.

Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lydie D.  
Wright, Martha S.  
Merlin, Ellis J.  
Launis, Karen L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Syngenta Biotechnology, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US 09/988,462  
FILING DATE: 20-NO. US20030046726A1-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/547,422  
FILING DATE: 11-APR-2000  
APPLICATION NUMBER: US 08/459,504  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-188051  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7  
Query Match 59.5%; Score 2236.5; DB 10; Length 1207;  
Best Local Similarity 64.1%; Pred. No. 5.1e-180;  
Matches 441; Conservative 76; Mismatches 156; Indels 15; Gaps 7;  
QY 40 EDCLKMSEYENVEPVASSTQIGTAGKILGTGVFPAGQVASYLSFILGELWPKGN 99  
DB 10 EDSLCIAEGNNIDPFVSASTVQTGINAGILGVLPVFPAGQVASYLSFILGELWPKGRD 69  
QY 100 QWEILFMEHVEE-INQKISTYARNKALTDLKLGDALAVYHDSLESWGNNTRARSV 158  
DB 70 QWEI-FLEHVEQLINQITENARTALRQLGDSFRAYQQSLEDWLENRRDARTSVL 128  
QY 159 RSQYALELMEVQKLPFASVGEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEIS 218  
DB 129 YTOYALELDFLNAFLPAIRNQVPLLMVTAQAANLHLLLRDASLFGSEFGLTSQEIQ 188  
QY 219 TFYNQVREAGDSDHCVKYSTGLNNLRGTNAESWRYNQFRDMTLMVLVLVPPSY 278  
DB 189 RYERQVETRDYSDYCVENWTGLNSLRGTNAESWRYNQFRDRLTLGLVLDLVLVPPSY 248  
QY 279 DTQMYPIKTTAQLTRVYTDATGTVHPHPSFTSTWNNNAPSFAIEAAVVRPHLLDF 338

DB 249 DIRTYPINTSAQLTRVYTDATGAT--GVNMASMNWNNNAPSFAIEAAAIRPHLLDF 305  
QY 339 LEQVTIYSLLSRWNTQYMMNMGHLEFRITGIGTLNISTOGSTNTSINPVTLPFTSRDV 398  
DB 307 LEQLTIFSSASRWNSNTRHTYWRGHTTQSRPIGGGLNTSTHGATNTSINPVTLPFASRDV 366  
QY 399 YRTESLAGLNLF--LTQPVNGVPRVDFHWKVFTHP-----IASDNFYYPGVAGIGTQLOD 451  
DB 367 YRTESYAGVLLWGIYLEPIHGVTVRFNF---TNPQNISDRGTANYSQP-YESFGLQKQD 422  
QY 452 SENELPPEATQOPNTYESYSHRLSHIGLSASHVKALVYSWTHRSADRNTTIEPNSITQIP 511  
DB 423 SETELPPTETTERPNTYESYSHRLSHIGIILQSRVNVVYSWTHRSADRNTTIGPRITQIP 482  
QY 512 LVKAFNLSSGAAVRPGFTGGDILRRNTGTGDIRVININPPPPFAQRVVRIRVASTTDL 571  
DB 483 MYKASELPQGTTVVRGPGFTGGDILRRNTGTGDIRVINGPLTQRYRIGFRVASTVDF 542  
QY 572 QFHTSINGKAINQGNFSATMRGEBLDYKTPFTVGTGFTFPFSLDVOSTFTIGAMNFSGN 631  
DB 543 DPFVSRGGTTVANNFRFLRMTNSGDELKYGNFVRRATFTPTFTQODIIRTSIQGLSNG 602  
QY 632 EVIDRIEFPVVEVYEAEDFEKAEKVYALFTSTNPRGLKTDVKDYHIDQVSNLVESL 691  
DB 603 EVIDIKIEIIPVTATFEAEYDLERAQEAANVALLFTWTFNPRKLTVDYHIDQVSNLVACL 662  
QY 692 SDEFYLDKRELFEIVKYANLHIERNM 719  
DB 663 SDEFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 6  
US-10-428-961-63  
Sequence 63, Application US/10428961  
Publication No. US20030237111A1  
GENERAL INFORMATION:  
APPLICANT: Baum, James A.  
APPLICANT: Chu, Chih-Rei  
APPLICANT: Donovan, William P.  
APPLICANT: Gilmer, Amy J.  
APPLICANT: Rupal, Mark J.  
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
FILE REFERENCE: MECO201--1  
CURRENT APPLICATION NUMBER: US/10/428,961  
CURRENT FILING DATE: 2003-05-02  
PRIOR APPLICATION NUMBER: 09/661,322  
PRIOR FILING DATE: 2000-09-13  
PRIOR APPLICATION NUMBER: 60/153,995  
PRIOR FILING DATE: 1999-09-15  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 63  
LENGTH: 1227  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis  
US-10-428-961-63

Query Match 57.4%; Score 2157.5; DB 15; Length 1227;  
Best Local Similarity 59.0%; Pred. No. 2.6e-173;  
Matches 422; Conservative 103; Mismatches 175; Indels 15; Gaps 5;  
QY 13 SSNAVKDKISTDSLKN-----ETDIELQNIHEDCLKMSEYENVEPVFVSASTVQTIG 65  
DB 7 NENEINALSIPAVSNHSAQWNLSTDARI-----EDSLCIAEGNNIDPFVSASTVQTIGIN 61  
QY 66 IAGKILGTIGVFPAGQVASYLSFILGELWPKGNOWELFMEHVEE-INQKISTYARNKA 124  
DB 62 IAGRILGVLPVFPAGQVASYLSFILGELWPKGRDPWEI-FLEHVEHLRQQVTENTRTA 120  
QY 125 LTDLKGLGDALAVYHDSLESWGNNTRARSVRSQYIALELMEVQKLPFASVGEVVP 184



NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1228  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-614-524-2

Query Match 55.5%; Score 2087; DB 15; Length 1228;  
Best Local Similarity 59.2%; Pred. No. 2.5e-167;  
Matches 423; Conservative 96; Mismatches 183; Indels 12; Gaps 9;

13 SNAKVDKISTDSLKN-ETDIELO-NINHEDCMKSEYENVEPVSASTIQTGIGIAGKI 70  
7 NENEIINALSPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINAGRI 66  
71 LGTLGVPPAGOVASLYFSLGELWPKGNQWELFMEHVEE-INQKISTYARKNALTDLK 129  
67 LGVLGVPPAGQIASFYSLVGLWELPKGRQWEL-FLHEVEQLINQOITENARNALTARLQ 125  
130 GLGDALAVYHDSLESVWGNRNNTARSVRSQYALIELMFQKLPSPFAVSGEEVPLPIY 189  
126 GLGDSFRAYQOSLEDWLENRDARTSVLYTQYIALELDFLAMPFLFAIRNQEVPLLMY 185  
190 AQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKVYSTGLNNLRGT 249  
186 AQANLHLLLRDASIFGSEFGLTSQEIORYERQVEQTRDYSYCEWYNTGLNSLRGT 245  
250 NAESVRYNQFRDMLTGLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAGTGVHPHPSF 309  
246 NAASVRYNQFRDMLTGLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAGTGVHPHPSF 303  
310 TSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMNWGGHKLFRFT 369  
304 ASMNWYNNAPSFSAIETAVIRSPHLLDFLEQVITYSLSRWSNTQYMNWGGHKLFRFT 363  
370 IGGTLNISTOGSTNTSINPVLTPFTSRDVTYTESLAGLNLF--LTOPVNGVPRVDFHWF 427  
364 IGGGLNTSTHGSTNTSINPVLTPFTSRDVTYTESLAGLNLF--LTOPVNGVPRVDFHWF 423  
428 V--THPIASDNFYPGYAGIGTQODSENELPPEATQPNYESYSHRLSHIGLISASHVK 485  
424 PONTFERGTANYSQP--YESPGLQKXDSLETLPETTERPNYESYSHRLSHIGLISASHVK 482  
486 ALVYSWTHRSADRTNTPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRNTGTGFG 545  
483 VPVYSWTHRSADRTNTPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRNTGTGFG 542  
546 DIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYKTFRTV 605  
543 SMGLNFNTSLQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYKTFRTV 602  
606 GFTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEVDEKAEKVTAFT 665  
603 EFPVGISASGSQ--TAGISISNNAGRTQFHFDEKIEFIPITATFEAEYDLERAQEAVALFT 661  
666 STNPRGLKTDVYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719  
662 NTNPRRLKTDVYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 715

Query Match 55.5%; Score 2087; DB 15; Length 1228;  
Best Local Similarity 59.2%; Pred. No. 2.5e-167;  
Matches 423; Conservative 96; Mismatches 183; Indels 12; Gaps 9;

13 SNAKVDKISTDSLKN-ETDIELO-NINHEDCMKSEYENVEPVSASTIQTGIGIAGKI 70  
7 NENEIINALSPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINAGRI 66  
71 LGTLGVPPAGOVASLYFSLGELWPKGNQWELFMEHVEE-INQKISTYARKNALTDLK 129  
67 LGVLGVPPAGQIASFYSLVGLWELPKGRQWEL-FLHEVEQLINQOITENARNALTARLQ 125  
130 GLGDALAVYHDSLESVWGNRNNTARSVRSQYALIELMFQKLPSPFAVSGEEVPLPIY 189  
126 GLGDSFRAYQOSLEDWLENRDARTSVLYTQYIALELDFLAMPFLFAIRNQEVPLLMY 185  
190 AQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKVYSTGLNNLRGT 249  
186 AQANLHLLLRDASIFGSEFGLTSQEIORYERQVEQTRDYSYCEWYNTGLNSLRGT 245  
250 NAESVRYNQFRDMLTGLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAGTGVHPHPSF 309  
246 NAASVRYNQFRDMLTGLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAGTGVHPHPSF 303  
310 TSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMNWGGHKLFRFT 369  
304 ASMNWYNNAPSFSAIETAVIRSPHLLDFLEQVITYSLSRWSNTQYMNWGGHKLFRFT 363  
370 IGGTLNISTOGSTNTSINPVLTPFTSRDVTYTESLAGLNLF--LTOPVNGVPRVDFHWF 427  
364 IGGGLNTSTHGSTNTSINPVLTPFTSRDVTYTESLAGLNLF--LTOPVNGVPRVDFHWF 423  
428 V--THPIASDNFYPGYAGIGTQODSENELPPEATQPNYESYSHRLSHIGLISASHVK 485  
424 PONTFERGTANYSQP--YESPGLQKXDSLETLPETTERPNYESYSHRLSHIGLISASHVK 482  
486 ALVYSWTHRSADRTNTPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRNTGTGFG 545  
483 VPVYSWTHRSADRTNTPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRNTGTGFG 542  
546 DIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYKTFRTV 605  
543 SMGLNFNTSLQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYKTFRTV 602  
606 GFTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEVDEKAEKVTAFT 665  
603 EFPVGISASGSQ--TAGISISNNAGRTQFHFDEKIEFIPITATFEAEYDLERAQEAVALFT 661  
666 STNPRGLKTDVYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719  
662 NTNPRRLKTDVYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 715

RESULT 9  
US-10-614-524-2  
; Sequence 2, Application US/10614524  
; Publication No. US20040016020A1  
; GENERAL INFORMATION:  
; APPLICANT: Arnaut, Greta  
; APPLICANT: Boets, Annemie  
; APPLICANT: Damme, Nicole  
; APPLICANT: Mathieu, Eva  
; APPLICANT: Vanneste, Stijn  
; APPLICANT: Van Rie, Jeroen  
; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.  
; FILE REFERENCE: NEWBTSUS2  
; CURRENT APPLICATION NUMBER: US/10/614,524  
; CURRENT FILING DATE: 2003-07-08  
; PRIOR APPLICATION NUMBER: US/09/739,243  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/173387  
; CURRENT FILING DATE: 1999-12-28



```

US-10-428-961-6
; Sequence 6, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-6

Query Match 44.1%; Score 1658.5; DB 15; Length 653;
Best Local Similarity 51.4%; Pred. No. 2.le-131;
Matches 346; Conservative 105; Mismatches 173; Indels 49; Gaps 16;

QY 13 SSNAKVDKISTDSLKN---ETDIELQNIHEDCLKMXEYENVPFVSASTIQTGIGIAGK 69
DB 2 NENEIINALSIPAVSNHSAQMDLSL-DARIEDSLCIAEGNNINPLVSASTVQTGINAGR 60

QY 70 ILGTGLVPFAGOVASLYSFLIGELWPKGNQWELTFMEHVEE-INOKIYIARNKALTDL 128
DB 61 ILGLVGPFPAGQLASFYSFLGELWPGSDRPWEI-FLYEYEQILRQOVTEHTAIAL 119

QY 129 KGLGDALAVYHDSLESVGNRRNTRASVRSQYIALELMFVKLFSAVSGSEVPLLP 188
DB 120 EGLGRGYSYQQALETWLDNRNDRSRIILERYVALELDITTAIPLFRIRNEBEVPLMV 179

QY 189 YQAANLHLLLRDASIPGKEWGLSSEISTFYNRQVERAGDYSDCHVKWYSTGLNNLRG 248
DB 180 YQAANLHLLLRDASLFGSEWGLSSDVNOYYQEIRYTEEYNSHCQWINTGLNNLRG 239

QY 249 TNAESWRYNCFRRDMLTLMVLDLVALPFSYDTQMPYIKTTAQLTREYVTDIAGTVHPHPS 308
DB 240 TNAESWRYNCFRRDMLTLMVLDLVALPFSYDTQMPYIKTTAQLTREYVTDIAGTVHPHPS 299

QY 309 FTSTTYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLSLRWNTQYMMWGGHKLFR 368
DB 300 FASTWFWNNNAPSFAIEAAIFRPPHLLDFPEQLTIYSASSRWSSTOHMYVWGHRLNFR 359

QY 369 TIGGTLNTSTOGST-NTSINPVTLPP-TRSDYRTESLAGLNLFLTOPVNGVPRVDPHWK 426
DB 360 PIGGTLNTSTOGLTNTSINPVTLHYVSRDVRRTESNAGTNILFTTPVNGVPWARFN- 417

QY 427 FVTHPIADSNFYYP-----GYAGIGTQLOQDSNELPPEATQOPNVESYSHRLSHIG- 477
DB 418 FITLRFKKEAPLTVNRIRELGFNYLIQKLNHOK-----QONDQIMNHIVIDISY 469

QY 478 -LISASHVVALYVSWTHRSADRTNIENSITQIPLVKAFNLSSGAAVVRPGFTGGDIL 536
DB 470 RLIIQNTLAPYVSWTHRSADRTNIGNRITQIPAVKGRFLFNG-SVIGSGFTGGDVV 528

QY 537 R-RTNGTGF--GDIRVNIN-PFFAQRVVRIRYASTTDLQFHTSINKAINQGNFSATM 591
DB 529 RLNRNNGNITQNGRYIEVPQFTSTSTRYRVRVRYASVTSIELNVNLGNSSIFTTTLPTATA 588

QY 592 NRGEDLDYKTRTVGTFTTFFSFLDVQSTFT-----IGANNFSSGNEVYIDIRIFVPVEV 645
DB 589 ASLDNLQ-----SGDFGVGEVNNAFSTATGIVGARNFSAEVLIDRFEPIPTA 639

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Qy	646	TYAEYDFEKAQE 658	:     : :
Db	640	TFEYEDLERAQK 652	:     : :
RESULT 13			
US-10-782-141-16			
; Sequence 16, Application US/10782141			
; Publication No. US20040197917A1			
; GENERAL INFORMATION:			
; APPLICANT: Carozzi, Nadine			
; APPLICANT: Hargiss, Tracy			
; APPLICANT: Koziel, Michael G.			
; APPLICANT: Duck, Nicholas B.			
; APPLICANT: Carr, Brian			
; TITLE OF INVENTION: AKMI-014, A Delta-Endotoxin Gene and			
; TITLE OF INVENTION: Methods for Its Use			
; FILE REFERENCE: 045600/274143			
; CURRENT APPLICATION NUMBER: US/10782,141			
; CURRENT FILING DATE: 2004-02-20			
; PRIOR APPLICATION NUMBER: 60/448,632			
; PRIOR FILING DATE: 2003-02-20			
; NUMBER OF SEQ ID NOS: 23			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 16			
; LENGTH: 1157			
; TYPE: PRT			
; ORGANISM: Bacillus thuringiensis			
US-10-782-141-16			
Query Match 43.7%; Score 1643.5; DB 16; Length 1157;			
Best Local Similarity 49.1%; Pred. No. 9.5e-130; Indels 61; Gaps 21;			
Matches 372; Conservative 96; Mismatches 229;			
Qy	1	MKLKNODKHQSFSSNAKVDKISTDS----	LKNETDIELQNIHEDCLKMSEYE-----N 50
Db	1	MEPNQNIYEIDA TPST-SVSSDSNRYPFANEPTD	ALQNNYKDYLKWSGGENPELFGN 59
Qy	51	VEPPFVASTIQTIGIAGKILGTGVPPAGVASIYS	FILGELWP-KGKNQW-EILFMEH 108
Db	60	PETFISSITQIGIGVGRILGALGVPPASQITASFS	PIVGQLWPSKSVDIVGEI--MER 117
Qy	109	VZE-INQISIVARNKALTDLKGIDALAVHDSLES	VMVGNRNTFRASVVRQVIALEL 167
Db	118	VEELVDQKIEKYVKDAAELKGLGNALDVYQOSLE	DWLENNRDARTSVVSNQFIALDL 177
Qy	168	MFVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDAS	IFGKEWGSSEISITFYNRQVER 227
Db	178	NFVSSIPSPFAVSGHEVLLAVYAQAVNHLHLLRDAS	IFGEEWGTPGEISRFYNRQVL 237
Qy	228	AGDSDHCYKVKYSTGLNNLRGNASWRYNQFRDM	TLVLDLVALPSPYDTQMPYKPT 287
Db	238	TAEYSDYCVKWKYKIGLDKLGKTTSKSWLNHYQFR	REMTLLVLDLVALFPNYDTHMYPDET 297
Qy	288	TAQLTRVYTDATGVHPHPSFTST-----TWYNN	NAPSFAEAAVVRNPHLLDFLEQVT 343
Db	298	TAQLTRDVYTDPIA-----FNIWTSFGCPNWS	THSGILFYEVENNVI RPHFLFDILSSVE 353
Qy	344	IYSLLSR-----WSNTOYMNWGHGKLEFR-----	TIGGTLNISTOGSTWTSINPVTLPFT 394
Db	354	INT--SRGGITLNDAYINWSGHTLYKRYRTADST	VTVYANYGRITSEKNS-----FALE 406
Qy	395	SRDVYRTESLAGNLFLTPQVNGVPRVDHFWKVF	HPHPIASDNFY-----YPGVAGIGTOL 449
Db	407	DRDIFEINSTAVMLANYOKAYGVPGSWFH--	MVKEGTSSITAYLYSKYTHLTALQGC-TQV 463
Qy	450	QDSENELPPEATQPNVYESYSHRLSHI-----	GLISASHVKALVYSWTHRSADRTNT 501
Db	464	YESDSEIDLPDRT--VPVAESYSHRLSHITSHS	FSKNG--SAYYGSFFPVVWTHTSADLNNT 520
Qy	502	IEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD	ILRRTWTGTGFDLRVINPFPFAQRYR 561

```
Db 521 IYSDKITQIPAVKDMYLGGSVVOGPGFTGGDILKRTNPSILGTFAVTNGSLSORVRV 580
Qy 562 RIRYASTTDLQPHSTSGKAINQGNFSAATMNRGEDLDYKTRTGVFTTFFSFLDVQSTFT 621
Db 581 RIRYASTTDFEF-TLYLGDITIEKRNFKMTMDNGASLTIVETPKFASFITDFQPREQDKIL 639
Qy 622 ICANWFSSGNEVYIDRIEFPVVEVYEAEDPEKAQEKVATLTFTNPRGLTKTDVKDHYH 681
Db 640 LSGMDFSSGQEVYIDRIEFPVDEYEAQDLEAAKAVNALFTNTKD-GLRPGVTDYEV 698
Qy 682 DOVSNLVSLSDEFYLDKRELFEIVKYANLHIERNM 719
Db 699 NQANLVECLSDLLYPNEKRLFLDAVREAKRLSGARNL 736

RESULT 14
US-10-032-717-2
; Sequence 2, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With
; FILE OF INVENTION: Pesticidal Activity Against Coleopterans
; CURRENT APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-032-717-2

Query Match 39.5%; Score 1485; DB 13; Length 1206;
Best Local Similarity 44.3%; Pred. No. 2.8e-116;
Matches 337; Conservative 127; Mismatches 231; Indels 66; Gaps 24;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDS----LKNETDIELQNINHEDECLM-----SEYE-N 50
Db 1 MSPNNQNEYEIIDATPST-SVSNDSNRYPPFANEPTNALQNDYKDYLNKNSAGNASEYFGS 59
Qy 51 VEPFVSA-STTQTGIGIAGKILGTGVPPAGOVASLYSFILGELWPKG-KNQWEILFMEH 108
Db 60 PEVLVSGQDAAKAADIIVGKLLSGLGVFPVGSIVSLYTLQIDILWPSGEKSQWEI-FMEQ 118
Qy 109 VEE-INQKISTYARKNALTDLKGLGDALAVHDSLESWGVRNNTNRARSVRSQVIALEL 167
Db 119 VEELNQKIAEYARKNALSLEGLGNNYQLYLTALEEWEENPNRSGRDLVRNREIFLDS 178
Qy 168 MFVOKLPSFVSGEVPPLPIYAOANLHLLLRDASIFGKEWGLSSSEISTFYNRQYER 227
Db 179 LFTQYMFSTRVNFVPELTVYAAANLHLLLRDASIFGKEWGLSSSEISTFYNRQYER 238
Qy 228 AGVSDHCWKVYSTGLANLRGNTAESWYRNQFRDMLTAMVLDLVALPSPYDTQMPIKT 287
Db 239 TAEYSDHCWKVYETGLAKLKGTSKQWVDYVNFQFRREMTLAVLDVVALFPNYDTRTPMET 298
Qy 288 TAQLTREYVYTAIGTVHPHPFTSTTWNNAAPSASAEAAVVRNPHLLDFLEQVYISL 347
Db 299 KAQLTREYVYDPLGAVNVS---SIGSWY-DKAPSEGVIESVIRPPHVFYITGLTVYVQ 354
Qy 348 LSRVSNTOYMNWGHKLEFRITGTLNISTQGSTNTSINPV-TLPFTSRDVRYESLAG 406
Db 355 SRSISSARIYRWAGHQISYHRVSRGSLNQMYGTNQNLHSTSTFDFTNYDIYKILSKDA 414
```

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Qy 407 LNLFLUTQP-----VNGVPRVDFHMKFVTHPTIASDN---FYYPGYAGIGTQLODSNEILPP 458
Db 415 VLLDVIYPGYTYIFPGMEVEFP---FMVQNLNTRKTLKYNPVSVDIIASTRDSLELPP 471
Qy 459 EATGQPNYESYSHRLSHLIGLISAS-HVKAL--VYSWTHRSADRTWTIEPNSITQIPLVKA 515
Db 472 ETSQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKC 531
Qy 516 FNLSSGAAVVRGPGFTGGDILR-RTNTGTGFDI---RVNINPPFAQRYVRIRYASTTDL 571
Db 532 WDNLPFPVVPVKGPGHTGGDLQYNRSTGSGVGLFLARYGLALEKAGKYRVLRYATDADI 591
Qy 572 QFHTSINGKALNQGNFSATMNRGEDLDYKTR-----TVGFTTTPFSFL-----DVOS 618
Db 592 VLH--VNDQAI---QMPKTMNPGEDLTSKTFKVAADAITTLNLTATDSSLALKHNLGEDPNS 646
Qy 619 TFTIGAWNFSSGNEVYIDRIEFPVVEVYEAEDPEKAQEKVATLTFTNPRGLTKTDVKD 678
Db 647 TLS-----GIVYVDRIEFPVDEYEAQDLEAAKAVNALFTNTKD-GLRPGVTD 696
Qy 679 YHIDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNM 719
Db 697 YEYVQAANLVECLSDLLYPNEKRLFLDAVREAKRLSEARNL 737

RESULT 15
US-10-414-637-2
; Sequence 2, Application US/10414637
; Publication No. US20030177528A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1 Proteins With
; FILE OF INVENTION: Pesticidal Activity Against Coleopterans
; CURRENT APPLICATION NUMBER: US/10/414,637
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-414-637-2

Query Match 39.5%; Score 1485; DB 14; Length 1206;
Best Local Similarity 44.3%; Pred. No. 2.8e-116;
Matches 337; Conservative 127; Mismatches 231; Indels 66; Gaps 24;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDS----LKNETDIELQNINHEDECLM-----SEYE-N 50
Db 1 MSPNNQNEYEIIDATPST-SVSNDSNRYPPFANEPTNALQNDYKDYLNKNSAGNASEYFGS 59
Qy 51 VEPFVSA-STTQTGIGIAGKILGTGVPPAGOVASLYSFILGELWPKG-KNQWEILFMEH 108
Db 60 PEVLVSGQDAAKAADIIVGKLLSGLGVFPVGSIVSLYTLQIDILWPSGEKSQWEI-FMEQ 118
Qy 109 VEE-INQKISTYARKNALTDLKGLGDALAVHDSLESWGVRNNTNRARSVRSQVIALEL 167
Db 119 VEELNQKIAEYARKNALSLEGLGNNYQLYLTALEEWEENPNRSGRDLVRNREIFLDS 178
Qy 168 MFVOKLPSFVSGEVPPLPIYAOANLHLLLRDASIFGKEWGLSSSEISTFYNRQYER 227
Db 179 LFTQYMFSTRVNFVPELTVYAAANLHLLLRDASIFGKEWGLSSSEISTFYNRQYER 238
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 9, 2005, 17:18:14 ; Search time 23.1512 Seconds  
(without alignments)  
2318.356 Million cell updates/sec

Title: US-10-019-823B-58  
Perfect score: 3761  
Sequence: 1 MKLNQKHQSFSSNAKVDK.....KRELFVIVKYNELHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3720	98.9	719	3	US-08-286-870A-8
2	3420	91.5	710	4	US-09-661-322A-42
3	3370	89.6	648	3	US-08-286-870A-4
4	3341	88.8	719	2	US-09-003-217-2
5	3336	88.7	719	3	US-09-218-942-2
6	2776	73.8	535	3	US-08-286-870A-6
7	2417.5	64.3	1229	1	US-08-100-709-4
8	2417.5	64.3	1229	1	US-08-176-865-4
9	2417.5	64.3	1229	1	US-08-474-038-4
10	2417.5	64.3	1229	2	US-08-779-046-4
11	2417.5	64.3	1229	2	US-08-881-340-4
12	2318.5	61.6	488	1	US-08-448-170-10
13	2318.5	61.6	488	3	US-08-961-803-10
14	2336.5	59.5	1207	1	US-07-951-715A-7
15	2336.5	59.5	1207	2	US-08-459-448A-7
16	2336.5	59.5	1207	3	US-08-459-595A-7
17	2336.5	59.5	1207	3	US-08-459-504B-7
18	2336.5	59.5	1207	3	US-08-459-444-7
19	2336.5	59.5	1207	3	US-09-053-549-8
20	2336.5	59.5	1207	3	US-09-547-422-7
21	2336.5	59.5	1207	4	US-09-988-462-7
22	2336.5	59.4	1227	3	US-09-053-549-2
23	2166.5	57.6	1227	1	US-08-448-170-8
24	2166.5	57.6	1227	3	US-08-961-803-9
25	2157.5	57.4	1227	4	US-09-661-322A-63
26	2142.5	57.0	1186	3	US-09-178-252-23
27	2142.5	57.0	1186	4	US-09-826-660-23

28 2087 55.5 1228 4 US-09-661-322A-38 Sequence 38, Appl  
29 1909.5 50.8 643 3 US-09-178-252-25 Sequence 25, Appl  
30 1909.5 50.8 643 4 US-09-826-660-25 Sequence 25, Appl  
31 1872 49.8 380 5 PCT-US91-02560-4 Sequence 4, Appl  
32 1658.5 44.1 653 4 US-09-661-322A-6 Sequence 6, Appl  
33 1643.5 43.7 1157 1 US-07-876-280-30 Sequence 30, Appl  
34 1643.5 43.7 1157 1 US-07-812-180A-2 Sequence 2, Appl  
35 1643.5 43.7 1157 1 US-08-315-468-2 Sequence 2, Appl  
36 1643.5 43.7 1157 3 US-07-941-650A-2 Sequence 2, Appl  
37 1481.5 39.4 1176 1 US-08-257-999-2 Sequence 2, Appl  
38 1466 39.0 1157 2 US-08-532-547-5 Sequence 5, Appl  
39 1466 39.0 1157 2 US-08-379-656B-5 Sequence 5, Appl  
40 1466 39.0 1157 3 US-08-458-838-5 Sequence 5, Appl  
41 1466 39.0 1157 3 US-09-019-809-5 Sequence 5, Appl  
42 1466 39.0 1157 4 US-09-471-177-5 Sequence 5, Appl  
43 1466 39.0 1157 4 US-09-220-806-5 Sequence 5, Appl  
44 1461 38.8 1168 1 US-08-291-368-4 Sequence 4, Appl  
45 1461 38.8 1168 2 US-08-962-190-4 Sequence 4, Appl

## ALIGNMENTS

## RESULT 1

US-08-286-870A-8  
; Sequence 8, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENN, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PAUL N. KOKULIS  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 70608/220720  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-286-870A-8

Query Match 98.9%; Score 3720; DB 3; Length 719;  
Best Local Similarity 99.2%; Pred. No. 0;  
Matches 714; Conservative 3; Mismatches 1; Indels 2; Gaps 2;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMSEYENVEPVSASTI 60  
DB 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMSEYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYSPILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
DB 61 QTGIGIAGKILGTGVPFAGQVASYSPILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
QY 120 ARNKALTDLKGDLALAVYHDSLESWGNRNNTARSVRSQYIALBELMFVKLPSPAVS 179  
DB 120 ARNKALTDLKGDLALAVYHDSLESWGNRNNTARSVRSQYIALBELMFVKLPSPAVS 179  
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKENGLSSEISTEYFNQVERAGDYSCHVKWY 239  
DB 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKENGLSSEISTEYFNQVERAGDYSCHVKWY 239  
QY 240 STGLNLRGNTAESWVRYNQFRDMLVLDLVALFPSTYDQMPYIKTTAQLTREVTDA 299  
DB 240 STGLNLRGNTAESWVRYNQFRDMLVLDLVALFPSTYDQMPYIKTTAQLTREVTDA 299  
QY 300 IGVHPPHPSFTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMM 359  
DB 300 IGVHPPHPSFTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMM 359  
QY 360 WGGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTSLAGLNLFLTPQVNGVP 419  
DB 360 WGGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTSLAGLNLFLTPQVNGVP 419  
QY 420 RVDHFKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATQPNYESYSHRSLHGLI 479  
DB 420 RVDHFKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATQPNYESYSHRSLHGLI 479  
QY 480 SASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFLSSGAAVVRGPGFTGGDILRRT 539  
DB 480 SASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFLSSGAAVVRGPGFTGGDILRRT 539  
QY 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599  
DB 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599  
QY 600 KTFRTVGTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
DB 600 KTFRTVGTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
QY 660 VTALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
DB 660 VTALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 2  
US-09-661-322A-42  
; Sequence 42, Application US/09661322A  
; Patent No. 6593293  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Ruper, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos  
; FILE REFERENCE: MECO201  
; CURRENT APPLICATION NUMBER: US/09/661.322A  
; CURRENT FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 42  
; LENGTH: 710  
; TYPE: PRT

ORGANISM: Bacillus thuringiensis  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (2007..(200)  
OTHER INFORMATION: No. 6593293-Coding  
US-09-661-322A-42

Query Match 91.5%; Score 3442.5; DB 4; Length 710;  
Best Local Similarity 91.9%; Pred. No. 3.5e-304;  
Matches 662; Conservative 16; Mismatches 31; Indels 11; Gaps 3;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMSEYENVEPVSASTI 60  
DB 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMSEYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYSPILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
DB 61 QTGIGIAGKILGTGVPFAGQVASYSPILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
QY 120 ARNKALTDLKGDLALAVYHDSLESWGNRNNTARSVRSQYIALBELMFVKLPSPAVS 179  
DB 120 ARNKALTDLKGDLALAVYHDSLESWGNRNNTARSVRSQYIALBELMFVKLPSPAVS 179  
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKENGLSSEISTEYFNQVERAGDYSCHVKWY 239  
DB 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKENGLSSEISTEYFNQVERAGDYSCHVKWY 239  
QY 240 STGLNLRGNTAESWVRYNQFRDMLVLDLVALFPSTYDQMPYIKTTAQLTREVTDA 299  
DB 240 STGLNLRGNTAESWVRYNQFRDMLVLDLVALFPSTYDQMPYIKTTAQLTREVTDA 299  
QY 300 IGVHPPHPSFTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMM 359  
DB 300 IGVHPPHPSFTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMM 359  
QY 360 WGGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTSLAGLNLFLTPQVNGVP 419  
DB 360 WGGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTSLAGLNLFLTPQVNGVP 419  
QY 420 RVDHFKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATQPNYESYSHRSLHGLI 479  
DB 420 RVDHFKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATQPNYESYSHRSLHGLI 479  
QY 480 SASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFLSSGAAVVRGPGFTGGDILRRT 539  
DB 480 SASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFLSSGAAVVRGPGFTGGDILRRT 539  
QY 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599  
DB 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599  
QY 600 KTFRTVGTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
DB 600 KTFRTVGTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
QY 660 VTALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
DB 660 VTALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 3  
US-08-286-870A-4  
; Sequence 4, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENN, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABY & CUSHMAN

```

; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-870A-4

Query Match      89.6%; Score 3370; DB 3; Length 648;
Best Local Similarity 99.5%; Pred. No. 1.2e-297;
Matches 646; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

Qy      1 MKLKNDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVEPFVSASTI 60
Db      1 MKLKNDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVEPFVSASTI 60

Qy      61 QTGIGIAGKILGTGVPFAGOVASLYSFTLGLWPKGNQWEILFMEHVEE-INOKISTY 119
Db      61 QTGIGIAGKILGTGVPFAGOVASLYSFTLGLWPKGNQWEILFMEHVEE-INOKISTY 119

Qy      120 ARNKALTDLKGIGDALAVYHDSLESWGVRNRRNTRARSVVRQYIALELMFVKLPSPFAVS 179
Db      120 ARNKALTDLKGIGDALAVYHDSLESWGVRNRRNTRARSVVRQYIALELMFVKLPSPFAVS 179

Qy      180 GEEVPLPIYAQAANLHLLLRDASIIFGKWLGLSSSEISTFTYNRQVERAGDYSDHCVKWY 239
Db      180 GEEVPLPIYAQAANLHLLLRDASIIFGKWLGLSSSEISTFTYNRQVERAGDYSDHCVKWY 239

Qy      240 STGLNLRGTAESVVRNQFRDMTAVLDLVALFPSTQYPIKTTAQLTREVVYDA 299
Db      240 STGLNLRGTAESVVRNQFRDMTAVLDLVALFPSTQYPIKTTAQLTREVVYDA 299

Qy      300 IGTVHPHPSFTSTTWNYNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNM 359
Db      300 IGTVHPHPSFTSTTWNYNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNM 359

Qy      360 WGGHKLFRRTTGGTGNISINPVLPTFSRDVYRTESLAGNLFITQPVNGVP 419
Db      360 WGGHKLFRRTTGGTGNISINPVLPTFSRDVYRTESLAGNLFITQPVNGVP 419

Qy      420 RVDHFWKFTVTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
Db      420 RVDHFWKFTVTHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479

; ADDRESS: Intellectual Property Group of
; ADDRESS: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09-003-217-2
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09003217
; FILING DATE: 09-MAY-1990
; GENERAL INFORMATION:
; APPLICANT: Madkour, Magdy A.
; APPLICANT: Bulla, Lee A.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH
; TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
; STREET: 3605 Glenwood Ave. Suite 310
; CITY: Raleigh
; STATE: NC
; COUNTRY: US
; ZIP: 27622
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003.217
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 5718-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2202
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-003-217-2

Query Match      88.8%; Score 3341; DB 2; Length 719;
Best Local Similarity 89.2%; Pred. No. 6.1e-295;
Matches 642; Conservative 35; Mismatches 41; Indels 2; Gaps 2;

Qy      1 MKLKNDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVEPFVSASTI 60
Db      1 MKLKNDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVEPFVSASTI 60

Qy      61 QTGIGIAGKILGTGVPFAGOVASLYSFTLGLWPKGNQWEILFMEHVEE-INOKISTY 119
Db      61 QTGIGIAGKILGTGVPFAGOVASLYSFTLGLWPKGNQWEILFMEHVEE-INOKISTY 119

Qy      120 ARNKALTDLKGIGDALAVYHDSLESWGVRNRRNTRARSVVRQYIALELMFVKLPSPFAVS 179
Db      120 ARNKALTDLKGIGDALAVYHDSLESWGVRNRRNTRARSVVRQYIALELMFVKLPSPFAVS 179

Qy      180 GEEVPLPIYAQAANLHLLLRDASIIFGKWLGLSSSEISTFTYNRQVERAGDYSDHCVKWY 239
Db      180 GEEVPLPIYAQAANLHLLLRDASIIFGKWLGLSSSEISTFTYNRQVERAGDYSDHCVKWY 239
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Db 180 GEEVPLPIYAQAANLHLLLDASIFKNGGLSASEISTFYNRQVVERTDYSDYCHVKWN 239  
Qy 240 STGLNNLRTNAESWVRNQFRDMTLMVLDLVALFPPSYDTOMYPIKTTAQLTREVYTD 299  
Db 240 NTGLNNLRATNGQSWVRNQFRKDIELMVLVDFVPPSYDTLVPIKTTSQLTREVYTD 299  
Qy 300 IGTVHPHPSFTSTWYNNNAPSFAIAEAAVVRNPHLLDLEQVTTIYSLLSRWNSNTQYMMN 359  
Db 300 IGTVDNQLRSTWYNNNAPSFAIAEAAVVRNPHLLDLEQVTTIYSLLSRWNSNTQYMMN 359  
Qy 360 WGHKLEPRTTGGTLNISTQGSTNTSINPVTLPFTSRDVRVTTESLAGLNLFTQPVNGVP 419  
Db 360 WGHRLSRPFGGALNTSTQGSTNTSINPVTLPFTSRDVRVTTESLAGLNLFTQPVNGVP 419  
Qy 420 RVDHFKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
Db 420 RVDHFKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
Qy 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
Db 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
Qy 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDY 599  
Db 540 KSGTFGHIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDY 599  
Qy 600 KTRFTVGTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659  
Db 600 KTRFTVGTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659  
Qy 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFLDKRELFEIVKYANELHIERNM 719  
Db 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFLDKRELFEIVKYANELHIERNM 719

RESULT 5  
US-09-218-942-2  
; Sequence 2, Application US/09218942  
; Patent No. 6232439  
; GENERAL INFORMATION:  
; APPLICANT: Osman, Yehia  
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum  
; FILE REFERENCE: CryII  
; CURRENT APPLICATION NUMBER: US/09/218,942  
; CURRENT FILING DATE: 1998-12-22  
; EARLIER APPLICATION NUMBER: 60/035,361  
; EARLIER FILING DATE: 1997-01-10  
; EARLIER APPLICATION NUMBER: 09/003,217  
; EARLIER FILING DATE: 1998-01-06  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-09-218-942-2

Query Match 88.7%; Score 3336; DB 3; Length 719;  
Best Local Similarity 89.2%; Pred. No. 1.7e-294;  
Matches 642; Conservative 35; Mismatches 41; Indels 2; Gaps 2;

Qy 1 MCLKNODKHOFSSNAKVDKISTDSLKNVETDIELQNIHEDCLMKSEYENVEPVSASTI 60  
Db 1 MCLKNPKHQTLSSNAKVDKIATDSLKNVETDIELKNWNEIDYLRMSEHESIDPFVSASTI 60  
Qy 61 QTGIGIAGKILGTGVFPAGVSLYSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
Db 61 QTGIGIAGKILGTGVFPAGVSLYSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
Qy 120 ARNKALTDKLGALAVYHDSLSWGVRNNTARSVRSQVYTALELMFVQKLPSFAVS 179  
Db 120 ARNKALTDKLGALAVYHDSLSWGVRNNTARSVRSQVYTALELMFVQKLPSFAVS 179

Qy 180 GEEVPLPIYAQAANLHLLLDASIFKNGGLSASEISTFYNRQVVERTDYSDYCHVKWY 239  
Db 180 GEEVPLPIYAQAANLHLLLDASIFKNGGLSASEISTFYNRQVVERTDYSDYCHVKWN 239  
Qy 240 STGLNNLRTNAESWVRNQFRDMTLMVLDLVALFPPSYDTOMYPIKTTAQLTREVYTD 299  
Db 240 NTGLNNLRATNGQSWVRNQFRKDIELMVLVDFVPPSYDTLVPIKTTSQLTREVYTD 299  
Qy 300 IGTVHPHPSFTSTWYNNNAPSFAIAEAAVVRNPHLLDLEQVTTIYSLLSRWNSNTQYMMN 359  
Db 300 IGTVDNQLRSTWYNNNAPSFAIAEAAVVRNPHLLDLEQVTTIYSLLSRWNSNTQYMMN 359  
Qy 360 WGHKLEPRTTGGTLNISTQGSTNTSINPVTLPFTSRDVRVTTESLAGLNLFTQPVNGVP 419  
Db 360 WGHRLSRPFGGALNTSTQGSTNTSINPVTLPFTSRDVRVTTESLAGLNLFTQPVNGVP 419  
Qy 420 RVDHFKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
Db 420 RVDHFKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
Qy 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
Db 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
Qy 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDY 599  
Db 540 KSGTFGHIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDY 599  
Qy 600 KTRFTVGTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659  
Db 600 KTRFTVGTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659  
Qy 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFLDKRELFEIVKYANELHIERNM 719  
Db 660 VTALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFLDKRELFEIVKYANELHIERNM 719

RESULT 6  
US-08-286-870A-6  
; Sequence 6, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989

```

; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-870A-6

Query Match 73.8%; Score 2776; DB 3; Length 535;
Best Local Similarity 99.4%; Pred. No. 1e-243;
Matches 533; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

Qy 1 MKLNQDQHQSFSSNAKVDKISTSLKNETDIELQINHHEDCLKMSYENVEPVSASTI 60
Db 1 MKLNQDQHQSFSSNAKVDKISTSLKNETDIELQINHHEDCLKMSYENVEPVSASTI 60

Qy 61 QTGIGIACKIILGTGVPPAGVASLYSFLGELMPKGNQWEILFMEHVEE-INQIKISTY 119
Db 61 QTGIGIACKIILGTGVPPAGVASLYSFLGELMPKGNQWEILFMEHVEE-INQIKISTY 119

Qy 120 ARNKALTDKLGIDALAVYHDSLSWGNRRNTRARSVVRQYIALELMFVKLPSPAVS 179
Db 120 ARNKALTDKLGIDALAVYHDSLSWGNRRNTRARSVVRQYIALELMFVKLPSPAVS 179

Qy 180 GEEVPLPIYQAANLHLLLRDASIFGKWLGSSEISTFYNRQVERAGDYSDHCVKWY 239
Db 180 GEEVPLPIYQAANLHLLLRDASIFGKWLGSSEISTFYNRQVERAGDYSDHCVKWY 239

Qy 240 STGLNLEGTAESWVRNQFRDMLMVLVDLVALFPSYDTOMYPIKTAQLTREVYTD 299
Db 240 STGLNLEGTAESWVRNQFRDMLMVLVDLVALFPSYDTOMYPIKTAQLTREVYTD 299

Qy 300 IGTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNM 359
Db 300 IGTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNM 359

Qy 360 WGGHKLFPRTIGTLNISTQSTNTSINPVLPTSDRYRTESLAGNLFLTPQVNGVP 419
Db 360 WGGHKLFPRTIGTLNISTQSTNTSINPVLPTSDRYRTESLAGNLFLTPQVNGVP 419

Qy 420 RVDPHMKFVTHPIASDNFYFGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
Db 420 RVDPHMKFVTHPIASDNFYFGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479

Qy 480 SASHVKALVYSWTHRSADRTNTIEPNSITQPLVKAFNLSSGAAVVRGPGFTGGDI 535
Db 480 SASHVKALVYSWTHRSADRTNTIEPNSITQPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
; Sequence 4, Application US/08100709
; Patent No. 5322687
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia

```

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; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,709
; FILING DATE: 19930729
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-100-709-4

Query Match 64.3%; Score 2417.5; DB 1; Length 1229;
Best Local Similarity 65.3%; Pred. No. 1.7e-210;
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

Qy 13 SSNAKVDKISTSLKIN-ETDIELQ-NINHHEDCLKMSYENVEPVSASTITGTGIGIACKI 70
Db 7 NENEIINALSIPTVNSPSTQNLSPDARIEDSLCAEVNINIDPFVSASTVQTGINIAGRI 66

Qy 71 LGTLGVPPAGVASLYSFLGELMPKGNQWEILFMEHVEE-INQIKISTYARNKALTDLK 129
Db 67 LGVLGVPPAGQALASIFLVLGELMPSGRDPWEI-FLHEVEQLIQQVTTENTRTAIARLE 125

Qy 130 GLGDALAVYHDSLSWGNRRNTRARSVVRQYIALELMFVKLPSPAVSGEEVPLPIY 189
Db 126 GLGRGYSYQQALETWLDNRNDARSRSIILERYVALELDITTAIPLFRIRNEEVPLLMVY 185

Qy 190 QAANLHLLLRDASIFGKWLGSSEISTFYNRQVERAGDYSDHCVKWYSLGLNLRGT 249
Db 186 QAANLHLLLRDASIFGSEMGWASSDVNQYQIRYTESYSHCHVQMYNTGLNLRGT 245

Qy 250 NAEWSWVRNQFRDMLMVLVDLVALFPSYDTOMYPIKTAQLTREVYTDAGTVHPHPSF 309
Db 246 NAEWSWVRNQFRDMLMVLVDLVALFPSYDTOMYPIKTAQLTREVYTDAGTVHPHPSF 305

Qy 310 TSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMGGHKLFPRT 369
Db 306 ASTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMGGHKLFPRT 365

Qy 370 IGTGLNISTQSTNTSINPVLPTSDRYRTESLAGNLFLTPQVNGVPVRDHPHFKV 428
Db 366 IGTGLNISTQSTNTSINPVLPTSDRYRTESLAGNLFLTPQVNGVPVRDHPHFKV 422

Qy 429 THPIASDNFYFGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISA 481
Db 423 ---INPQNIYERGATTYSQYQVIGIQLFDESELPETTERPNYESYSHRLSHIGLIIG 479

Qy 482 SHVKALVYSWTHRSADRTNTIEPNSITQPLVKAFNLSSGAAVVRGPGFTGGDILRRNT 541
Db 480 NTLRAPVYSWTHRSADRTNTIEPNSITQPLVKAFNLSSGAAVVRGPGFTGGDILRRNT 539

Qy 542 GTFGDIRVNWNPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSAATMRGDDLYKT 601
Db 540 GTFGDIRVNWNPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSAATMRGDDLYKT 599

Qy 602 FRTVGFPTPFSFLDVQSTFTIGAMNFSNGNEVYDRIEFVPEVTEYAEYDFEKAQKVT 661
Db 600 FRTAGFSTPPFNLAQSTFTLGAQFSN-QEYVIDRVEFVPAEYTFEABYDLERAQKAVN 658

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Qy	662	ALFTSTNPRGLKTDVQKDHIDQVNLVESLSDEFYLDKELFEIYKYNELHIERNM	719
Db	659	ALFTSTNPRRLKTDVTDYHIDQVNMVACLSDFCDEKRELFEKVYAKRLSDERNL	716
RESULT 8			
US-08-176-865-4			
; Sequence 4, Application US/08176865			
; Patent No. 5616319			
; GENERAL INFORMATION:			
; APPLICANT: Donovan, William P.			
; APPLICANT: Tan, Yuping			
; APPLICANT: Jany, Christine S.			
; APPLICANT: Gonzalez Jr., Jose M.			
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5			
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS			
; NUMBER OF SEQUENCES: 5			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.			
; ADDRESS: Nadel			
; STREET: 1601 Market Street, 36th Floor			
; CITY: Philadelphia			
; STATE: Pennsylvania			
; COUNTRY: U.S.A.			
; ZIP: 19103			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent In Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/176,865			
; FILING DATE: 30-DEC-1993			
; CLASSIFICATION: 435			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/100,709			
; FILING DATE: 29-JUL-1993			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Egoif, Christopher			
; REGISTRATION NUMBER: 27633			
; REFERENCE/DOCKET NUMBER: 7205-49			
; TELEPHONE: 215-757-1590			
; INFORMATION FOR SEQ ID NO: 4:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1229 amino acids			
; TYPE: amino acid			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-08-176-865-4			
Query Match 64.3%; Score 2417.5; DB 1; Length 1229;			
Best Local Similarity 65.3%; Pred. No. 1.7e-210;			
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;			
Qy	13	SSNAKVDKISTSLKN-ETDIELQ-NINHEDECLKSEYENVEPFFVSASTIQIGIAGKI	70
Db	7	NENEINAIISPTVSNPSTQMLSPDARIEDSLCAEVANNIDPFFVSASTIQIGIAGRI	66
Qy	71	LGTGLVFPFAGQVASYLSFILGELWPKGNQWELFMEHVEE-INOKISTYARNKALTDLK	129
Db	67	LGLVGFVFPAGQLASFYSFLVGLWPGSRDPWEI-FLEHVEQLIRQOQVTEINTAIALR	125
Qy	130	GLGDALAVHDSLSWVGNNRNNTRASVRSQVIALELMFVQKLPSFAVSGEVPLLPT	189
Db	126	GLGRGYSRYSQALETWLDNRNDARSIIILERVVALELDITTAIPLFRNVEVPLLMY	185
Qy	190	AQANLHLILLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSCHCVKWTGLANLRGT	249
Db	186	AQANLHLILLRDASLFGSEWGMASDVNQYQEQIRYREYSNHCQVWNTGLANLRGT	245
Qy	250	NAESWRYNQFRDMLMLDLVALPFSYDTQMPYIKTTAQLTREYVTDIAITGVHPHPSF	309

Db	246	NAESWRYNQFRDMLTLGLVDLVALPFSYDTRTYPTNTSAQLTREIYTDPIGRTNAPSQF	305
Qy	310	TSTTWANNAPSALEAAAVNPNHLLDFLEQVTTYSLLSRWSNTQYMMNMGHKLFPRT	369
Db	306	ASTNWFNNAPSALEAAAFPPHLLDPPEQLTTYSASSRWSSTQHNNYWGHRNLFRP	365
Qy	370	IGGTLNISTQGST-NTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPRVDFHWKFV	428
Db	366	IGGTLNISTQGLTNNTSINPVTLPFTSRDVRTESNAGTNILFTTPVNGVPPWAFNPF	422
Qy	429	THPIASDNFYPG-----YAGIGTLOQDSNELPPEATGQPNYESYSHRLSHIGLISA	481
Db	423	---INPQNIYERGATTYSQYQGVGLFSDSETLPETTERPNYESYSHRLSHIGLIG	479
Qy	482	SHVKALVYSWTHESADRTNIENSITQPLVKAFNLSSGAAVVRGPGTGGDILARTNT	541
Db	480	NTRAPVYSWTHESADRTNIENRITQPLVKALNLHSGVTVVGGPGTGGDILARTNT	539
Qy	542	GTFGDIRVNIINPPFAQRYRVIRYASTTDLQFHTSINGKAINQGNFSAATNRGEDIJYKT	601
Db	540	GTFGDIRLNIINVLPSQRYRVIRYASTTDLQFTRINGTIVNIGNFSRTMNRGDNLEYS	599
Qy	602	FRTVGTTPSPFLDVQSTFTIGAWNFSSGNEWIDRIEFVPEVTVYEAAYDEKAQEKVT	661
Db	600	FRTAGFSTPFNFLNAQSTFTLGAQSPSN-QEVVIDRVEFPVPAEVTFEAEVDLERAQAVN	658
Qy	662	ALFTSTNPRGLKTDVQKDHIDQVNLVESLSDEFYLDKELFEIYKYNELHIERNM	719
Db	659	ALFTSTNPRRLKTDVTDYHIDQVNMVACLSDFCDEKRELFEKVYAKRLSDERNL	716
RESULT 9			
US-08-474-038-4			
; Sequence 4, Application US/08474038			
; Patent No. 5679343			
; GENERAL INFORMATION:			
; APPLICANT: Donovan, William P.			
; APPLICANT: Tan, Yuping			
; APPLICANT: Jany, Christine S.			
; APPLICANT: Gonzalez Jr., Jose M.			
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5			
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS			
; NUMBER OF SEQUENCES: 5			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.			
; ADDRESS: Nadel			
; STREET: 1601 Market Street, 36th Floor			
; CITY: Philadelphia			
; STATE: Pennsylvania			
; COUNTRY: U.S.A.			
; ZIP: 19103			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent In Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/474,038			
; FILING DATE: 07-JUN-1995			
; CLASSIFICATION: 514			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/176,865			
; FILING DATE: 30-DEC-1993			
; APPLICATION NUMBER: US 08/100,709			
; FILING DATE: 29-JUL-1993			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Egoif, Christopher			
; REGISTRATION NUMBER: 27633			
; REFERENCE/DOCKET NUMBER: 7205-49			
; TELEPHONE: 215-757-1590			
; INFORMATION FOR SEQ ID NO: 4:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1229 amino acids			
; TYPE: amino acid			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-08-176-865-4			
Query Match 64.3%; Score 2417.5; DB 1; Length 1229;			
Best Local Similarity 65.3%; Pred. No. 1.7e-210;			
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;			

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1229 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-474-038-4

Query Match 64.3%; Score 2417.5; DB 1; Length 1229;  
 Best Local Similarity 65.3%; Pred. No. 1.7e-210;  
 Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPFSASTIQTGIGIAGKI 70  
 DB 7 NENEIINALSIPTVSNPSTQMLSPDARIEDSLCAEVNNDIPFVSASTVQTGINIAGRI 66  
 QY 71 LGTLGVPPAGQVASYLSIFGLMFKGNQWEILFMEHVEE-INOKISTYARNKALTDLK 129  
 DB 67 LGVLGVPPAGQVASYLSIFGLMFKGNQWEILFMEHVEE-INOKISTYARNKALTDLK 125  
 QY 130 GLGDALAVYHDSLSWGVNRRNTRARSVVRQYIALELMFVQKLPSPFVSGVEVPLLIY 189  
 DB 126 GLGRYRSYQOALSTWLDNRDARSILERYVALELDITTAIPLFIRNEEVPLLMVY 185  
 QY 190 AQAANLHLLLRDASIFGKWLSSSEISTFVNRQVERAGDYSDHCVKWYSTGLNNLRGT 249  
 DB 186 AQAANLHLLLRDASIFGKWLSSSEISTFVNRQVERAGDYSDHCVKWYSTGLNNLRGT 245  
 QY 250 NAESWVRYNQRRDMLVLDLVALFPSYDTQMPYIKTTAQITREYVYDAITGVHPHPSF 309  
 DB 246 NAESWVRYNQRRDMLVLDLVALFPSYDTQMPYIKTTAQITREYVYDAITGVHPHPSF 305  
 QY 310 TSTWYNNNAPSFAIEAAVVRNPHLLDFLQVITYLSLLRSWNTQYNNMGGHKLERT 369  
 DB 306 ASTWYNNNAPSFAIEAAVVRNPHLLDFLQVITYLSLLRSWNTQYNNMGGHKLERT 365  
 QY 370 IGGTLNISTQGST-NTSINPVTLPSTRDVRATESLAGNLFLTPQVNGVPRVDFHWFV 428  
 DB 366 IGGTLNISTQGST-NTSINPVTLPSTRDVRATESLAGNLFLTPQVNGVPRVDFHWFV 422  
 QY 429 THPIASDNFYYPG-----YAGIGTQLQDSENELPPEATGQPNYESYSHRSLHIGLISA 481  
 DB 423 ---INPQNIYERGATTYSQYQGVIGLQFDESETLPPTTERPNYESYSHRSLHIGLIG 479  
 QY 482 SHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVRGPGFTGCDILRRNT 541  
 DB 480 NTLRAPVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVRGPGFTGCDILRRNT 539  
 QY 542 GTFGDIRVNPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAIWMRGEDLDYKT 601  
 DB 540 GTFGDIRVNPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAIWMRGEDLDYKT 599  
 QY 602 FRTVGTTPFPFGLDQVSTFTIGAMFSSGNEVYIDRIEFPVPEVTEAYEDPEKAQKV 661  
 DB 600 FRTAGSTFPFPLNAQSTFTIGAQSFN-QEVIDRVEFVAEVTFAEYDLEAQAQAVN 658  
 QY 662 ALFTSTNPRGLTKDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNM 719  
 DB 659 ALFTSTNPRGLTKDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNM 716

RESULT 10  
 US-08-779-046-4  
 Sequence 4, Application US/08779046  
 Patent No. 5854053  
 GENERAL INFORMATION:  
 APPLICANT: Donovan, William P.  
 APPLICANT: Tan, Yiping  
 APPLICANT: Jan, Christine S.  
 APPLICANT: Gonzalez Jr., Jose M.  
 TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5  
 TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ADDRESSEE: Nadel  
 STREET: 1601 Market Street, 36th Floor  
 CITY: Philadelphia  
 STATE: Pennsylvania  
 COUNTRY: U.S.A.  
 ZIP: 19103

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/779,046  
 FILING DATE: 06-JAN-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/100,709  
 FILING DATE: 29-JUL-1993

ATTORNEY/AGENT INFORMATION:  
 NAME: Egoif, Christopher  
 REGISTRATION NUMBER: 27633  
 REFERENCE/DOCKET NUMBER: 7205-49  
 TELEPHONE: 215-757-1590

INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1229 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-779-046-4

Query Match 64.3%; Score 2417.5; DB 2; Length 1229;  
 Best Local Similarity 65.3%; Pred. No. 1.7e-210;  
 Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPFSASTIQTGIGIAGKI 70  
 DB 7 NENEIINALSIPTVSNPSTQMLSPDARIEDSLCAEVNNDIPFVSASTVQTGINIAGRI 66  
 QY 71 LGTLGVPPAGQVASYLSIFGLMFKGNQWEILFMEHVEE-INOKISTYARNKALTDLK 129  
 DB 67 LGVLGVPPAGQVASYLSIFGLMFKGNQWEILFMEHVEE-INOKISTYARNKALTDLK 125  
 QY 130 GLGDALAVYHDSLSWGVNRRNTRARSVVRQYIALELMFVQKLPSPFVSGVEVPLLIY 189  
 DB 126 GLGRYRSYQOALSTWLDNRDARSILERYVALELDITTAIPLFIRNEEVPLLMVY 185  
 QY 190 AQAANLHLLLRDASIFGKWLSSSEISTFVNRQVERAGDYSDHCVKWYSTGLNNLRGT 249  
 DB 186 AQAANLHLLLRDASIFGKWLSSSEISTFVNRQVERAGDYSDHCVKWYSTGLNNLRGT 245  
 QY 250 NAESWVRYNQRRDMLVLDLVALFPSYDTQMPYIKTTAQITREYVYDAITGVHPHPSF 309  
 DB 246 NAESWVRYNQRRDMLVLDLVALFPSYDTQMPYIKTTAQITREYVYDAITGVHPHPSF 305  
 QY 310 TSTWYNNNAPSFAIEAAVVRNPHLLDFLQVITYLSLLRSWNTQYNNMGGHKLERT 369  
 DB 306 ASTWYNNNAPSFAIEAAVVRNPHLLDFLQVITYLSLLRSWNTQYNNMGGHKLERT 365  
 QY 370 IGGTLNISTQGST-NTSINPVTLPSTRDVRATESLAGNLFLTPQVNGVPRVDFHWFV 428  
 DB 366 IGGTLNISTQGST-NTSINPVTLPSTRDVRATESLAGNLFLTPQVNGVPRVDFHWFV 422  
 QY 429 THPIASDNFYYPG-----YAGIGTQLQDSENELPPEATGQPNYESYSHRSLHIGLISA 481  
 DB 423 ---INPQNIYERGATTYSQYQGVIGLQFDESETLPPTTERPNYESYSHRSLHIGLIG 479  
 QY 482 SHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVRGPGFTGCDILRRNT 541  
 DB 480 NTLRAPVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVRGPGFTGCDILRRNT 539

QY 542 GTFGDIRVNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFATNRGDLDT 601  
 DB 540 GTFGDIRVNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFATNRGDLDT 599  
 QY 602 FRTVGFTTTPFSDVQSTFTTICANFSGNEVYIDRIEFVFPVETVYAEAEFKAQEKVT 661  
 DB 600 FRTAGFTFPFNLNAQSTFTLGAQFSN-QEVYIDRVFVPAEVTFAEYDLERAKAVN 658  
 QY 662 ALFTSTNPRGLKTDVYHIDQVNSLVESLDEFLDEKRELFKVKYAKLSDERNL 719  
 DB 659 ALFTSTNPRGLKTDVYHIDQVNSLVESLDEFLDEKRELFKVKYAKLSDERNL 716

RESULT 11  
 ; Sequence 4, Application US/08881340  
 ; Patent No. 5942658  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yiping  
 ; APPLICANT: Jany, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESSEE: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/881,340  
 ; FILING DATE: 24-JUN-1997  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/100,709  
 ; FILING DATE: 29-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egolf, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1229 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLESCULE TYPE: protein  
 ; US-08-881-340-4

Query Match 64.3%; Score 2417.5; DB 2; Length 1229;  
 Best Local Similarity 65.3%; Pred. No. 1.7e-210;  
 Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;  
 QY 13 SNAKVDKLSTSLKN-ETDIEIQ-NINHEDCIKSEVENVFPFVSASTIQTGIGIAGKI 70  
 DB 7 NENEINAIISIPTVSNPSTQMLNSDPARIEDSLCAEVNNDIPFVSASTVQGINIAGRI 66  
 QY 71 LGTLGVFPAGQVASYLSFTLIGELWPKQKQWELFMFHEVEE-INQKISTYARNKALTDIK 129  
 DB 67 LGVLGVFPAGQVASYLSFTLIGELWPKQKQWELFMFHEVEE-INQKISTYARNKALTDIK 125  
 QY 130 GLGDALAVYHDSLESVWGNRNTTRARSVRSQVIALELMFVOKLPSFAVSGEEVPLPIY 189

DB 126 GLGRGYRSVQQALETWLDNRNDARSIIILERYVALELDITTAIPLFIRNEEVPILMVY 185  
 QY 190 AQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRERAGDYSDCHCKVYSTGLNNLRGT 249  
 DB 186 AQANLHLLLRDASIFGSEWGMASDVNQYQEQIRYTEEYSNHCQVQWINTGLNNLRGT 245  
 QY 250 NAESWRYNQFRDRLTMDLVLPSPVDTOMYPIKTTAQLTREVYTTDAIGTVHHPSPF 309  
 DB 246 NAESWRYNQFRDRLTMDLVLPSPVDTOMYPIKTTAQLTREVYTTDAIGTVHHPSPF 305  
 QY 310 TSTTWNANAPSAAEAAVVRNPHLLDLEQVTTIYSLSRWSNTOMVMNMGHKLFR 369  
 DB 306 ASTWNNFNNAPSAAEAAVVRNPHLLDLEQVTTIYSLSRWSNTOMVMNMGHKLFR 365  
 QY 370 IGGTLNISTQGST-NTSINPVTLPFTSRDVRTTESLAGNLFLTQPVNGVPRVDFHWKFV 428  
 DB 366 IGGTLNISTQGST-NTSINPVTLPFTSRDVRTTESLAGNLFLTQPVNGVPRVDFHWKFV 422  
 QY 429 THPIASDNFYYPG-----YAGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLISA 481  
 DB 423 ---INPQNIYERGATTYSQPYQVGIQLEFSETLPETTERPNEYSYSHRLSHIGLII 479  
 QY 482 SHVKALVYSWTHRSADRTNTEIPNSITQIPLKAFNLSSGAAVVRGPGFTGGDILARTNT 541  
 DB 480 NTLRAPVYSWTHRSADRTNTEIPNSITQIPLKAFNLSSGAAVVRGPGFTGGDILARTNT 539  
 QY 542 GTFGDIRVNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFATNRGDLDT 601  
 DB 540 GTFGDIRVNPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFATNRGDLDT 599  
 QY 602 FRTVGFTTTPFSDVQSTFTTICANFSGNEVYIDRIEFVFPVETVYAEAEFKAQEKVT 661  
 DB 600 FRTAGFTFPFNLNAQSTFTLGAQFSN-QEVYIDRVFVPAEVTFAEYDLERAKAVN 658  
 QY 662 ALFTSTNPRGLKTDVYHIDQVNSLVESLDEFLDEKRELFKVKYAKLSDERNL 719  
 DB 659 ALFTSTNPRGLKTDVYHIDQVNSLVESLDEFLDEKRELFKVKYAKLSDERNL 716

RESULT 12  
 ; Sequence 10, Application US/08448170  
 ; Patent No. 5723758  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Payne, Jewel  
 ; APPLICANT: Cummings, David A.  
 ; APPLICANT: Cannon, Raymond J.C.  
 ; APPLICANT: Narva, Kenneth E.  
 ; APPLICANT: Steiman, Steve  
 ; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted  
 ; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes  
 ; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: David R. Saliwanchik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/448,170  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/069,902  
 ; FILING DATE: 01-JUNE-1993  
 ; CLASSIFICATION: 424





QY 360 WGGHKLFRITGGTNTSTOGSTNTSINPVTLPFTSRDVTYRTSLAGLNFLFTQPVNGVP 419  
Db 351 WGGHKLFRITGGTNTSTOGSTNTSINPVTLPFTSRDVTYRTSLAGLNFLFTQPVNGVP 410  
QY 420 RVDPHKFWTHPIASDNFYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLI 479  
Db 411 RVDPHKFWTHPIASDNFYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLI 470  
QY 480 SASHVKALVYSWTHRSAD 497  
Db 471 SASHVKALVYSWTHRSAD 488

RESULT 14  
US-07-951-715A-7  
; Sequence 7, Application US/07951715A  
; Patent No. 5625136  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/951,715A  
; FILING DATE: 25-SEP-1992  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sprulli, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8615  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1207 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-951-715A-7

Query Match 59.5%; Score 2236.5; DB 1; Length 1207;

Best Local Similarity 64.1%; Pred. No. 5e-194;  
Matches 441; Conservative 76; Mismatches 156; Indels 15; Gaps 7;  
QY 40 EDCCKMSEYENVPFVSASTIQIGIAGKILGTGVPFAGQVASYSLFGLBWPXGKN 99  
Db 10 EDCCLCAEAGNIDPFVSASTVQIGINAGRIAGILGVLGVPFAGQVASYSLFGLBWPXGRD 69  
QY 100 QWEILFWEHVEE-INOKISTYARNKALTDLKGIGDALAVYHDSLESVGNVNNTRASVV 158  
Db 70 QWEI-FILEHVEQLINQOITENARNTALARLQGLGDSFRAYQQSLEDWLENRDDARTSVL 128  
QY 159 RSOYIALELMFVOKLPSFAVSGEVPPLPIYAQAANLHLLILDASIFGKWSLSSEIS 218  
Db 129 YTOYIALELDFLNPFLFAIRNQEVPLLMVYAQAANLHLLILDASIFGSEFGLTSQEIQ 188  
QY 219 TFYNROVERAGDYSDHCWKYSTGLNLRGTNAESVRYNQFRDRTMLVLDLVALPSPY 278  
Db 189 RYTERQVTRDYSYDCEWYNTGLSLRGTNAASVRYNQFRDRLTLGLVLDLVALPSPY 248  
QY 279 DTQMPYIKTTAQLTREYVYTDAGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDF 338  
Db 249 DTRTPINTSAQLTREYVYTDAGT--GVNWSMNWYNNNAPSFAIEAAAIRSPHLLDF 306  
QY 339 LEQVTIYSLSRWSNTQYMMWGHKLEFRTIGGTINISTOGSTNTSINPVTLPFTSRDV 398  
Db 307 LEQLTIFSSASSWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTSRDV 366  
QY 399 YRTESLAGLNLF--LTOPVNGVPRVDPHMFVTHP-----IASDNFYPGYAGIGTQLOD 451  
Db 367 YRTESYAGVLLWGIYLEPIHGVTVRNF---INPQISDRGTANYSQP-YESPLQLKD 422  
QY 452 SENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADTNTIEPNSITQIP 511  
Db 423 SETELPPTETTERPNYESYSHRLSHIGLILQSRVNVVYVSWTHRSADRTNTIGPNRIQIP 482  
QY 512 LVKAPNLSSGAAYVVRGPGFTGGILRETNTGTGDIRVNNPAPQAVRVIRVASTDL 571  
Db 483 MVKASELPQGTTVVRGPGFTGGILRETNTGTGDIRVNNPAPQAVRVIRVASTVDF 542  
QY 572 QFHTSINGKAINQGNFSATMNRGEDLDYKTRFTVGTTPFTSFLDVQSTFTTIGAWNFSGN 631  
Db 543 DFFVSRGCTTVNNFRFLRTWNSGDELKYGNFVRAFTPTFTTQIDIRTSIQGLSGNG 602  
QY 632 EVIDIRIEFVPEVTEYAEVDFEKAQKVTALFTSTNPRGLKTDVKYHIDQVSNLVESL 691  
Db 603 EVIDIKIEIIPVTATFEAYDLERAQAVNALFTNTNPRKLKTDVTDYHIDQVSNLVACL 662  
692 SDEFYLDKRELPEIVKYNELHIERNM 719  
663 SDEFCLDEKRELEKVKYAKRLSDERNL 690

RESULT 15  
US-08-459-448A-7  
; Sequence 7, Application US/08459448A  
; Patent No. 5859336  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2005, 20:32:21 ; Search time 16.5835 Seconds  
(without alignments)  
4171.616 Million cell updates/sec

Title: US-10-019-823B-59  
Perfect score: 3742  
Sequence: 1 MKLKNPDKHQSLSNAKVDK.....KRELFEIVKAKOIHIRM 719  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3742	100.0	719	2 I40590	cryV465 protein -
2	3520	94.1	719	2 I39815	insecticidal prote
3	3511	93.8	719	2 S25383	parasporal crystal
4	3503	93.6	719	2 I39814	insecticidal prote
5	2321.5	62.0	1228	2 S00873	parasporal crystal
6	1813	48.5	380	2 B42459	hypothetical prote
7	1507	40.3	1157	1 S49247	parasporal crystal
8	1503.5	40.2	1166	2 S32645	parasporal crystal
9	1491.5	39.9	1174	2 S32649	parasporal crystal
10	1487.5	39.8	1155	2 A26513	parasporal crystal
11	1480.5	39.6	1155	2 JD0002	parasporal crystal
12	1480.5	39.6	1156	2 A29125	parasporal crystal
13	1463.5	39.1	1155	2 S02134	parasporal crystal
14	1463.5	39.1	1181	2 A41052	parasporal crystal
15	1461.5	39.1	1155	2 I39838	parasporal crystal
16	1459	39.0	934	2 A22798	parasporal crystal
17	1457	38.9	1176	2 JT0241	parasporal crystal
18	1451	38.8	1176	2 JC2219	parasporal crystal
19	1447	38.7	1176	2 A22617	parasporal crystal
20	1447	38.7	1176	2 S02215	parasporal crystal
21	1367	36.5	1174	2 A42459	parasporal crystal
22	1348	36.0	1156	2 A29838	parasporal crystal
23	1343	35.9	1138	2 A48944	parasporal crystal
24	1340.5	35.8	823	2 S04181	parasporal crystal
25	1331.5	35.6	1189	2 S00944	parasporal crystal
26	1326	35.4	1154	2 S39536	parasporal crystal
27	1292	34.5	1171	2 I40572	parasporal crystal
28	1292	34.5	1171	2 A37829	parasporal crystal
29	1286	34.4	1176	2 A48970	parasporal crystal

30	1232	32.9	1160	2 S32647	parasporal crystal
31	1230.5	32.9	1165	2 S11446	parasporal crystal
32	1220.5	32.6	655	2 JC7140	protoxin - Bacillu
33	1196.5	32.0	1172	2 S32689	parasporal crystal
34	1179	31.5	1160	2 I40589	parasporal crystal
35	1178	31.5	652	2 A27323	parasporal crystal
36	1165	31.1	1178	1 US85XH	parasporal crystal
37	1164.5	31.1	1177	2 A49785	parasporal crystal
38	1159	31.0	659	2 S10228	parasporal crystal
39	1124.5	30.1	652	2 I39811	parasporal crystal
40	995	26.6	649	1 JH0261	parasporal crystal
41	938.5	25.1	618	2 S11445	parasporal crystal
42	896	23.9	1156	2 S19306	parasporal crystal
43	845	22.6	1136	1 US8581	parasporal crystal
44	662.5	17.7	934	2 B29838	parasporal crystal
45	637	17.0	1180	2 I39870	parasporal crystal

ALIGNMENTS

RESULT 1

I40590  
cryV465 protein - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change\_09-Jul-2004  
C:Accession: I40590  
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis  
tomocidus.  
A:Reference number: I39814; MUID:95314293; PMID:7793960  
A:Accession: I40590  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:G467234; PIDN:AAA82114.1; PID:G467234  
C:Genetics:  
C:Gene: cryV465  
C:Superfamily: parasporal crystal protein

Query Match	100.0%	Score	3742	DB	2	Length	719
Best Local Similarity	100.0%	Pred. No.	3.1e-258				
Matches	719	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	1	1	1	1	1	1
Db	1	1	1	1	1	1	1
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Qy	301	1	1	1	1	1	1
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Qy	361	1	1	1	1	1	1
Db	361	1	1	1	1	1	1

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Db 421 VDFHWKPTPLIASDNFYLYGAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480  
Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
Qy 541 TGTFGDIRVNNPFPFAQRVVRIRYASTTDLQPHSTINGKAINQGNFSATMNRGEDLDYK 600  
Db 541 TGTFGDIRVNNPFPFAQRVVRIRYASTTDLQPHSTINGKAINQGNFSATMNRGEDLDYK 600  
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Db 601 TFRIGTFTTFFSFDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVVTYEAAYDPEKAQEKV 660  
Qy 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFVYKAKQIHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFVYKAKQIHIERNM 719

RESULT 2  
I39815  
insecticidal protein cryv - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I39815  
R:Gleave, A.P.; Williams, R.; Hedges, R.J.  
Appl. Environ. Microbiol. 59, 1683-1687, 1993  
A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for  
iensis subsp. kurataki.  
A:Reference number: I39815; MUID:93298009; PMID:8517758  
A:Accession: I39815  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:Cross-references: UNIPROT:Q45752; GB:M98544; NID:g142767; PIDN:AAA22354.1; PID:g142768  
C:Genetics:  
A:Gene: cryv  
C:Superfamily: parasporal crystal protein

Query Match 94.1%; Score 3520; DB 2; Length 719;  
Best Local Similarity 92.9%; Pred. No. 2e-242;  
Matches 668; Conservative ~31; Mismatches 20; Indels 0; Gaps 0;  
Qy 1 MRLKNPDKHQSLSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSHESIDPFVSASTI 60  
Db 1 MRLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVSASTI 60  
Qy 61 QTGIGIAGKILGTGVFPAGQIASLYSFILGELWPKGKSOWEIMFHVVEEIIINOKILTYA 120  
Db 61 QTGIGIAGKILGTGVFPAGQVASLYSFILGELWPKGKNQWEIMFHVVEEIIINOKISTYA 120  
Qy 121 RNKALSDLRGDGLAVYHDSLESWENNRNTRARSVVVKQYIALELMFVKLSPFAVSG 180  
Db 121 RNKALTDLKLGLDALAVYHDSLESWGNRNTRARSVVVKQYIALELMFVKLSPFAVSG 180  
Qy 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSASEISTFYNNROVERTDYSDHCIKWYN 240  
Db 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSCHVKWYS 240  
Qy 241 TGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSYDTLVPYPIKTTSQLTREYITDAI 300  
Db 241 TGLNNLRGTNAESWRYNQFRDMTLMVLDLVALFPSYDTQWYPIKTTAQLTREYITDAI 300  
Qy 301 GTVHPNQAFSTTWNNNAPSAIEAAVIRSPHLLDFLEKVTIYSLLSRNSNTQYNNMW 360  
Db 301 GTVHPHPSFTSTTWNNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRNSNTQYNNMW 360  
Qy 361 GGHRLSPRIGGALNTSQGSTNTSINPVTLOFTSRDVRYESLAGLNLFILTPQVNGVPR 420  
Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLFILTPQVNGVPR 420

Qy 421 VDFHWKPTPLIASDNFYLYGAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480  
Db 421 VDFHWKPTPLIASDNFYLYGAGVGTQLODSENELPPEATGPNYESYSHRLSHIGLIS 480  
Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
Qy 541 TGTFGDIRVNNPFPFAQRVVRIRYASTTDLQPHSTINGKAINQGNFSATMNRGEDLDYK 600  
Db 541 TGTFGDIRVNNPFPFAQRVVRIRYASTTDLQPHSTINGKAINQGNFSATMNRGEDLDYK 600  
Qy 601 TFRIGTFTTFFSFDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVVTYEAAYDPEKAQEKV 660  
Db 601 TFRIGTFTTFFSFDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVVTYEAAYDPEKAQEKV 660  
Qy 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFVYKAKQIHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFVYKAKQIHIERNM 719

RESULT 3  
S25383  
parasporal crystal protein cryIIaI - Bacillus thuringiensis  
N:Alternate names: delta-endotoxin; parasporal crystal protein cryv  
C:Species: Bacillus thuringiensis  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C:Accession: S25383  
R:Tailor, R.; Tippet, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.  
Mol. Microbiol. 6, 1211-1217, 1992  
A:Title: Identification and characterization of a novel Bacillus thuringiensis delta-end  
toxin subunit.  
A:Reference number: S25383; MUID:92269502; PMID:1588820  
A:Accession: S25383  
A:Molecule type: DNA  
A:Residues: 1-719 <TAI>  
A:Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:g40289; PIDN:CAA44633.1; PID:g40290  
C:Genetics:  
A:Gene: cryv  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 93.8%; Score 3511; DB 2; Length 719;  
Best Local Similarity 92.8%; Pred. No. 8.6e-242;  
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;  
Qy 1 MRLKNPDKHQSLSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSHESIDPFVSASTI 60  
Db 1 MRLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPVSASTI 60  
Qy 61 QTGIGIAGKILGTGVFPAGQIASLYSFILGELWPKGKSOWEIMFHVVEEIIINOKILTYA 120  
Db 61 QTGIGIAGKILGTGVFPAGQVASLYSFILGELWPKGKNQWEIMFHVVEEIIINOKISTYA 120  
Qy 121 RNKALSDLRGDGLAVYHDSLESWENNRNTRARSVVVKQYIALELMFVKLSPFAVSG 180  
Db 121 RNKALTDLKLGLDALAVYHDSLESWGNRNTRARSVVVKQYIALELMFVKLSPFAVSG 180  
Qy 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSASEISTFYNNROVERTDYSDHCIKWYN 240  
Db 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWS 240  
Qy 241 TGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSYDTLVPYPIKTTSQLTREYITDAI 300  
Db 241 TGLNNLRGTNAESWRYNQFRDMTLMVLDLVALFPSYDTQWYPIKTTAQLTREYITDAI 300  
Qy 301 GTVHPNQAFSTTWNNNAPSAIEAAVIRSPHLLDFLEKVTIYSLLSRNSNTQYNNMW 360  
Db 301 GTVHPHPSFTSTTWNNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRNSNTQYNNMW 360  
Qy 361 GGHRLSPRIGGALNTSQGSTNTSINPVTLOFTSRDVRYESLAGLNLFILTPQVNGVPR 420  
Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLFILTPQVNGVPR 420

421 VDFHWKFPPTLPASDNFYVLGVAGVGTQLODSENELPPTTGPQPNVESHRLSHIGLIS 480  
421 VDFHWKFPVTHPTIASNDFYYPGVAGICTQLODSENELPPEATGPQPNVESHRLSHIGLIS 480  
481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGCDILRRTN 540  
481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGCDILRRTN 540  
541 TGTFGDIRVINPPPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600  
541 TGTFGDIRVINPPPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600  
601 TPTTGTTPPFSFSDVQSTFTIGAMNFFSGNEVYIDRIEFVPEVYIYEAEDFEKAQEKV 660  
601 TPTTGTTPPFSFSDVQSTFTIGAMNFFSGNEVYIDRIEFVPEVYIYEAEDFEKAQEKV 660  
661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLDSDEFYLDKRELFEIVKYAKQIHIERNM 719  
661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLDSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 4  
I39814  
insecticidal protein cryVI - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text change 26-Aug-1999  
C:Accession: I39814  
R.Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis  
comocidus.  
A:Reference number: I39814; MUID:95314293; PMID:7793960  
A:Accession: I39814  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:Cross-references: GB:I36338; NID:G540281; PIDN:AAC36999.1; PID:G540282  
C:Genetics:  
A:Gene: cryVI  
C:Superfamily: parasporal crystal protein

Query Match 93.6%; Score 3503; DB 2; Length 719;  
Best Local Similarity 92.5%; Pred. No. 3.2e-241;  
Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;

QY 1 MKLNPKDKHQSLSSNAKVDKIATDSLKNETDIELKMNNEGYLRMSEHESIDPFVSASTI 60  
DB 1 MKLNPKDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEFFVSASTI 60

QY 61 QTGIGIAGKILGTLGVPPAGQIASLYSFTLGEMLWPKGQWEIFMEHVEEIIINQKILTYA 120  
DB 61 QTGIGIAGKILGTLGVPPAGQIASLYSFTLGEMLWPKGQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALSDRLGLDALAVYHESLESWENNRNTRARSVVKQYIALELMFQKLPSPAVSG 180  
DB 121 RNKALTDRLGLDALAVYHESLESWGNRNTRARSVVKSVQYIALELMFQKLPSPAVSG 180

QY 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVETRDYSDHCKIKNYN 240  
DB 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVETRDYSDHCKIKNYN 240

QY 241 TGLNNLRGTNAKSWRYNQFRKDMTLMVLVDLVALFPSSYDTLVYPIKTTSQLTREVVYDAI 300  
DB 241 TGLNNLRGTNAKSWRYNQFRKDMTLMVLVDLVALFPSSYDTLVYPIKTTSQLTREVVYDAI 300

QY 301 GTVHPNQAFSTWYNNAPSPSAIAAAVIRSPHLLDFLEKVTIYSLLSRWNSQTMMNW 360  
DB 301 GTVHPNPFSTWYNNAPSPSAIAAAVIRSPHLLDFLEKVTIYSLLSRWNSQTMMNW 360

QY 361 GGHRLSRPTGGALNTSTOGSTNTSINPVLTQFTSRDVYRTESLAGLNFLTPQVNGVPR 420  
DB 361 GGHKLEFRITGGTINLTSTOGSTNTSINPVLTQFTSRDVYRTESLAGLNFLTPQVNGVPR 420

421 VDFHWKFPPTLPASDNFYVLGVAGVGTQLODSENELPPTTGPQPNVESHRLSHIGLIS 480  
421 VDFHWKFPVTHPTIASNDFYYPGVAGICTQLODSENELPPEATGPQPNVESHRLSHIGLIS 480  
481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGCDILRRTN 540  
481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGCDILRRTN 540  
541 TGTFGDIRVINPPPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600  
541 TGTFGDIRVINPPPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600  
601 TPTTGTTPPFSFSDVQSTFTIGAMNFFSGNEVYIDRIEFVPEVYIYEAEDFEKAQEKV 660  
601 TPTTGTTPPFSFSDVQSTFTIGAMNFFSGNEVYIDRIEFVPEVYIYEAEDFEKAQEKV 660  
661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLDSDEFYLDKRELFEIVKYAKQIHIERNM 719  
661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLDSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 5  
S00873  
parasporal crystal protein cryBal - Bacillus thuringiensis subsp. thuringiensis  
N:Alternate names: parasporal crystal protein cryA4  
C:Species: Bacillus thuringiensis subsp. thuringiensis  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C:Accession: S00873  
R.Brizzard, B.L.; Whiteley, H.R.  
Nucleic Acids Res. 16, 2723-2724, 1988  
A:Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus  
A:Reference number: S00873; MUID:88203216; PMID:3362680  
A:Accession: S00873  
A:Molecule type: DNA  
A:Residues: 1-1228 <BRI>  
A:Cross-references: UNIPROT:P05517; EMBL:X06711; NID:G40264; PIDN:CAA29898.1; PID:G58094;  
C:Genetics:  
A:Gene: cryA4  
A:Start codon: TTG  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 62.0%; Score 2321.5; DB 2; Length 1228;  
Best Local Similarity 63.6%; Pred. No. 1e-156;  
Matches 453; Conservative 80; Mismatches 162; Indels 17; Gaps 4;

QY 23 TDSLKNETDI-----ELKMNNEGYLRMSEHESIDPFVSASTIQTGIGIAGKI 70  
DB 2 TSNRKNEEIIINAVSNHSAQMOLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61

QY 71 LGTLGVPPAGQIASLYSFTLGEMLWPKGQWEIFMEHVEEIIINQKILTYARNKALSDLRG 130  
DB 62 LGVLGVPPAGQIASLYSFTLGEMLWPKGQWEIFLEHVEQLINQKITENARNALTALQOG 121

QY 131 LGDALAVYHESLESWENNRNTRARSVVKQYIALELMFQKLPSPAVSGEVPPLPIYA 190  
DB 122 LGDSFRAYQQSLEDLENDRDARTSVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYA 181

QY 191 QAANLHLLLRDASIFGKEWGLSASEISTFYNRQVETRDYSDHCKIKNYNLTGLNNLRGTN 250  
DB 182 QAANLHLLLRDASIFGSEFGLTSQEIQRVQVETRDYSDYCVWNTGLNSLRGTN 241

QY 251 AKSWRYNQFRKDMTLMVLVDLVALFPSSYDTLVYPIKTTSQLTREVVYDAIGTVPNQAFSA 310  
DB 242 AASWRYNQFRDLTLGVLDLVALFPSSYDTLVYPIKTTSQLTREVVYDAIGATGVN--MA 299

QY 311 STWYNNAPSPSAIAAAVIRSPHLLDFLEKVTIYSLLSRWNSQTMMNWGHRLESRPI 370  
DB 300 SMWYNNAPSPSAIAAAVIRSPHLLDFLEKVTIYSLLSRWNSRTRMTYWRGHTIQSRPI 359

QY 371 GGALNTSTOGSTNTSINPVLTQFTSRDVYRTESLAGLNLF--LTQPVNGVPRVDFHWKFP 428  
DB 360 GGGLNTSTHGATNTSINPVLTQFTSRDVYRTESYAGVLLWGLYLEPIHGVTVPVRFNTNP 419





Db 714 KMLEAVRAAKRLSRERL 732

RESULT 8

S32645  
parasporal crystal protein crylGal - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S32645  
R:Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A:Reference number: S32645  
A:Accession: S32645  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1166 <LAM>  
A:Cross-references: UNIPROT:Q45746; EMBL:Z22510; NID:g295861; PIDN:CAA80233.1; PID:g295861  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 40.2%; Score 1503.5; DB 2; Length 1166;  
Best Local Similarity 46.6%; Pred. No. 1.6e-98;  
Matches 330; Conservative 97; Mismatches 210; Indels 71; Gaps 15;  
QY 28 NETDIELKNNNEDYLRMSSEHSIDPFVSASTQTGIGIAGKILGTGLVPPFAGQIASLYS 87  
Db 16 NPPESEIFNARNSEN-----FGLVSQVSSGL---TRFLLEAAVPEAGFALGLFD 60  
QY 88 FILGELWPKGKOWEIEFMEHVEEIIKILTYARNKALSDLRGLGALAVYHESLESWE 147  
Db 61 IHWGAL---GVQWLSFLRQIEQLRQETELERNRATALTGLSSYNLYVEALREWEN 117  
QY 148 NRNTRARSVVKNQYIALELMFVQKLPFAVSGEEVPLPIYQAQANLHLLLRDASIFG 207  
Db 118 DPNNPASQEVRRFRRLTDVAITGLPTLAIRNLEVNVLSVYQAANLHLLRDVAVFG 177  
QY 208 KEWGLGASEISTFYNROVERTRDYSDHCIKWYNTGLNLRGTNAKSWRYNQPRKDMTLM 267  
Db 178 ERWGLTQANTIEDLYRLTSLIQSYSDHCARWYNQGLNEIGGISR---RYLDPQRDLTIS 233  
QY 268 VLDLVALFPSYDVLVPIKTTLSQLTREVVYDAI--GVVHPNQAFASTTWNNNAPSFAI 325  
Db 234 VLDLVALFPYDITRTPIQSQLTREIYTPVVGNI-----NFGLS 276  
QY 326 EAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMMWGHRLSRPI---GGALNTSTQGS 381  
Db 277 IANVLAPHLMDRIDRIVITNSVR--STPY---WAGHEVISRRTGGQGNFRFPYGV 331  
QY 382 TNTSINPVTIQ---FT--SRDVTRESLAGNLFLTPQVNGVPRVDFHMKFPPLPIASDN 436  
Db 332 AANAEPVTTIRPGFTDEQRQWRARSRRVVSFRSSGQDFSLVDVAVGFLATIFSASVYRNG 391  
QY 437 FYVLGVAGVCTIQDSNELPPTTGPQNPYESYSHRLSHGLISAS-----HVKALVYSW 491  
Db 392 F-----GFNT---DTIDEIPIE--GVDPTGYSHRLCHVGFLASSPFIQYARAPIFSW 440  
QY 492 THRSADRTNTEPNSITQIPLVKAFNLSGAAVVVRGPGFTGGDILRRTNTGTGDIRVNI 551  
Db 441 THRSATLTNTIADPVITQIPLVKAFNLSGATIVKGGFTGGDILRRTNVGSGDNRVNI 500  
QY 552 NPPFAQRYRIRIYASTDLOFHTSINGKAINGNFSATNNRGEDLDYKTFRTIGTTPP 611  
Db 501 TAPLSQRYRIRIYASTDLOFHTSINGKAINGNFSATNNRGEDLDYKTFRTIGTTPP 560  
QY 612 SFSDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVTVYEAEDYFEKAQEKYALTSTNPRG 671  
Db 561 TFSANSTFTIGAFGSPNNEVYIDRIEFVPAEYVTEAEYDLEKAQKAVNALFTSSNQIG 620  
QY 672 LKTDVQDYHIDQVSNLVESLSDFYLDKRELPFVYKAKQIHIERNM 719  
Db 621 LKTDVTDYHIDQVSNLVESLSDFYLDKRELPFVYKAKQIHIERNM 668

RESULT 9

S32649  
parasporal crystal protein crylFa3 - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S32649  
R:Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A:Reference number: S32645  
A:Accession: S32649  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1174 <LAM>  
A:Cross-references: UNIPROT:Q45749; EMBL:Z22512; NID:g295865; PIDN:CAA80235.1; PID:g295865  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 39.9%; Score 1491.5; DB 2; Length 1174;  
Best Local Similarity 47.4%; Pred. No. 1.2e-97;  
Matches 323; Conservative 88; Mismatches 179; Indels 91; Gaps 14;  
QY 76 VFPAGQIASLYGFIILGELWPKGKOWEIEFMEHVEEIIKILTYARNKALSDLRGLGDAL 135  
Db 49 VPGVGAFGLFDLIWGFTIP---SEWSLFLQIEQLRQETELERNRATITLRLGLADSY 105  
QY 136 AVYHESLESWENNRNTRARSVVKNQYIALELMFVQKLPFAVSGEEVPLPIYQAQANL 195  
Db 106 EYVLEALREWEENPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANL 165  
QY 196 HLLLRDASIFKEWGLGASEISTFYNROVERTRDYSDHCIKWYNTGLNLRGTNAKSWV 255  
Db 166 HLLSLRDVAVSFGQWGLDIAITNNHYNRLNLIHRYTEHCLDTYNQGLNLRGTNRQMS 225  
QY 256 RYNQPRKDMTLMVLDLVALFPSYDVLVPIKTTLSQLTREVVYDAI--GVVHPNQAFSTTWY 315  
Db 226 RFNQFRRLTTLVLDLVALFPYDARAYFIQSSQLTREIYTSVSVIEDSPVSA----- 278  
QY 316 NNNAPS--PSAEEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMMWGHRLSRPIGGAL 374  
Db 279 --NIPNGFNRAEFGV--RPPHLMDFNN-----SLFVTAETVRSQTVWGHVSSR----- 324  
QY 375 NTSTQGSTWTSINPVTIQF-----TSRDVYRTRESLAGNLFLTPQVNGVP 419  
Db 325 -----NTAGNPINFPIYIGIFNPGGAIWIADEDPRPFYRT-----LSDPV--FV 365  
QY 420 RYDHEHMKFPTLPASDNFYVLGVAGVGTQLQ-----DSENELPPTTGPQN 465  
Db 366 RGGF-----GNPHVVLGLRGVAFQGTGNTNHTRTFRNSGTIDSLDEIPQDMSGAP 415  
QY 466 YESYSHRLSHI-----GLISASHV--KALVYSWTHRSADRTNTEPNSITQIPLVKAFNL 518  
Db 416 WNDYSHVLNHNVTFRWPGEAGSDSWRAPMFSWTHRSADRTNTEPNSITQIPLVKAFNL 475  
QY 519 SGAAVVVRGPGFTGGDILRRTNTGTGDIRVNI--PPFAQRYRIRIYASTDLOFHTSIN 578  
Db 476 HSGTIVVRGPGFTGGDILRRTNTGTGDIRVNI--PPFAQRYRIRIYASTDLOFHTSIN 535  
QY 579 GKAINGNFSATNNRGEDLDYKTFRTIGTTPFSFSDVQSTFTIGAWNFSNGNEVYIDRI 638  
Db 536 GTSVNGNQRNTRNNGNLSGNFRTAGTSTTFPSFNAOSTTFLGTAQFSN--QEVYIDRI 594  
QY 639 EFVPEVTVYEAEDYFEKAQEKYALTSTNPRGLKTDVQDYHIDQVSNLVESLSDFYLD 698  
Db 595 EFVPAEYVTEAEYDLEKAQKAVNALFTSTSQLGKTNVTGYHIDQVSNLVESLSDFYLD 654  
QY 699 EKRELPFVYKAKQIHIERNM 719  
Db 655 EKRELPFVYKAKQIHIERNM 675

RESULT 10

A26513  
parasporal crystal protein - Bacillus thuringiensis (strain aizawai)

C:Species: Bacillus thuringiensis  
C:Date: 11-Mar-1988 #sequence\_revision 11-Mar-1988 #text\_change 09-Jul-2004  
C:Accession: A26513  
R:Oeda, K.; Ohnishi, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, H.; Ohkawa, H.  
Gene 53, 113-119, 1987  
A:Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis  
A:Reference number: A26513; MUID:87248103; PMID:3297927  
A:Accession: A26513  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1155 <ORF>  
A:Cross-references: UNIPROT:P06578; GB:M16463; NID:g143098; PIDN:AAA22551.1; PID:g143098  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 39.8%; Score 1487.5; DB 2; Length 1155;  
Best Local Similarity 46.5%; Pred. No. 2.2e-97;  
Matches 309; Conservative 106; Mismatches 196; Indels 55; Gaps 11;

QY 76 VPGAQIASLYSFILGELWPKGQWEIFMEHVEEINQKILTYARNKALSDRLGLGDAL 135  
DB 51 VPGAQIASLYSFILGELWPKGQWEIFMEHVEEINQKILTYARNKALSDRLGLGDAL 135  
QY 136 AVYHESLESWVENNTRARSVKQYIALELMFVKQLPSFVSGEEVPLPIYAQAANL 195  
DB 108 QIYAESFREWEADPTNPALREEMRIQFNDMNSALTTPALFAVQNYQVPLLSVTVQAANL 167  
QY 196 HLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHICIKWYNTGLNLRGNKASWV 255  
DB 168 HLLVRDVSFVGQRGDPAATINSRYNDLTRIGNYTHAVRWYNTGLERWVGPSRDWI 227  
QY 256 RYNQFRKMDTLMLVDLVALFSPSYDTLVPKITSQITREVTDAIGTVHPNQAFASITWY 315  
DB 228 RYNQFRKMDTLMLVDLVALFSPSYDTLVPKITSQITREVTDAIGTVHPNQAFASITWY 315  
QY 316 NNAPSFSAIEAAV---TRSPHLLDFLEKVTYISLLSRWSNTQYNNMGHRLSRPIG- 371  
DB 274 ENPDGFRALAOGIEGSRPHMLDLINSITTYTDAHR--GEY--YWSGHQIMASPVGF 328  
QY 372 -----GAL-NTSTQGSTNTINPVTLQFTQRTDVRTESLAGLNLFTQPVNGVPR 420  
DB 329 SGPEFTFPLYGTMGNAAPQORIVAQLOGGVYRTLSLTLYRRFPNIGIN---NQQLSVLDG 385  
QY 421 VDFHWKFTPLTASDNFYLYGAGVGTQLODSENLPPETTGQPNVESYSHRLSHIGLI- 479  
DB 386 TEPAYG-----TSSNLPDANTKSGT--VDSLDHIPPQNNVPPRQGFSHRLSHVSMFR 437  
QY 480 -----SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGGAADVVRGPGFTGG 533  
DB 438 SGFSNSSVSITRAPMFSWIHRSAEFNNIIPSSQITQIPLTSTNLGSGTSVVKGPFTGG 497  
QY 534 DILRRNTGTFDIRNINPPFAQRYRVRIRYASTTDLPHTSINGKALINQGNFSAATWNR 593  
DB 498 DILRRTPSGQISTRLVNTAPUSQRYRVRIRYASTTNLFQHTSIDGRPINQGNFSAATWSS 557  
QY 594 GEDLDYKTRFTTGTFPFSFDSVQSTFTICAMNFSSGNEVYIDRIEFVPEVTEAEYDF 653  
DB 558 GSNLQSGSFRTVGTFTFPFNSGSSVFTLSAHVFNSGNEVYIDRIEFVPEVTEAEYDF 617  
QY 654 EKAQEKVTLFTSTNPRGLTVDKVDHIDQVSNLVSLSDEFDLDEKRLFEIVKYAKOI 713  
DB 618 ERAQKAVNELTSSNQIGLKTDTVDYHIDQVSNLVSLSDEFDLDEKRLFEIVKYAKOI 677  
QY 714 HIERNM 719  
DB 678 SDERNL 683

Query Match 39.8%; Score 1487.5; DB 2; Length 1155;  
Best Local Similarity 46.5%; Pred. No. 2.2e-97;  
Matches 309; Conservative 106; Mismatches 196; Indels 55; Gaps 11;

QY 76 VPGAQIASLYSFILGELWPKGQWEIFMEHVEEINQKILTYARNKALSDRLGLGDAL 135  
DB 51 VPGAQIASLYSFILGELWPKGQWEIFMEHVEEINQKILTYARNKALSDRLGLGDAL 135  
QY 136 AVYHESLESWVENNTRARSVKQYIALELMFVKQLPSFVSGEEVPLPIYAQAANL 195  
DB 108 QIYAESFREWEADPTNPALREEMRIQFNDMNSALTTPALFAVQNYQVPLLSVTVQAANL 167  
QY 196 HLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHICIKWYNTGLNLRGNKASWV 255  
DB 168 HLLVRDVSFVGQRGDPAATINSRYNDLTRIGNYTHAVRWYNTGLERWVGPSRDWI 227  
QY 256 RYNQFRKMDTLMLVDLVALFSPSYDTLVPKITSQITREVTDAIGTVHPNQAFASITWY 315  
DB 228 RYNQFRKMDTLMLVDLVALFSPSYDTLVPKITSQITREVTDAIGTVHPNQAFASITWY 315  
QY 316 NNAPSFSAIEAAV---TRSPHLLDFLEKVTYISLLSRWSNTQYNNMGHRLSRPIG- 371  
DB 274 ENPDGFRALAOGIEGSRPHMLDLINSITTYTDAHR--GEY--YWSGHQIMASPVGF 328  
QY 372 -----GAL-NTSTQGSTNTINPVTLQFTQRTDVRTESLAGLNLFTQPVNGVPR 420  
DB 329 SGPEFTFPLYGTMGNAAPQORIVAQLOGGVYRTLSLTLYRRFPNIGIN---NQQLSVLDG 385  
QY 421 VDFHWKFTPLTASDNFYLYGAGVGTQLODSENLPPETTGQPNVESYSHRLSHIGLI- 479  
DB 386 TEPAYG-----TSSNLPDANTKSGT--VDSLDHIPPQNNVPPRQGFSHRLSHVSMFR 437  
QY 480 -----SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGGAADVVRGPGFTGG 533  
DB 438 SGFSNSSVSITRAPMFSWIHRSAEFNNIIPSSQITQIPLTSTNLGSGTSVVKGPFTGG 497  
QY 534 DILRRNTGTFDIRNINPPFAQRYRVRIRYASTTDLPHTSINGKALINQGNFSAATWNR 593  
DB 498 DILRRTPSGQISTRLVNTAPUSQRYRVRIRYASTTNLFQHTSIDGRPINQGNFSAATWSS 557  
QY 594 GEDLDYKTRFTTGTFPFSFDSVQSTFTICAMNFSSGNEVYIDRIEFVPEVTEAEYDF 653  
DB 558 GSNLQSGSFRTVGTFTFPFNSGSSVFTLSAHVFNSGNEVYIDRIEFVPEVTEAEYDF 617  
QY 654 EKAQEKVTLFTSTNPRGLTVDKVDHIDQVSNLVSLSDEFDLDEKRLFEIVKYAKOI 713  
DB 618 ERAQKAVNELTSSNQIGLKTDTVDYHIDQVSNLVSLSDEFDLDEKRLFEIVKYAKOI 677  
QY 714 HIERNM 719  
DB 678 SDERNL 683

RESULT 11  
JD0002  
Parasporal crystal protein cryIIab3 - Bacillus thuringiensis  
N:Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal pr  
C:Species: Bacillus thuringiensis

[illegible]

RESULT 13  
S02134

parasporal crystal protein cryIC1 - Bacillus thuringiensis (strain aizawai IC1)  
N;Alternate names: Delta-endotoxin IC1; entomocidal crystal protein  
C;Species: Bacillus thuringiensis  
A;Variety: strain aizawai IC1  
C;date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: S02134; S04994  
R;Haider, M.Z.; Ellar, D.J.  
Nucleic Acids Res. 16, 19027, 1988  
A;Title: Nucleotide sequence of a Bacillus thuringiensis aizawai IC1 entomocidal crystal  
A;Reference number: S02134; MUID:89083518; PMID:3205732  
A;Accession: S02134  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-1155 <HAI>  
A;Cross-references: UNIPROT:P06578; EMBL:X13233; NID:g40277; PIDN:CAA31620.1; PID:g40278  
A;Experimental source: strain aizawai IC1  
R;Haider, M.Z.; Ellar, D.J.  
J. Mol. Biol. 208, 183-194, 1989  
A;Title: Functional mapping of an entomocidal delta-endotoxin. Single amino acid changes  
A;Reference number: S04994; MUID:89362455; PMID:2769751

J. Molec. Biol. 208, 133-134, 1985  
 A>Title: Functional mapping of an entomocidal delta-endotoxin. Single amino acid changes  
 A:Reference number: S04994; MUID:89362455; PMID:2769751  
 A:Accession: S04994  
 A:Molecule type: DNA  
 A:Residues: 429-449, 'A', 451-724 <HAW>  
 A:Cross-references: EMBL:X16315  
 A:Experimental source: strain aizawai IC1  
 C:Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.  
 C:Superfamily: parasporal crystal protein  
 C:Keywords: delta-endotoxin  
  
 Query Match 39.1%; Score 1463.5; DB 2; Length 1155;  
 Best Local Similarity 46.0%; Pred. No. 11e-95;  
 Matches 307; Conservative 105; Mismatches 198; Indels 57; Gaps 12;  
  
 Qy 76 VPFGAQIASLYSFYLGELWLPKQSGWEIIFMEHVEIINQILTYARNKALSDIRLGLDAL 135  
 Db 51 VPFGAGFVLGLVDITWGIF---GPSQWDAPFLVQIEQLINQRIEERFARNQATSRLEGLSNLY 107

QY	136	AVYHESLESWENRNNTRASVVKQVIALELMFVOKLPSPFAVSGEVPLLPYQAANL	195
Db	108	QIYAESFREWEADPTNPALREEMRIQFNDMNSALTATPLFAVQVYVPLLSVYQAANL	167
QY	196	HLLLRDASIFGKEMGLSASEISFTFYNRQVTRDYSDHCIKWYNTGLNLRGTNAKSW	255
Db	168	HLSVLRDVSGFQWKGWLDVATINSRYNDLRLGLTYDYAVRWYNTGLERWGPDSRDW	227
QY	256	RYNFRKDMTLMVLDLVALPESYDTLVYPIKTTSQLTREVYTDAGTVHPNQAFSTTWY	315
Db	228	RYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNFV	273
QY	316	NNAPSP-----SATEAAVIRSPHLLDFLEKVTIYSLLRWSNTQYMMWGGHLSRPIG	371
Db	274	ENFDGFRGSAQGIEGS--IRSPHLMILNSITITDAHR---GEY--YWSGHQIMASPVG	327
QY	372	-----GAL-NTSTQGSTNTSINPVTLOQTSRDVYRTESLAGLNLFLTQPVNGVP	419
Db	338	FSGPEFTPLYGTMGNAAPQQRIVAQLOGVYRTLSLTYRRPNIGIN---NQQLSVLD	384
QY	420	RVDFHWKFTPLPIASDNFYLYGAGVGTQLODSENELPETTGQPNYESYSHRLSHIGLI	479
Db	385	GTEPAYG-----TSSNLPASAVYRKSGT--VDSLDEIPPNQNNVPPRQGFSHRLSHVSMF	436
QY	480	-----SASHVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTG	532
Db	437	RSFGNSSVSIIRPPMFWIHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTG	496
QY	533	GDILRTNTGTGDIRVNNPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMN	592
Db	497	GDILRTSPQISTLRVNITAPLSQRYRIRYASTTNLQHTSIDGRINQGNFSATMS	556
QY	593	RGEDLDYKTRTGTFTTSPFSQVOSTTIGAMWPNSSGNEVYIDRIEVPVVEYAEYD	652
Db	557	SGSNLQSGSFRTVGTFTTFFNSGSSVFTLSAHVFNSSGNEVYIDRIEVPVVEYAEYD	616
QY	653	FKAQSKVTALTFTSNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQ	712
Db	617	LERAQKAVNELFTSSNQIGLTKDVTVDYHIDQVSNLVESLSDEFYLDKRELSEKVKHAKR	676
QY	713	IHIERNM 719	
Db	677	LSDERNL 683	
RESULT 14			
A41052			
parasporal crystal protein cryAel - Bacillus thuringiensis (strain alesti)			
C:Species: Bacillus thuringiensis			
C>Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004			
C:Accession: A41052			
R:Lee, C.S.; Aronson, A.I.			
J. Bacteriol. 173, 6635-6638, 1991			
A:Title: Cloning and analysis of delta-endotoxin genes from Bacillus thuringiensis subsp			
A:Reference number: A41052; PMID:92011442; PMID:1655719			
A:Accession: A41052			
A:Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-1181 <RES>			
A:Cross-references: UNIPROT:Q03748; GB:M65252; NID:g142874; PIDN:AAA22410.1; PID:g142875			
C:Superfamily: parasporal crystal protein			
C:Keywords: delta-endotoxin			
Query Match 39.1%; Score 1463.5; DB 2; Length 1181;			
Best Local Similarity 45.9%; Pred. No. 1.2e-95;			
Matches 306; Conservative 104; Mismatches 201; Indels 55; Gaps 11;			
QY	76	VPPAQGTASLYSFTLGEINWPKGSQWEIFMEHVEEIIINOKILTYARNKALSDLRGLGDAL	135
Db	51	VPGAGFVLGLTDLWGFV---GPSQWDAFLVQIEQLISQRIEFARQAISRLGSLNLY	107
QY	136	AVYHESLESWENRNNTRASVVKQVIALELMFVOKLPSPFAVSGEVPLLPYQAANL	195

Db	108	QIYAESFREWEADPTNPALREEMRIQFNDMNSALTATPLFTVQVYVPLLSVYQAANL	167
QY	196	HLLLRDASIFGKEMGLSASEISFTFYNRQVTRDYSDHCIKWYNTGLNLRGTNAKSW	255
Db	168	HLSVLRDVSGFQWKGWLDVATINSRYNDLRLGLTYDYAVRWYNTGLERWGPDSRDW	227
QY	256	RYNFRKDMTLMVLDLVALPESYDTLVYPIKTTSQLTREVYTDAGTVHPNQAFSTTWY	315
Db	228	RYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNFV	273
QY	316	NNAPSP-----IRSPHLLDFLEKVTIYSLLRWSNTQYMMWGGHLSRPIG	371
Db	274	ENFDGFRGSAQRIEQSIRSPLMDILNSITIT--DAHGGYY--WSGHQIMASPVGF	328
QY	372	-----GAL-NTSTQGSTNTSINPVTLOQTSRDVYRTESLAGLNLFLTQPVNGVPR	420
Db	329	SGPEFTPLYGTMGNAAPQQRIVAQLOGVYRTLSSTFYRNPFFIGIN---NQRLSVLDG	385
QY	421	VDPHWKFTPLPIASDNFYLYGAGVGTQLODSENELPETTGQPNYESYSHRLSHIGLI	479
Db	386	TEPAYG-----SSNLPASAVYRKSGT--VDSLOBIPODNNVPPRQGFSHRLSHVSWPR	437
QY	480	-----SASHVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTG	533
Db	438	SGFSNSSVSIIRAPMFWIHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTG	497
QY	534	DILRTNTGTGDIRVNNPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMN	593
Db	498	DILRTSPQISTLRVNITAPLSQRYRIRYASTTNLQHTSIDGRINQGNFSATWSS	557
QY	594	GEDLDYKTRTGTFTTSPFSQVOSTTIGAMWPNSSGNEVYIDRIEFPVVEYAEYDF	653
Db	558	GGNLQSGSFRTVGTFTTFFNSGSSVFTLSAHVFNSSGNEVYIDRIEFPVVEYAEYDL	617
QY	654	EKAQSKVTALTFTSNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQI	713
Db	618	ERAQKAVNALFTSPNQIGLTKDVTVDYHIDQVSNLVESLSDEFYLDKRELSEKVKHAKEL	677
QY	714	IHIERNM 719	
Db	678	SDERNL 683	
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I39838			
parasporal crystal protein - Bacillus thuringiensis			
C:Species: Bacillus thuringiensis			
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004			
C:Accession: I39838			
R:Hefford, M.A.; Brousseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J.A.; Lau, P.C.K.			
J. Biotechnol. 6, 307-322, 1987			
A:Title: Sequence of a lepidopteran toxin gene of Bacillus thuringiensis subsp kurstaki			
A:Reference number: I39838			
A:Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: DNA			
A:Residues: 1-1155 <RES>			
A:Cross-references: UNIPROT:P06578; GB:M37263; NID:g142885; PIDN:AAA22420.1; PID:g142886			
C:Superfamily: parasporal crystal protein			
C:Keywords: delta-endotoxin			
Query Match 39.1%; Score 1461.5; DB 2; Length 1155;			
Best Local Similarity 46.2%; Pred. No. 1.5e-95;			
Matches 308; Conservative 103; Mismatches 199; Indels 57; Gaps 12;			
QY	76	VPPAQGTASLYSFTLGEINWPKGSQWEIFMEHVEEIIINOKILTYARNKALSDLRGLGDAL	135
Db	51	VPGAGFVLGLTDLWIGTF---GPSQWDAFLVQIEQLINQRIEFARQAISRLGSLNLY	107
QY	136	AVYHESLESWENRNNTRASVVKQVIALELMFVOKLPSPFAVSGEVPLLPYQAANL	195
Db	108	QIYAESFREWEADPTNPALREEMRIQFNDMNSALTATPLFAVQVYVPLLSVYQAANL	167



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:22:09 ; Search time 60.0945 Seconds  
(without alignments)  
3909.384 Million cell updates/sec

Title: US-10-019-823B-59  
Perfect score: 3742  
Sequence: 1 MKLKNPDKHQSSNAKVDK.....KRELFEIVKYAKOIHIRMN 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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2: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pap.\*  
3: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pap.\*  
4: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pap.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3520	94.1	719	16	US-10-782-020-10
2	3520	94.1	719	16	US-10-782-141-8
3	3368.5	90.0	710	15	US-10-428-961-42
4	2324.5	62.1	1228	16	US-10-809-953-10
5	2314.5	61.9	1207	10	US-09-988-462-7
6	2234	59.7	1227	15	US-10-428-961-63
7	2219	59.3	1186	9	US-09-826-660-23
8	2170.5	58.0	1228	15	US-10-428-961-38
9	2170.5	58.0	1228	15	US-10-614-524-2
10	1982	53.0	643	9	US-09-826-660-25
11	1734.5	46.4	1167	14	US-10-089-678-1
12	1683.5	45.0	653	15	US-10-428-961-6
13	1657.5	44.3	1157	16	US-10-782-141-16

14	1514	40.5	1206	13	US-10-032-717-2	Sequence 2, Appli
15	1514	40.5	1206	14	US-10-414-637-2	Sequence 2, Appli
16	1514	40.5	1206	15	US-10-606-320-2	Sequence 2, Appli
17	1500.5	40.1	1156	14	US-10-099-285-72	Sequence 72, Appl
18	1500.5	40.1	1156	15	US-10-428-961-28	Sequence 28, Appl
19	1494	39.9	1210	13	US-10-032-717-4	Sequence 4, Appli
20	1494	39.9	1210	14	US-10-414-637-4	Sequence 4, Appli
21	1494	39.9	1210	15	US-10-606-320-4	Sequence 4, Appli
22	1480.5	39.6	1155	9	US-09-756-643-2	Sequence 2, Appli
23	1480.5	39.6	1155	10	US-09-988-462-9	Sequence 9, Appli
24	1480.5	39.6	1155	15	US-10-136-998A-2	Sequence 2, Appli
25	1480.5	39.6	1181	10	US-09-988-462-11	Sequence 11, Appl
26	1480.5	39.6	1181	10	US-09-988-462-13	Sequence 13, Appl
27	1480.5	39.6	1181	10	US-09-988-462-15	Sequence 15, Appl
28	1480.5	39.6	1181	10	US-09-988-462-17	Sequence 17, Appl
29	1480.5	39.6	1181	10	US-09-988-462-28	Sequence 28, Appl
30	1480.5	39.6	1181	15	US-10-136-998A-4	Sequence 4, Appli
31	1480.5	39.6	1181	15	US-10-136-998A-8	Sequence 8, Appli
32	1480.5	39.6	1181	15	US-10-136-998A-10	Sequence 10, Appl
33	1480.5	39.6	1181	15	US-10-136-998A-12	Sequence 12, Appl
34	1472.5	39.4	1177	14	US-10-035-060-6	Sequence 6, Appli
35	1472.5	39.4	1177	14	US-10-102-469-24	Sequence 24, Appl
36	1470.5	39.3	1177	14	US-10-035-060-2	Sequence 2, Appli
37	1470.5	39.3	1177	14	US-10-035-060-8	Sequence 8, Appli
38	1447	38.7	1176	16	US-10-782-141-6	Sequence 6, Appli
39	1436.5	38.4	1176	11	US-09-837-961-2	Sequence 2, Appli
40	1436.5	38.4	1176	16	US-10-825-751-2	Sequence 2, Appli
41	1391	37.2	1167	15	US-10-428-961-40	Sequence 40, Appl
42	1386.5	37.1	1177	9	US-09-873-873-26	Sequence 26, Appl
43	1386.5	37.1	1177	10	US-09-916-956A-26	Sequence 26, Appl
44	1386.5	37.1	1177	10	US-09-997-914-26	Sequence 26, Appl
45	1386.5	37.1	1177	14	US-10-365-645-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1

US-10-782-020-10  
; Sequence 10, Application US/10782020  
; Publication No. US20040197916A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMT-004, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274139  
; CURRENT APPLICATION NUMBER: US/10/782,020  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,810  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-020-10

Query Match 94.1%; Score 3520; DB 16; Length 719;  
Best Local Similarity 92.9%; Pred. No. 5.4e-287;  
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKLKNPDKHQSSNAKVDKIATDLSKNETDIELKNMNEYLRMSEHSIDPFVSASTI 60

Db 1 MKLKNPDKHQSSNAKVDKIATDLSKNETDIELKNMNEYLRMSEHSIDPFVSASTI 60

QY 61 QTGIGTAGIKLTGLGVPPFAGQATASLYSFILGELWPKQKQWEIFMEHVEIINOKILTYA 120

Db 61 QTGIGTAGIKLTGLGVPPFAGQATASLYSFILGELWPKQKQWEIFMEHVEIINOKILTYA 120





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; NAME/KEY: misc_feature
; LOCATION: (200)..(200)
; OTHER INFORMATION: The 'xaa' at location 200 stands for any naturally occurring amino acid
US-10-428-961-42

Query Match
Best Local Similarity 90.0%; Score 3368.5; DB 15; Length 710;
Matches 641; Conservative 32; Mismatches 37; Indels 9; Gaps 1;

QY 1 MKLNKPKQKQSSNAKVDKIADTSLKNETDIELKNNEDYLRMSHESIDPFVSASTI 60
DB 1 MKSKNQWQSLNNATVDKNTFGLSNNNTNTELQNFN-----HGIEFVSSTI 51

QY 61 QTGIGIAGKILGTLPVFPAGQIASLYSFILGELWPKGQWEIFMEHVEEIIINOKILTLYA 120
DB 52 QTGIGIAGKILGNLGVFPAGQVASLYSFILGELWPKGQWEIFMEHVEELINQKISTYA 111

QY 121 RNKALSDRLGLDALAVYHESLESVENNNTARSVVKQYIALBMLFVQKLPSPAVSG 180
DB 112 RNKALADLKLGLDALAVYHESLESVENNNTARSVVKQYIALBMLFVQKLPSPAVSG 171

QY 181 EEPVLPPIVAQAANLHLLLRDASIFGKXWGLSDSEISIFYNQKSGKSEYSDHCWKYN 240
DB 172 EEPVLPPIVAQAANLHLLLRDASIFGKXWGLSDSEISIFYNQKSGKSEYSDHCWKYN 231

QY 241 TGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREYVTDAL 300
DB 232 TGLNRLMGNNAESWRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREYVTDAL 291

QY 301 GTVHPNQAFASFTWYNNAPSPFAIAEAAVRSRPHLLDFLEKVTIYSLLSRWSTQYNNMW 360
DB 292 GTVHPHPSEFTSTWYNNAPSPFSTIEAAVVRNPHLLDFLEKVTIYSLLSRWSTQYNNMW 351

QY 361 GGHRLSRPITGGALNTSTQSTNTSINPVTLOFTSRDVRTESLAGNLFLTPQVNGVPR 420
DB 352 GGHKLFRTIGGLNTSTQSTNTSINPVTLOFTSRDVRTESLAGNLFLTPQVNGVPR 411

QY 421 VDFHMKFPTLPASDNFYLGYAGVGTQLODSNELPPTGQPNYESYSHRLSHIGLIS 480
DB 412 VDFHMKFVTHPIASDNFYLGYAGVGTQLODSNELPPTGQPNYESYSHRLSHIGLIS 471

QY 481 ASHVKALVSWTHRSADRTNTIENPVTLOFTSRDVRTESLAGNLFLTPQVNGVPR 540
DB 472 ASHVKALVSWTHRSADRTNTIENPVTLOFTSRDVRTESLAGNLFLTPQVNGVPR 531

QY 541 TGFPGDIRVNNPFAQRVRYRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600
DB 532 TGFPGDIRVNNPFAQRVRYRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 591

QY 601 TFRITGFTTFFSFDVQSTFTIGAMNFSNGNEVYIDRIEFPVPVEVTEAYEYDPEKAQEV 660
DB 592 TFRITGFTTFFSFDVQSTFTIGAMNFSNGNEVYIDRIEFPVPVEVTEAYEYDPEKAQEV 651

QY 661 TALFTSTNPRGLKTDVQKHYDIDQVSNLVESLSDEFYLDKRELFELFVVKYAKQIHIERM 719
DB 652 TALFTSTNPRGLKTDVQKHYDIDQVSNLVESLSDEFYLDKRELFELFVVKYAKQIHIERM 710

RESULT 4
US-10-809-953-10
; Sequence 10, Application US/10809953
; Publication No. US2004018125A1
; GENERAL INFORMATION:
; APPLICANT: Van Mellaert, Herman
; APPLICANT: Botterman, Johan
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Joos, Henk
; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTICIDAL PROTEINS
; FILE REFERENCE: 021565-078
; CURRENT APPLICATION NUMBER: US/10/809,953
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/09/661,016
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; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: PCT/EP90/00905
; PRIOR FILING DATE: 1990-05-30
; PRIOR APPLICATION NUMBER: GB 89401499.2
; PRIOR FILING DATE: 1989-05-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-809-953-10

Query Match
Best Local Similarity 62.1%; Score 2324.5; DB 16; Length 1228;
Matches 454; Conservative 85; Mismatches 166; Indels 9; Gaps 5;

QY 12 LSSNAKVDKIADTSLKNN---ETDIELKNNEDYLRMSHESIDPFVSASTIQTGTGIAG 68
DB 1 LTSNRKNEEIIINASNHSQAQMDL-LPDARIEDSLCIAEGNNIDPFVSASTVQTGTGINIAG 59

QY 69 KILGTLGVFPAGQIASLYSFILGELWPKGQWEIFMEHVEEIIINOKILTLYAARNKALS 128
DB 60 RILGVLGVFPAGQIASLYSFILGELWPKGQWEIFMEHVEEIIINOKILTLYAARNKALS 119

QY 129 RGLGDALAVYHESLESVENNNTARSVVKQYIALBMLFVQKLPSPAVSGEVPPLPI 188
DB 120 QGLGDSFRAYQQSLDLEWLNRRDDARTSRVLTQYIALELDLFLNAPLFAIRNQEVPPLMV 179

QY 189 YAAQANLHLLLRDASIFGKXWGLSDSEISIFYNQKSGKSEYSDHCWKYNGLNLRG 248
DB 180 YAAQANLHLLLRDASIFGKXWGLSDSEISIFYNQKSGKSEYSDHCWKYNGLNLRG 239

QY 249 TNAKSWRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREYVTDALGTVHPNQ 308
DB 240 TNAKSWRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREYVTDALGTVHPNQ 297

QY 309 FASTTWNYNNAFSAIAEAAVRSRPHLLDFLEKVTIYSLLSRWSTQYNNMWGGHRLSR 368
DB 298 MASMNNYNNAFSAIAEAAVRSRPHLLDFLEKVTIYSLLSRWSTQYNNMWGGHRLSR 357

QY 369 PIGGALNTSTQSTNTSINPVTLOFTSRDVRTESLAGNLFLTPQVNGVPRVDFHWK 426
DB 358 PIGGGLNTSTHGATNTSINPVTLOFTSRDVRTESLAGNLFLTPQVNGVPRVDFHWK 417

QY 427 FP-TLPIASDNFYLGYAGVGTQLODSNELPPTGQPNYESYSHRLSHIGLISASHVK 485
DB 418 NFQNISDRGTANYSQYSPFGLQKDSDELPPETTERPNYESYSHRLSHIGLISASHVK 477

QY 486 ALVYSWTHRSADRTNTIENPVTLOFTSRDVRTESLAGNLFLTPQVNGVPRVDFHWK 545
DB 478 VPVYSWTHRSADRTNTIENPVTLOFTSRDVRTESLAGNLFLTPQVNGVPRVDFHWK 537

QY 546 DIRVNNPFAQRVRYRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYKFTFI 605
DB 538 PIRVTNNGLTQRYRIGFYASTVDFDFVFRSGGTTVNNFRFLRTNWSGDELKYNFVR 597

QY 606 GFTTPEFSDVQSTFTIGAMNFSNGNEVYIDRIEFPVPVEVTEAYEYDPEKAQEV 665
DB 598 AFTTPTFTTQIQTIRTSIQGLSGNGEVYIDRIEFPVPVEVTEAYEYDPEKAQEV 657

QY 666 STNPRGLKTDVQKHYDIDQVSNLVESLSDEFYLDKRELFELFVVKYAKQIHIERM 719
DB 658 NTNPRGLKTDVQKHYDIDQVSNLVESLSDEFYLDKRELFELFVVKYAKQIHIERM 711

RESULT 5
US-09-988-462-7
; Sequence 7, Application US/09988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Desai, Nalini M.
```

Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Lauais, Karen L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Syngenta Biotechnology, Inc.  
STREET: 3054 Cornwalis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/988,462  
FILING DATE: 20-NOV-98  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/547,422  
FILING DATE: 11-APR-2000  
APPLICATION NUMBER: US 08/459,504  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-188051  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7  
Query Match 61.9%; Score 2314.5; DB 10; Length 1207;  
Best Local Similarity 65.4%; Pred. No. 3.6e-185;  
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;  
QY 40 EDYLRMSEHIDPFVSASTIOTGIAGKILGTGVPFAGQIASYFILGELWPKGKS 99  
DB 10 EDLSCTAEGNNIDPFVSASTVQTGINIAGRIILGVLPFAGQLASFSYFLVGLWPRGRD 69  
QY 100 QWEIFMEHVEEIIINQKILTVARNKALSDRLGLGDALAVTHESLWENRNNTRARSVVK 159  
DB 70 QWEIFLEHVEEIIINQKILTVARNKALSDRLGLGDALAVTHESLWENRNNTRARSVVK 129  
QY 160 NOYIALELMEVQKLPSPFVSGEVEPLPIYQAQANLHLLLRDASIFGKEWGLSASEIST 219  
DB 130 TQYIALELDPINAWPLFAINQNEVPLVMYQAQANLHLLLRDASIFGSEFGLTSQEIQR 189  
QY 220 FYNRQVETRDYSDHCIKWTNTGLNRLGTNAKSWRYNQFRKMTLMVLIDLVALPPSYD 279  
DB 190 YNRQVETRDYSDYCVEMWTNTGLNRLGTNAKSWRYNQFRKMTLMVLIDLVALPPSYD 249  
QY 280 TLVYPIKTSQTLREVYTDIGIVHPNQAFASITWYNNNAPSFAEAAVIRSPHLLDFL 339

DB 250 FTETYPINTSAQLTREVYTDIGATGVN--MASMWNYNNAAPSFSAIEAAAIRSPHLLDFL 307  
QY 340 EKVTIYSLLSRWNTQYNNMGGHLESRPPIGGALNTSTQGTNTSINPVTLOFTSRDYY 399  
DB 308 EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLRFASRDYY 367  
QY 400 RTESLAGLNLFF--LTQPVNGVPRVDFHWKFP--TLPIASDNFYILGYAGVGTQLOQDSENEL 456  
DB 368 RTESVAGVLLMGIYLEPHGVPTVRFNFTNQNSIDRGCTANYSQPYESFGLQKDSSETEL 427  
QY 457 PPETTGQPNYESYSHRLSHIGLISASHKALVYVSWTHRSADRTNTIEPNSITQIPLVXAF 516  
DB 428 PPETTERPNYESYSHRLSHIGLISASHKALVYVSWTHRSADRTNTIEPNSITQIPLVXAF 487  
QY 517 NLSSGAAVVRGPGFTGGDILRETNTGTGDIRVNNPPPAQRYRVRIRYASTDLDQFHHS 576  
DB 488 ELPGQTTVVVRGPGFTGGDILRETNTGTGDIRVNNPPPAQRYRVRIRYASTDLDQFHHS 547  
QY 577 INGKAINQGNFSATMNRGDDLDYKTFRTIGTTPFSFSDVQSTFTTIGAMNFSGNEVYID 636  
DB 548 RGTTVNNFRFLRTMNSGDELAYGNFVREAFPTTFTQIIDIIRTSIQGLSGNGEVYID 607  
QY 637 RIEFVPEVYTYAEYDFEKAQKVLTFTSTNPRGLKTDVQKDYHIDQVSNLVESLSDEFY 696  
DB 608 KIEIIPVTATFEAEYDLERAQAVNALFTNTPRRLKTDVTDYHIDQVSNLVACLSDEFY 667  
QY 697 LDEKRELFEIVKYAKOIHIERNM 719  
DB 668 LDEKRELLEKVKYAKLSDERNL 690

RESULT 6

US-10-428-961-63  
Sequence 63 Application US/10428961  
Publication NO. US20030237111A1  
GENERAL INFORMATION:  
APPLICANT: Baum, James A.  
APPLICANT: Chu, Chih-Rei  
APPLICANT: Donovan, William P.  
APPLICANT: Gilmer, Amy J.  
APPLICANT: Rupar, Mark J.  
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)  
FILE REFERENCE: MECO201--1  
CURRENT APPLICATION NUMBER: US/10/428,961  
CURRENT FILING DATE: 2003-05-02  
PRIOR APPLICATION NUMBER: 09/661,322  
PRIOR FILING DATE: 2000-09-13  
PRIOR APPLICATION NUMBER: 60/153,995  
PRIOR FILING DATE: 1999-09-15  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: Patent In version 3.2  
SEQ ID NO 63  
LENGTH: 1227  
TYPE: PRF  
ORGANISM: Bacillus thuringiensis  
US-10-428-961-63

Query Match 59.7%; Score 2234; DB 15; Length 1227;  
Best Local Similarity 60.8%; Pred. No. 2.2e-178;  
Matches 434; Conservative 100; Mismatches 162; Indels 18; Gaps 3;  
QY 23 TDSLKNETDI----ELKNMNN-----EDYLRMSEHIDPFVSASTIQTIGIG 65  
DB 2 TSNRKNNEIINALSIPAVSNHSAQMLSTDAIEDSLCTAEGNNIDPFVSASTVQTGIN 61  
QY 66 IAGKILGTGVPFAGQIASYFILGELWPKGKSQWEIFMEHVEEIIINQKILTVARNKAL 125  
DB 62 IAGRIILGVLPFAGQIASFSYFLVGLWPRGRDPEIFLEHVEHLLRQQVTNTRDAL 121  
QY 126 SDRLGLGDALAVTHESLWENRNNTRARSVVKNOYIALELMEVQKLPSPFVSGEVEPL 185

Db	122	ARLOGLGNSFRAYQOOSLEDWLENRRDDARTREVLVTQYIALBELDFLNAMPLFAIRNQEVPL	181
Qy	186	LPIYAQAANLHLLLLRDASIPGKEWGLSASISITFYNRQVTRTDYSDHCIKWYNTGLNN	245
Db	182	LWYTAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEKTRREYSDYCARWYNTGLNN	241
Qy	246	LRGTNAKSWRYNQFRKDMTLMWLDLVALPPSYDTLVPIKYTTSQLTREVYTDAGTVHP	305
Db	242	LRGTNAESWLRYNQFRDLTLGLVLDLVALPPSYDTRVYPMNTSQAQLTREIYTDPIGTNA	301
Qy	306	NQAFASITWYNNNAAPSASAEAAVIRSPHLLDLEKVTIYVLLSRWSNTQYNNWGGHRL	365
Db	302	PSGFASTNWENNNAAPSASAEAAVIRPHLLDFFPEQLTIFSVLSRWSTQYNNWVGHRL	361
Qy	366	ESRPIGALNATSTOGSTNTSINPVTLOFTSRDVTYRTESLAGINLFLTOPVNGVPRVDPHW	425
Db	362	ESRTIRGSLSTWTHGNTNTSINPVTLOFTSRDVTYRTESFAGINILLITPVNGVPPWAREFW	421
Qy	426	KPPTLPASDNFYVLGVAGVGTQLOSENELPPETGQPNYESYSHRLSHGLISASHVK	485
Db	422	RNPLNSLRGSLLYTIGYTGVTQQLFDSETELPETTERPNYESYSHRLSNLRLLISGNTLR	481
Qy	486	ALVYSWTHRSADRNTTIEPHSITOIPLVKAENLSSGAAVRGPGFTGGDIILRRNTGTFG	545
Db	482	APVTSWTHRSADRNTTSSOSITQIPLVKSFLNSGTSVWSGPGFTGGDIILRTNVNGSVL	541
Qy	546	DIRVINPPFAQRVVRIRVASTTDLQPHTSINGKAINQGNFSAATMRGEDLDYKTFRTI	605
Db	542	SMGLNFNTSILQRVVRVRYAASQTMVLRVTVGGSTTFDQGFPTMSANESLTSQSFRFA	601
Qy	606	GFTPTPFSFVQSTFTTGANNFSSGNEVYIDRIEFVPVEVTEYAEYDPEKAQEKVTLFT	665
Db	602	EPFVGISASGSQ-TAGISISNNAGRQTFHPDKIEFIPITATFEAEYDLDERAQEAVALFT	660
Qy	666	STWPRGLKTDVKDHYHDQVSNLVESLDSDEFVLDEKRELFELVYKAKQIHISNM	719
Db	661	NTNPRRLKTVGTDYHIDEVSNLACLSDSEFCLEKRELLKVKYAKRLSDERNL	714
RESULT 7			
US-09-826-660-23			
; Sequence 23, Application US/09826660			
; Patent No. US20010026940A1			
; GENERAL INFORMATION:			
; APPLICANT: Cardineau, Guy A.			
; APPLICANT: Steلمان, Steven J.			
; APPLICANT: Narva, Kenneth E.			
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins			
; FILE REFERENCE: MA-714XC2D1			
; CURRENT APPLICATION NUMBER: US/09/826,660			
; CURRENT FILING DATE: 2001-04-05			
; PRIOR APPLICATION NUMBER: 09/178,252			
; PRIOR FILING DATE: 1998-10-23			
; PRIOR APPLICATION NUMBER: 60/065,215			
; PRIOR FILING DATE: 1997-11-12			
; PRIOR APPLICATION NUMBER: 60/076,445			
; PRIOR FILING DATE: 1998-03-02			
; NUMBER OF SEQ ID NOS: 27			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 23			
; LENGTH: 1186			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene			
US-09-826-660-23			
Query Match 59.3%; Score 2219; DB 9; Length 1186;			
Best Local Similarity 60.5%; Pred. No. 3.8e-177;			
Matches 432; Conservative 103; Mismatches 161; Indels 18; Gaps 3			
Qy	23	TDSLKNETDI----ELKNMNN-----EDYLRMSEHSIDPFVSASTIQTGIG	65

Db 2 TSNRKNENIEINALSIPAVNSHSAQNNLSTDARIEDSLCIAEGNNIDPFGVSASTVQTGIN 61  
 Qy 66 IAGKILGTGLVFPAGQIASLYFIIIGELWPKGSKQWEIFMEHVEBIIINQKILITYARNKAL 125  
 Db 62 IAGRILGLVGFPAQGIASFYSFLVGLWPRGRDPWEIFLEHVEQLIRQVVTENTRDTAL 121  
 Qy 126 SDLRGLGDALAYTHSLSLWENRNNTRARSVVKNQYITALELMMFVOKLPSFPAVSGEEVPL 185  
 Db 122 ARLOQGLGNSFRAYQQSLEDWLENRRDDARTSRVLYTYQYIALELDFLNAWPLFAIRNQEVPL 181  
 Qy 186 LPYIAQAANLHLLLRDASIFCKEKLGSASEISTFVNRQVETTRDYSDHCIKWNVTGLNN 245  
 Db 182 LMVYIAQAANLHLLLRDASLGFSEFGLTSQEQIRYIERQVEKTRISYDCAWYNTGLNN 241  
 Qy 246 LRGTNAKSVRYNRQKQMTLMVLDLVALFPSTYDLTVPIKTTSQLTREVYTDAGTVHP 305  
 Db 242 LRGTNAESWLRYNQFRDLTLGLVDLVALFPSTYDTRVYPMNTSAQLTREIYTDPIGRNA 301  
 Qy 306 NOAFASTTWNNNAPSFAIAEAAVIRSPHLLDFLEKVTIYLLSWSNTOYNNMMGGHRL 365  
 Db 302 PSGFASTWNFNNAAPSFAIAEAAVIRPHLLDFPEQLATFSLVLSWSNTQYNNYVVGHRL 361  
 Qy 366 ESRPIGALNTQGSTNTSINPVTLOFTSRDVTETSLAGLNLFLTOPVNGVPRVDHFW 425  
 Db 362 ESKTRGSLUSTHGTNTSINPVTLOFTSRDVTETSPAGINILLTTPVNGVPMWARFNW 421  
 Qy 426 KPETPLPIASDNFVYLGACVGTQLODSENELPPTTGPNTYESYSHRLSHIGLISASHVK 485  
 Db 422 RNPLNSLRGSLYTYGYTGVGTQLODFDSETELPETTERPNYESYSHRLSNIRLISGNTLR 481  
 Qy 486 ALVYSWTHRSADRTNTEPNSITQPLVKAFNLSSGAAVVRGPGTGGDILRRTWTGTFG 545  
 Db 482 APVYSWTHRSADRTNTESSDITQPLVKSFNLSGTSVVSQPGTGGDILRRTNVGSLV 541  
 Qy 546 DIRVINPFFAORYVRTRYASTTDLQHTSINGKAINQGFSAWNRGDLDYKTFRTI 605  
 Db 542 SMGLNFNNTSLQRYVRVRYAAASQWMLRVLTGVGGSTTTFDQGPSTSANESLTSQSFRA 601  
 Qy 606 GFTTPSPFDVGSTFTIGAWNFSSGNEVVYIDRIEFPVPEVTVEAEYDPEKAQEKVTLFT 665  
 Db 602 EFPVGISASGSQ-TAGISISNNAGQTQTHFDKIEFIPITATLEASDLERAQKAVNALFT 660  
 Qy 666 STNPRLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEBIVKYAKQIHIERNM 719  
 Db 661 SSNQIGLKTDVTDYHIDRVSNLVECLSDDEFCLDEKKELSEKVKHAKRLSDERNL 714  
 RESULT 8  
 US-10-428-961-38  
 ; Sequence 38, Application US/10428961  
 ; Publication No. US20030237111a1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baum, James A.  
 ; APPLICANT: Chu, Chih-Rei  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Gilmer, Amy J.  
 ; APPLICANT: Rupa, Mark J.  
 ; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
 ; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)  
 ; FILE REFERENCE: MECO201--1  
 ; CURRENT APPLICATION NUMBER: US/10/428,961  
 ; CURRENT FILING DATE: 2003-05-02  
 ; PRIOR APPLICATION NUMBER: 09/661,322  
 ; PRIOR FILING DATE: 2000-09-13  
 ; PRIOR APPLICATION NUMBER: 60/153,995  
 ; PRIOR FILING DATE: 1999-09-15  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 38  
 ; LENGTH: 1228  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-428-961-38

Query Match 58.0%; Score 2170.5; DB 15; Length 1228;  
Best Local Similarity 60.5%; Pred. No. 4.9e-173;  
Matches 435; Conservative 98; Mismatches 171; Indels 15; Gaps 8;  
Qy 12 LSSNAK-----VDKIATDSLKN-ETDIELK-NMNNEDYLMSEHESIDPFSASTIQTGI 64  
Db 1 LTSNRKNEINEINALSPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60  
Qy 65 GIACKILGTGVPAGQIASLSPFLGELWPKGKSQWEIFMEHVEEIIINQKILTYARNKA 124  
Db 61 NIAGRIILGVLPAGQIASLSPFLGELWPKGQDQWEIFLEHVEQLINQITENARNTA 120  
Qy 125 LSDRLGLGDALAVHYESLESWVENNRNTRASVVKVQYIALELMFVKQLSPFAVSGEVP 184  
Db 121 LARLQGLGDSFRAYQOQSLDLEWLNRRDARTSRVLYTQYIALELDFLNAMPLFAIRNOEVP 180  
Qy 185 LPIYAQAANLHLLLRDASIFGKEMGLSASEISTFYNRQVTRDYSDHCIKWYNTGLN 244  
Db 181 LLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYRYERQVEQTRDYSDYCVWYNTGLN 240  
Qy 245 NLRGNTAKSWRYNQFRKDMTLMVLDLVALFPSYDTLVPYPIKTSQLTREVTYDAIGTVH 304  
Db 241 SLRGNTAKSWRYNQFRKDMTLMVLDLVALFPSYDTLVPYPIKTSQLTREVTYDAIGTVH 300  
Qy 305 PNOAFSTTWNNNAPSPSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYMMNMGCHR 364  
Db 301 VN--MASMWNWNNAPSPSAIETAVIRSPHLLDFLEKVTIYSLLSRWSTQYMMNMGCHR 358  
Qy 365 LESRPIGGALNTSTQGSTNTSINPVLTQFTSRDVTYTESLAGLNF--LTQPVNGVPRVD 422  
Db 359 IQSRPIGGALNTSTQGSTNTSINPVLTQFTSRDVTYTESLAGLNF--LTQPVNGVPRVD 418  
Qy 423 FHWKFP--TLPIASDNFYVLGAVGTQLODSENELPPTTQPNVYESYSHLSHIGLIS 480  
Db 419 FNRPNQNTFERGTAN--YSQPYESPLQDKSETLPEPPTTERPNYESYSHLSHIGLIS 477  
Qy 481 ASHVKALVSWTHRSADRNTTIEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540  
Db 478 QSRVHVVPVSWTHRSADRNTTIEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 537  
Qy 541 TGTFGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
Db 538 NGSVLSMGLNFNTSLQRYVRVRVYAAASQTMVLRVTVGSTTTFDQGFSTMSANESLTSQ 597  
Qy 601 TFRITGFTTFFSDVQSTFTICAMNFFSGNEVYIDRIEFVVEVYEAEDYDFAKAEKV 660  
Db 598 SFRFAEPFVGISASGSQ--TAGISISNNAAGRTFHFKIEFIPITATFEAYDLERAQAV 656  
Qy 661 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFELIVYKAKQIHIERNM 719  
Db 657 NALFTNTNPRKLTVDYHIDQVSNLVESLSDEFYLDKRELFELIVYKAKQIHIERNM 715

RESULT 9  
US-10-614-524-2  
; Sequence 2, Application US/10614524  
; Publication No. US2004016020A1  
; GENERAL INFORMATION:  
; APPLICANT: Arnaut, Greta  
; APPLICANT: Boets, Anemie  
; APPLICANT: Damme, Nicole  
; APPLICANT: Mathieu, Eva  
; APPLICANT: Vanneste, Stijn  
; APPLICANT: Van Rie, Jeroen  
; TITLE OF INVENTION: Insecticidal proteins from *Bacillus thuringiensis*.  
; FILE REFERENCE: NEWBISUS2  
; CURRENT APPLICATION NUMBER: US/10/614,524  
; CURRENT FILING DATE: 2003-07-08  
; PRIOR APPLICATION NUMBER: US/09/739,243  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/173387  
; PRIOR FILING DATE: 1999-12-28

; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1228  
; TYPE: PRT  
; ORGANISM: *Bacillus thuringiensis*  
US-10-614-524-2  
Query Match 58.0%; Score 2170.5; DB 15; Length 1228;  
Best Local Similarity 60.5%; Pred. No. 4.9e-173;  
Matches 435; Conservative 98; Mismatches 171; Indels 15; Gaps 8;  
Qy 12 LSSNAK-----VDKIATDSLKN-ETDIELK-NMNNEDYLMSEHESIDPFSASTIQTGI 64  
Db 1 LTSNRKNEINEINALSPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60  
Qy 65 GIACKILGTGVPAGQIASLSPFLGELWPKGKSQWEIFMEHVEEIIINQKILTYARNKA 124  
Db 61 NIAGRIILGVLPAGQIASLSPFLGELWPKGQDQWEIFLEHVEQLINQITENARNTA 120  
Qy 125 LSDRLGLGDALAVHYESLESWVENNRNTRASVVKVQYIALELMFVKQLSPFAVSGEVP 184  
Db 121 LARLQGLGDSFRAYQOQSLDLEWLNRRDARTSRVLYTQYIALELDFLNAMPLFAIRNOEVP 180  
Qy 185 LPIYAQAANLHLLLRDASIFGKEMGLSASEISTFYNRQVTRDYSDHCIKWYNTGLN 244  
Db 181 LLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYRYERQVEQTRDYSDYCVWYNTGLN 240  
Qy 245 NLRGNTAKSWRYNQFRKDMTLMVLDLVALFPSYDTLVPYPIKTSQLTREVTYDAIGTVH 304  
Db 241 SLRGNTAKSWRYNQFRKDMTLMVLDLVALFPSYDTLVPYPIKTSQLTREVTYDAIGTVH 300  
Qy 305 PNOAFSTTWNNNAPSPSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYMMNMGCHR 364  
Db 301 VN--MASMWNWNNAPSPSAIETAVIRSPHLLDFLEKVTIYSLLSRWSTQYMMNMGCHR 358  
Qy 365 LESRPIGGALNTSTQGSTNTSINPVLTQFTSRDVTYTESLAGLNF--LTQPVNGVPRVD 422  
Db 359 IQSRPIGGALNTSTQGSTNTSINPVLTQFTSRDVTYTESLAGLNF--LTQPVNGVPRVD 418  
Qy 423 FHWKFP--TLPIASDNFYVLGAVGTQLODSENELPPTTQPNVYESYSHLSHIGLIS 480  
Db 419 FNRPNQNTFERGTAN--YSQPYESPLQDKSETLPEPPTTERPNYESYSHLSHIGLIS 477  
Qy 481 ASHVKALVSWTHRSADRNTTIEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540  
Db 478 QSRVHVVPVSWTHRSADRNTTIEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 537  
Qy 541 TGTFGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
Db 538 NGSVLSMGLNFNTSLQRYVRVRVYAAASQTMVLRVTVGSTTTFDQGFSTMSANESLTSQ 597  
Qy 601 TFRITGFTTFFSDVQSTFTICAMNFFSGNEVYIDRIEFVVEVYEAEDYDFAKAEKV 660  
Db 598 SFRFAEPFVGISASGSQ--TAGISISNNAAGRTFHFKIEFIPITATFEAYDLERAQAV 656  
Qy 661 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFELIVYKAKQIHIERNM 719  
Db 657 NALFTNTNPRKLTVDYHIDQVSNLVESLSDEFYLDKRELFELIVYKAKQIHIERNM 715

RESULT 10  
US-09-826-660-25  
; Sequence 25, Application US/09826660  
; Patent No. US20010026940A1  
; GENERAL INFORMATION:  
; APPLICANT: Cardineau, Guy A.  
; APPLICANT: Stelman, Steven B.  
; APPLICANT: Narva, Kenneth B.  
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins  
; FILE REFERENCE: MA-714XC2D1  
; CURRENT APPLICATION NUMBER: US/09/826,660  
; CURRENT FILING DATE: 2001-04-05

```

; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-25

```

Query Match	53.0%;	Score 1982;	DB 9;	Length 643;
Best Local Similarity	59.6%;	Pred. No.1.3e-157;		
Matches 383;	Conservative	94;	Mismatches 148;	Indels 18; Gaps 3;
QY	23	TDSLKNETDI-----ELKMNK-----	EDVLRMSEHSIDPFVSASTIQTGIG	65
DB	2	TSRKNEVEINALSIFAVSNHSAQMMNLSTDA	IEDSLCTAEGNNIIDPFVSASTVQIGIN	61
QY	66	IAGKILGTGVPPAQGIASLYSIFILGELMPKGSQ	WEIFMEHVEBIIINQKILTYARNKAL	125
DB	62	IAGRILGVLPVPPAQGIASPSYFLVGLWPRGRDP	WEIFLEHVQOLIRQQVTTENTRDTAL	121
QY	126	SDLRGLGDALAVHESIESVVENNNTRASVVKNO	YIALELMFVKQLPSFAVSGEEVPL	185
DB	122	ARLOGLGNSPRAVOOSEDLENDDEDDARTSRV	LTQYIALELDELNAMPFAIRNRQVPL	181
QY	186	LPYIAQAANLHLLLRDASIFGKEWGLSASBIS	TFYNRQVERTDYSDHCIKWNTGLNN	245
DB	182	LMVYQAANLHLLLRDASLFGSSEGLTSQBIQ	RYRYERQVEKTRSYDYCARWYNTGLNN	241
QY	246	LRGTNAKSWRYNQFRKDMILMWLDLVALPSP	SYDTLVYPKITSQLTREYVTDGIVHP	305
DB	242	LRGTNAESWLRYNQFRDLTLGVLDLVALPSP	YDTRYVPMNTSQAQLTREIYTDPIGTNA	301
QY	306	NQAFASITWYNNNAPSATAAVIRGPHLLDFLE	KVTIYSLSRWNTQYMMNWGHRLL	365
DB	302	PSGFASINWFNNNAPSATAAVIRPPLLDFPE	QLTIFSVLSRWNTQYMMYVWGHRL	361
QY	366	ESRPIGALNTSTOGSTNTSINPVTLOFTSRD	VYRTESLAGNLFLTPQVNGVPRVDFHW	425
DB	362	ESKTRIGSLSTHGNTNTSINPVTLOFTSRD	VYRTESFAGINILLTTPVNGVPAWFNFW	421
QY	426	KFPTLPASDNFYVLGVAGVGTQLQDSENELP	PETTGPNYESYSHRLSHGLLSASHVK	485
DB	422	RNPUNSRGSLLYTIGYTGVTQLFDESETLP	PETTERPNYESYSHRLSNIRLLSGNLT	481
QY	486	ALVYSWTHRSADRNTTIEPNSITQIPLVKAP	NLSGGAAVVRGPGFTGCDILRRTNTFTFG	545
DB	482	APVYSWTHRSADRNTTSSDSITQIPLVKS	FNLSNGTSVWSGPGFTGCDIIRTVNWSVL	541
QY	546	DIRWINPPAQRVRVIRVASYATDLOPHSTS	INGKAINQGNFSATMNRGEDLDYKTRTI	605
DB	542	SMGLNFNNTSLQIRVRVRVAASQTMVLRT	VVGSTTTFDQGFPSPTMANSLSLTQSFRFA	601
QY	606	GFTPTPFSFSDVQSTFTTICAMFNSSGNEV	YIDRIEFVPEVYFE	648
DB	602	EPFVGISASGSO-TAGISINNACROTHPEK	IFRITATIE	643

```

RESULT 11
US-10-089-678-1
; Sequence 1, Application US/10089678
; Publication No. US20030017967A1
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shinichiro
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A
; TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD

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; FILE REFERENCE: Q69821
; CURRENT APPLICATION NUMBER: US/10/089,678
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: JP 2000-236140
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/JP01/066650
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-089-678-1

```

Query Match	46.4%; Score 1734.5; DB 14; Length 1167;
Best Local Similarity	48.2%; Pred. No. 2.3e-136;
Matches	366; Conservative 123; Mismatches 210; Indels 61; Gaps 14
Qy	1 MKLKPNPKDHOSI---SSNAKVYDKIATDSLKNETDIELKNNNEDYLKMSHE-----SI 51
Db	1 MSPNQNEVEILDASSSTSVSDNSVVRPLANDQTTTLQNNYKYDYLRMSGEINPELFGNP 60
Qy	52 DPFVSASTIQTGIGIAGKILGTGLVPFAGQIASLYSFILGELMPKGK-SQWEIFMERHVEE 110
Db	61 ETFFISSSTVQTGIGIVGVQVGLGALGVPPFAGQIASFYSFIVGQLWPSSTSVWEMIMKQVED 120
Qy	111 IINQKILYARNKALSDLRGLGDALAVYHESLESWEVRNNTRRSVVKNQYITALELMFV 170
Db	121 LIDQKITSVRKTALAGLGGIDGLDYQKSLKNLENRNDTRRSVVVVYITALELDFV 180
Qy	171 QKLPSFVSGEVRPLPTIYAQANLHLLLRDASIFGKEWGLSGASEISTTFYNRQVETR 230
Db	181 AKIPFAISGQEVPLLSVYAQANLHLLLRDASIFGAENGWTFPGELISTFYDQVTRTAQ 240
Qy	231 YSDHCIKWYNTGLNNLRGTNAKSVRYRNQFQKMTLMLDLVALFPSYDTLVVPYPIKTTSQ 290
Db	241 YSDYCVKWYNTGLDKTGNNAASWLKYHQFRREMTLLVLDLVALFPNYDTRTYPIETTAQ 300
Qy	291 LTRFVYVTAIGTVHPNQAFSTTWNNNAFSFAIEAAVIRSHPLLDFLEKVTIYSLLS- 349
Db	301 LTRFVYVTDIPVNRRTSGGFCRRWSLNSDISFSFEVASVIRSHPLFDILSEIFYITTRAG 360
Qy	350 -RWSNTQYNNMMGGHRLBSRPIGGALANTSTQGSTNTSINPVT-----LOFTSRDYYRTE 402
Db	361 LPLNTEYLEYVGHGSIKYK-----NTNASSALERNYGITSNKIKYDLANKDIFQVR 414
Qy	403 SL-AGNLFLPTQVNGVRPVDVPHWKPTPLPIASDNFYLYGVAGV-----T 447
Db	415 SLGADLANYYAQ-VYGVFPYASF-----TLLDKN---TGSGSVGGFTYSKPHTTMQVCT 463
Qy	448 QLQDSENELPPETTCQPNYESYSHRLSHIGLIS-----ASHVKALVYSWTHRGADRT 499
Db	464 QNYNTIDEIPB--NEPLSRGYSHRLSHITSYFSKNASSPARYGNLPVPAWTHRGADVT 521
Qy	500 NTIEPNSITQIPLVKAFNLSSGAAVWRPGPTGGDILERTNTGTGDIRYNINPPFAQRY 559
Db	522 NTWYSDKITQIPVVKHAHTLVSGTTVIKPGPGTGCNLLKRTSSGSPLAYTSVSVKSPLSQRY 581
Qy	560 RVRIRYASTTDLOFHTSINGKAINQGHSPATMRGELDLYKTRTGTGFTTFPFSPFSVDQST 619
Db	582 RARIIRYASTNLRVLTISGTRIYSINVNKTMKGGDLTFTNTFDLATIGTAFTFSNYSDS 641
Qy	620 FTIGAWNFSSGNVEYIDRIEFVPVEVTVEAEYDEPEKAQEKVTALFTSTNPRGLKTDVKDY 679
Db	642 LTVGADSFASGGEVYVDKFEELIPVNAFTEAEEDLDVAKAVGLFTSKKD-ALQTSVTDY 700
Qy	680 HIDQVSNLVESLDSFYLDKRELFELVVKYAKQIHIERNM 719
Db	701 OVNOANILVECLSDLYPNKRMKLWDVAKEAKRLVQARNL 740

**RESULT 12**

US-10-428-961-6  
; Sequence 6, Application US/10428961  
; Publication No. US20030237111A1  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chin-Rel  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Rugar, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)  
; FILE REFERENCE: MECO201-1  
; CURRENT APPLICATION NUMBER: US/10/428,961  
; CURRENT FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: 09/661,322  
; PRIOR FILING DATE: 2000-09-13  
; PRIOR APPLICATION NUMBER: 60/153,995  
; PRIOR FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 6  
; LENGTH: 653  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-428-961-6

Query Match 45.0%; Score 1683.5; DB 15; Length 653;  
Best Local Similarity 51.3%; Pred. No. 1.8e-132; Indels 47; Gaps 15;  
Matches 345; Conservative 111; Mismatches 169;

QY 13 SSNAVKDIATDSLN--ETDIEKNNMNDYLRMSHESIDPFVSASTIQTGIGIAGK 69  
DB 2 NENEIINALSPAVNSHAQWDLSL-DARIEDSLCIAEGNNINPLVSASTVQTGGINAGR 60

QY 70 ILGTGVPFAGQIASLYSIFILGELWPKGKOWEIPMEHVEIINOKILTYARNKALSDLR 129  
DB 61 ILGVLGVPFAGQIASLYSIFILGELWPKGKOWEIPMEHVEIINOKILTYARNKALSDLR 120

QY 130 GLGDALAVTHESLESWENNRTRARSVVVKQYIALELMFVQKLPSPAVSGEEVPLPIY 189  
DB 121 GLGRGYSYQOALETWLDRNDARSILERYALELDITTAIPLFIRNEEVPLLMVY 180

QY 190 AQAAHLHLLLRDASIFGKWEGLSASEISTFYNRQVTRDYSDHCIKWYNTGLNLRGT 249  
DB 181 AQAAHLHLLLRDASIFGSEWGWASSDVNQYQOEQIRVTEESYHCVQWNTGLNLRGT 240

QY 250 NAKSWRYNQFRKDMTLMVLDLVALPSPYDTLYPIKITSOLTREVYTDALGTVHPNOAF 309  
DB 241 NAKSWRYNQFRKDMTLMVLDLVALPSPYDTLYPIKITSOLTREVYTDALGTVHPNOAF 300

QY 310 ASTTWYNNAPSPSAEAAVIRSPHLLDFLEKVTIYSLLSRWNSNTQYMMMGHRLSRP 369  
DB 301 ASTTWYNNAPSPSAEAAVIRSPHLLDFLEKVTIYSLLSRWNSNTQYMMMGHRLSRP 360

QY 370 IGGALNTSTQGST-NTSINPVTLOF-TSRDVRTESLAGNLFLETPQVNGVRVDFHWKF 427  
DB 361 IGGALNTSTQGST-NTSINPVTLOF-TSRDVRTESLAGNLFLETPQVNGVRVDFHWKF 418

QY 428 PTL-----PIASDN-FYVLGAGVGTQLODSENELPETTGQPNYESYHRLSHIG-- 477  
DB 419 ITRIRFMEAPLPTVNRIRLEGNLYLIQKLYHQK-----QQNDQIMHIVIDISVR 470

QY 478 LISASHVKALVYSWTHRSADRTNIFNSITQPLVKAFNLGSGAAVVRGPGFTGGDIUR 537  
DB 471 LIIGNTLRAPVYSWTHRSADRTNIFNSITQPLVKAFNLGSGAAVVRGPGFTGGDIUR 529

QY 538 -RTNWTGTF---GDIRVNN-PPFAQRYRVRIRVASTDLDQFHTSINGKAINQCNFSATWN 592  
DB 530 LNRNNGNIQNGYIEVPIQFTSTSTRYRVRVRYASVTSIELNVLNNGSSIFNTWLPATAA 589

QY 593 RGEDLDYKTFRTIGFTTTPFSFDSQSTFT-----IGAMFSSGNEVYIDRIEFVPEVT 646  
DB 590 SLDNLQ-----SGDFGVGEINNAFTSATGNIVGARNFSANAEEVIDRPEFIPVTAT 640

QY 647 YBAEYDPEKAOE 658  
DB 641 FEVEYDLERAOK 652

RESULT 13  
US-10-782-141-16  
; Sequence 16, Application US/10782141  
; Publication No. US20040197917A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274143  
; CURRENT APPLICATION NUMBER: US/10/782,141  
; CURRENT FILING DATE: 2004-02-20  
; PRIOR APPLICATION NUMBER: 60/448,632  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 1157  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-141-16

Query Match 44.3%; Score 1657.5; DB 16; Length 1157;  
Best Local Similarity 48.9%; Pred. No. 6.8e-130; Indels 49; Gaps 19;  
Matches 368; Conservative 107; Mismatches 228;

QY 1 MCLKNDPKHQSSNAKVKIATDS---LKNETDIEKNNMNDYLRMSHE-----S 50  
DB 1 MSPNNQNEVEIIDATST-SVSDSNRYPFANEPTDALQNMVYKDYLMKSGCGENPELFCN 59

QY 51 IDPFVSASTIQTGIGIAGKILGTLPVPFAGQIASLYSIFILGELWPKGKOWEIPMEHVE 109  
DB 60 PETFISSTIQTGIGIAGKILGTLPVPFAGQIASLYSIFILGELWPKGKOWEIPMEHVE 119

QY 110 EIINOKILTYARNKALSDLRGDLAVTHESLESWENNRTRARSVVVKQYIALELMF 169  
DB 120 ELVDQKLEKVKYKOKALAEKGLGNALDVQOSLEDLENRDARTSVVSNQFIALDLNF 179

QY 170 VQKLPSFAVSGEEVPLPIYIAQAANLHLLLRDASIFGKWEGLSASEISTFYNRQVTR 229  
DB 180 VSSIPSPAVSGEEVPLPIYIAQAANLHLLLRDASIFGKWEGLSASEISTFYNRQVTR 239

QY 230 DYSDHCIKWYNTGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPYDTLYPIKITS 289  
DB 240 EYSDYCVKWKYKIGLQKLGKTSKSNLYHQFRREMILLLDLVALPFPNYDTHMYPIETTA 299

QY 290 QLREVTYDAIG-TVHPNQAFASITWYNNAPSPSAEAAVIRSPHLLDFLEKVTIYSL 348  
DB 300 QLREVTYDAIG-TVHPNQAFASITWYNNAPSPSAEAAVIRSPHLLDFLEKVTIYSL 356

QY 349 SR-----WSNTQYMMMGHRLSRPISGALNTST--QGSTNTSINPVTLOFTSRDVRT 402  
DB 357 SRGGITLNDAYINWSGHTLKRYRTADSTVYTYTANYGRITSEKNSFALB--DRDIFEIN 414

QY 403 SLAGNLPLTOPVNGVRVDFHW-KFPTLPIASDNFYVLGAGVGTQLOQ-----DSENE 455  
DB 415 STVANLANYQKAVGPGSWFHWKRG-SSSTAYL-YSKTHLTALQCTQVYESSDE 469

QY 456 LPPETTGQPNYESYHRLSHI-----GLISASHVKALVYSWTHRSADRTNIFNSI 507  
DB 470 IPLDRT-VPVAESYHRLSHITSHFSKNG--SAYYGSFPVFWMTHTSADLNNTIYSDKI 526

QY 508 TOIPLVKAFNLGSGAAVVRGPGFTGGDIILRTNTGTGDIRVNNPPFAQRYRVRIRYAS 567  
DB 508 TOIPLVKAFNLGSGAAVVRGPGFTGGDIILRTNTGTGDIRVNNPPFAQRYRVRIRYAS 567

```
Db 527 TQIPAVKDMXYLGGSVVQPGFTGGDILKRTNPSILGTFVAVTVNGSLSQRYVRIRYAS 586
QY 568 TTDLOFHTSINGKAINQGNFSAATMRGDELDTYKFTTIGTFTTFFSDVQSTFTIGAMNF 627
Db 587 TTDPEF-TLYLGDPTIEKNRENKTMNDGASLYTETFFASFIPTDFQRETDKILLSMGDP 645
QY 628 SSGNEVIIDRIEVPVEVYEABYDEKAEKVTAFTSTNPRGLKTDVKYHIDQVSNL 687
Db 646 SSGQEVYIDRIEPIPVDETYEABQDLEAAKAVNALFTNTKO-GLRPGVTDEYVQAAANL 704
QY 688 VESLSDEFYLDKRELFEIVKAKQIHIERNM 719
Db 705 VECLSDLYPNEKRLLFDAVREAKRUSGARNL 736

RESULT 14
US-10-032-717-2
; Sequence 2, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE OF INVENTION: Pesticidal Activity Against Coleopterans
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-032-717-2

Query Match 40.5%; Score 1514; DB 13; Length 1206;
Best Local Similarity 44.1%; Pred. No. 8.7e-118;
Matches 338; Conservative 126; Mismatches 226; Indels 76; Gaps 22;

QY 1 MCLKNPKDQKQSLSSNAKVDKIATDS----LKNETDIELKMNNDYLRMSEHSID---- 52
Db 1 MSPNQNEYEIIDATPST-SVNSDSNRYPPFANEPTNALQNM DYKLYKWSAGNASYPGS 59

QY 53 PFVSAS---TIQTGIGIAGKILGTGVPFAGQIASLYSIFILGELWPKG-KSQWEIFMEHV 108
Db 60 PEVLVSGDAAKAAIDIVGKLLSGLGVPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQV 119

QY 109 EEIINOKILTYARNKALSDIRGLGDALAVYHESLSWENRNTRARSVVVKQYIALELM 168
Db 120 EELINOKIAEYARNKALSELEGLGNNYQLYLTALBEEENPNNGSRALRDVNRNFEILDSL 179

QY 169 FVQKLPSEAVSGEVPPLPIYAQAANLHLLLDASIFGKEWGLSASESTFVNROVERT 228
Db 180 FTQYMPFSRVNTEVPFLTVYAAANLHLLLDKASIFGEEWGWSTTTNNYYDROMKLT 239

QY 229 RYSDSDHCKWYNTGLNLRGNTAKSVRYNQFRKDMTLMVLDLVALFPSPYDLYVPIKTT 288
Db 240 AEYSDHCVKWYETGLAKLKTSAQWVDYQNFREMTLAVLDVVALFPYDLYVPIKTT 299

QY 289 SQTREYVYDAIGTVHPNOAFSTWYNNNAPSFAIEAAVRSRPHLDFLEKVTIYSL 348
Db 300 AQLTRVYTDPLGAVNVS---SIGSWY-DKAPSGVIESVIRPPHFVDFYITGLTYTQS 355

QY 349 SRNSNTQYMMWGHRLSPICGALNTSQGSTNTSINPV-TLOQTSRDVYTESLAGL 407
Db 356 RSISSARYIRHWHAGHIOISVHRVSRGSLNQMYCTGNQLHSTSTFDFTNYDIYKLSKDAV 415
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QY 408 NLELTQP-----VNGVPRVDFHM-----KFTPL-----PIASDNFFYLVGAGVGTQLODSE 453
Db 416 LLDIVPGVTYIFFGMEPEFEMVQNLNTRKTKLVNPSKD-----IIASTRDS 466

QY 454 NELPETTCOPNYESVSHRLSHIGLISAS-HVKAL--VYSWTHRSADRTNTEPNSITQI 510
Db 467 LSELPPETSQPNYESVSHRLCHITSIPATGNTGLVPFVSWTHRSADLNNIYSDKITQI 526

QY 511 PLVKAFNLSSGAAVRGPQFTGGDILR-RTNTGTGFDI---RVNINPPFAQRYVRIRYA 566
Db 527 PAVKCDNLFPFVPVVGKPGHTGGDILLQYNRSTGSGVGTFLFARYGLALEKAGKRVRLRYA 586

QY 567 STTDLOFHTSINGKAINQGNFSAATMRGDELDTYKFTF-----TIGFTTFFSFS 614
Db 587 TDADIVLH--VNDQI---QMPKTNWPGEDLTSKTFKVADAITTLNLATDSSLALKHNLG 641

QY 615 -DVQSTFTTIGAMNPFSSGNEVYIDRIEFPVEVYEABYDEKAEKVTAFTSTNPRGLK 673
Db 642 EDPNSTLS-----GIVYVDRIEFIPVDETYEABQDLEAAKAVNALFTNTKO-GLR 691

QY 674 TDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQIHIERNM 719
Db 692 PGVTDEYVQAAANLVECLSDLYPNEKRLLFDAVREAKRUSGARNL 737

RESULT 15
US-10-414-637-2
; Sequence 2, Application US/10414637
; Publication No. US20030177528A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With
; FILE OF INVENTION: Pesticidal Activity Against Coleopterans
; CURRENT APPLICATION NUMBER: US/10/414,637
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-414-637-2

Query Match 40.5%; Score 1514; DB 14; Length 1206;
Best Local Similarity 44.1%; Pred. No. 8.7e-118;
Matches 338; Conservative 126; Mismatches 226; Indels 76; Gaps 22;

QY 1 MCLKNPKDQKQSLSSNAKVDKIATDS----LKNETDIELKMNNDYLRMSEHSID---- 52
Db 1 MSPNQNEYEIIDATPST-SVNSDSNRYPPFANEPTNALQNM DYKLYKWSAGNASYPGS 59

QY 53 PFVSAS---TIQTGIGIAGKILGTGVPFAGQIASLYSIFILGELWPKG-KSQWEIFMEHV 108
Db 60 PEVLVSGDAAKAAIDIVGKLLSGLGVPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQV 119

QY 109 EEIINOKILTYARNKALSDIRGLGDALAVYHESLSWENRNTRARSVVVKQYIALELM 168
Db 120 EELINOKIAEYARNKALSELEGLGNNYQLYLTALBEEENPNNGSRALRDVNRNFEILDSL 179

QY 169 FVQKLPSEAVSGEVPPLPIYAQAANLHLLLDASIFGKEWGLSASESTFVNROVERT 228
Db 180 FTQYMPFSRVNTEVPFLTVYAAANLHLLLDKASIFGEEWGWSTTTNNYYDROMKLT 239
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**Tue Feb 15 10:07:57 2005**

[illegible]

Search completed: February 14, 2005, 20:56:50  
Job time : 62.0945 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:24:54 ; Search time 22.3302 Seconds  
(without alignments)  
2403.590 Million cell updates/sec

Title: US-10-019-823B-59  
Perfect score: 3742  
Sequence: 1 MKLKNPDKHQSLSNAKVDK.....KRELFEIVKYAKQIHHRNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/prodata/1/iaa/5A COMB.pcp.\*  
2: /cgn2\_6/prodata/1/iaa/5B COMB.pcp.\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pcp.\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB.pcp.\*  
5: /cgn2\_6/prodata/1/iaa/PCUS COMB.pcp.\*  
6: /cgn2\_6/prodata/1/iaa/backfileseq.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3546	94.8	719	2	US-09-003-217-2
2	3541	94.6	719	3	US-09-218-942-2
3	3516	94.0	719	3	US-08-286-870A-8
4	3368.5	90.0	710	4	US-09-661-322A-42
5	3160	84.4	648	3	US-08-286-870A-4
6	2573	68.8	535	3	US-08-286-870A-6
7	2459	65.7	1229	1	US-08-100-709-4
8	2459	65.7	1229	1	US-08-176-865-4
9	2459	65.7	1229	1	US-08-474-038-4
10	2459	65.7	1229	1	US-08-779-046-4
11	2459	65.7	1229	1	US-08-881-340-4
12	2314.5	61.9	1207	2	US-07-951-715A-7
13	2314.5	61.9	1207	2	US-08-459-448A-7
14	2314.5	61.9	1207	3	US-08-459-595A-7
15	2314.5	61.9	1207	3	US-08-459-504B-7
16	2314.5	61.9	1207	3	US-08-459-444-7
17	2314.5	61.9	1207	3	US-09-053-549-8
18	2314.5	61.9	1207	3	US-09-547-422-7
19	2314.5	61.9	1207	4	US-09-988-462-7
20	2308.5	61.7	1227	3	US-09-053-549-2
21	2243	59.9	1227	1	US-08-448-170-8
22	2243	59.9	1227	3	US-08-961-803-9
23	2234	59.7	1227	1	US-09-661-322A-63
24	2233.5	59.7	488	1	US-08-448-170-10
25	2233.5	59.7	488	3	US-08-961-803-10
26	2219	59.3	1186	3	US-09-178-252-23
27	2219	59.3	1186	4	US-09-826-660-23

28	2168.5	58.0	1228	4	US-09-661-322A-38	Sequence 38, Appl
29	1982	53.0	643	3	US-09-178-252-25	Sequence 25, Appl
30	1982	53.0	643	4	US-09-826-660-25	Sequence 25, Appl
31	1813	48.5	380	5	PCT-US91-02560-4	Sequence 4, Appl
32	1683.5	45.0	653	4	US-09-661-322A-6	Sequence 6, Appl
33	1657.5	44.3	1157	1	US-07-876-280-30	Sequence 30, Appl
34	1657.5	44.3	1157	1	US-07-812-180A-2	Sequence 2, Appl
35	1657.5	44.3	1157	1	US-08-315-468-2	Sequence 2, Appl
36	1657.5	44.3	1157	3	US-07-941-650A-2	Sequence 2, Appl
37	1519.5	40.6	1176	1	US-08-257-999-2	Sequence 2, Appl
38	1507	40.3	1157	2	US-08-532-547-5	Sequence 5, Appl
39	1507	40.3	1157	2	US-08-379-656B-5	Sequence 5, Appl
40	1507	40.3	1157	3	US-08-455-838-5	Sequence 5, Appl
41	1507	40.3	1157	3	US-09-019-809-5	Sequence 5, Appl
42	1507	40.3	1157	4	US-09-471-177-5	Sequence 5, Appl
43	1507	40.3	1157	4	US-09-220-806-5	Sequence 5, Appl
44	1506.5	40.3	1168	1	US-08-291-368-4	Sequence 4, Appl
45	1506.5	40.3	1168	2	US-08-962-190-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1  
US-09-003-217-2  
; Sequence 2, Application US/09003217  
; Patent No. 5986177  
; GENERAL INFORMATION:  
; APPLICANT: Osman, Yehia A.  
; APPLICANT: Madkour, Magdy A.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH  
; TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)  
; STREET: 3605 Glenwood Ave. Suite 310  
; CITY: Raleigh  
; STATE: NC  
; COUNTRY: US  
; ZIP: 27622  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/003,217  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: 5718-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919 420 2202  
; TELEFAX: 919 881 3175  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-003-217-2

Query Match 94.8%; Score 3546; DB 2; Length 719;  
Best Local Similarity 95.0%; Pred. No. 6.1e-318;  
Matches 683; Conservative 11; Mismatches 25; Indels 0; Gaps 0;  
Qy 1 MKLKNPDKHQSLSNAKVDKATDSLKNETDLKMNNDYLRMSEHSIDPFVSASTI 60  
Db 1 MKLKNPDKHQSLSNAKVDKATDSLKNETDLKMNNDYLRMSEHSIDPFVSASTI 60

QY

61

QTGIGIAGKILGTGVFPAGQIASLYSFIIGELWPKGSOWEIFMEHVBEIINOKILTYA

120

Db

61

QTGIGIAGKILGTGVFPAGQIASLYSFIIGELWPKGSOWEIFMEHVBEIINOKILTYA

120

QY

121

RNKALSDLRGLGDALAVYHSHESLVNRRNTRARSVVKNQYIALELMFVKQLPSFAVSG

180

Db

121

RNKALSDLRGLGDALAVYHSHESLVNRRNTRARSVVKNQYIALELMFVKQLPSFAVSG

180

QY

181

BEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSYHCVKWN

240

Db

181

BEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSYHCVKWN

240

QY

241

TGLNLRGTNAKSWRYNQFRKQMTLWLDLVALFSPYDITLVPIKTTLSOLTREVTDAI

300

Db

241

TGLNLRGTNAKSWRYNQFRKQMTLWLDLVALFSPYDITLVPIKTTLSOLTREVTDAI

300

QY

301

GTVHPNQAFASITWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWNSNTQYNNMW

360

Db

301

GTVHPNQAFASITWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWNSNTQYNNMW

360

QY

361

GGHRESPIGALNTSGSTNTSINPVTLOFTSRDVRTESLAGLNFLTQPVNGVPR

420

Db

361

GGHRESPIGALNTSGSTNTSINPVTLOFTSRDVRTESLAGLNFLTQPVNGVPR

420

QY

421

VDPHWKFPPLTASDNFYVLGAGVGTQLODSENELPETTGQPNYESYSHRSLHIGLIS

480

Db

421

VDPHWKFPPLTASDNFYVLGAGVGTQLODSENELPETTGQPNYESYSHRSLHIGLIS

480

QY

481

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Db

481

ASHVKALVSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN

540

QY

541

TGTFGDIRVNINPPPAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK

600

Db

541

TGTFGDIRVNINPPPAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK

600

QY

601

TERTIGTTPFSFSDVQSTFTIGANFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV

660

Db

601

TERTIGTTPFSFSDVQSTFTIGANFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV

660

QY

661

TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFLDKRELFEIVKAKQIHIERNM

719

Db

661

TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFLDKRELFEIVKAKQIHIERNM

719

QY

1

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Db

1

MLKKNPDKHQSLSSNAKVDKIATDSLKTNETDILKNNMNEYLRMSEHESIDPFFVSASTI

60

QY

61

QTGIGIAGKILGTGVFPAGQIASLYSFIIGELWPKGSOWEIFMEHVBEIINOKILTYA

120

Db

61

QTGIGIAGKILGTGVFPAGQIASLYSFIIGELWPKGSOWEIFMEHVBEIINOKILTYA

120

QY

121

RNKALSDLRGLGDALAVYHSHESLVNRRNTRARSVVKNQYIALELMFVKQLPSFAVSG

180

Db

121

RNKALSDLRGLGDALAVYHSHESLVNRRNTRARSVVKNQYIALELMFVKQLPSFAVSG

180

QY

181

BEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSYHCVKWN

240

Db

181

BEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSYHCVKWN

240

QY

241

TGLNLRGTNAKSWRYNQFRKQMTLWLDLVALFSPYDITLVPIKTTLSOLTREVTDAI

300

Db

241

TGLNLRGTNAKSWRYNQFRKQMTLWLDLVALFSPYDITLVPIKTTLSOLTREVTDAI

300

QY

301

GTVHPNQAFASITWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWNSNTQYNNMW

360

Db

301

GTVHPNQAFASITWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWNSNTQYNNMW

360

QY

361

GGHRESPIGALNTSGSTNTSINPVTLOFTSRDVRTESLAGLNFLTQPVNGVPR

420

Db

361

GGHRESPIGALNTSGSTNTSINPVTLOFTSRDVRTESLAGLNFLTQPVNGVPR

420

QY

421

VDPHWKFPPLTASDNFYVLGAGVGTQLODSENELPETTGQPNYESYSHRSLHIGLIS

480

Db

421

VDPHWKFPPLTASDNFYVLGAGVGTQLODSENELPETTGQPNYESYSHRSLHIGLIS

480

QY

481

ASHVKALVSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN

540

Db

481

ASHVKALVSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN

540

QY

541

TGTFGDIRVNINPPPAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK

600

Db

541

TGTFGDIRVNINPPPAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK

600

QY

601

TERTIGTTPFSFSDVQSTFTIGANFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV

660

Db

601

TERTIGTTPFSFSDVQSTFTIGANFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV

660

QY

661

TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFLDKRELFEIVKAKQIHIERNM

719

Db

661

TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFLDKRELFEIVKAKQIHIERNM

719

QY

1

MLKKNPDKHQSLSSNAKVDKIATDSLKTNETDILKNNMNEYLRMSEHESIDPFFVSASTI

60

RESULT 3

US-08-286-870A-8

; Sequence 8, Application US/08286870A

; Patent No. 6063605

GENERAL INFORMATION:

APPLICANT: ELY, S

APPLICANT: TAILOR, RH

APPLICANT: TIPPEIT, JM

APPLICANT: BLENN, RG

TITLE OF INVENTION: BACTERIAL GENES

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DAREY & CUSHMAN

ADDRESSEE: Intellectual Property Group of

ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP

STREET: 1100 New York Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286, 870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PAUL N. KOKULIS  
; REGISTRATION NUMBER: 16, 773  
; REFERENCE/DOCKET NUMBER: 70608/220720  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-286-870A-8

Query Match 94.0%; Score 3516; DB 3; Length 719;  
Best Local Similarity 92.8%; Pred. No. 3e-315;  
Matches 667; Conservative 33; Mismatches 20; Indels 0; Gaps 0;  
QY 1 MRLKNDPKHQSLSSNAKVDKIATDSLKNETDIELKNNEDYLRMSHEHSDIPFVSASTI 60  
DB 1 MRLKNDPKHQSLSSNAKVDKIATDSLKNETDIELKNNEDYLRMSHEHSDIPFVSASTI 60  
QY 61 QTGIGTAGKILGTLPVPPAGQIASLVSFILGELWPKGKQWEIEMFMEHVEIINQKILTYA 120  
DB 61 QTGIGTAGKILGTLPVPPAGQIASLVSFILGELWPKGKQWEIEMFMEHVEIINQKILTYA 120  
QY 121 RNKALSDLRLGLDALAVYHESLESWVENNRNTRARSVVKNOYIALELMFVKLPSPFAVSG 180  
DB 121 RNKALSDLRLGLDALAVYHESLESWVENNRNTRARSVVKNOYIALELMFVKLPSPFAVSG 180  
QY 181 EHVPLLPPIYAQAANLHLLLRDASIFGKWLSDSEISTFYNRQSRKSEYSDHCWKYN 240  
DB 181 EHVPLLPPIYAQAANLHLLLRDASIFGKWLSDSEISTFYNRQSRKSEYSDHCWKYN 240  
QY 241 TGLNNLRGTNAKSWRVYNOFRDMLVLDLVALFPSYDTLVYPIKTTSQLTRVYTDAL 300  
DB 241 TGLNNLRGTNAKSWRVYNOFRDMLVLDLVALFPSYDTLVYPIKTTSQLTRVYTDAL 300  
QY 301 GTVHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYNNMW 360  
DB 301 GTVHPNPSFTSTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYNNMW 360  
QY 361 GGHRLSRPIGGALNTSTQSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPR 420  
DB 361 GGHKLEFRTIGTLNISTQSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPR 420  
QY 421 VDFHMKFPTLPASDNFYLYAGVGTQLQDSNELPPEATGPNYESYSHRLSHGLIS 480  
DB 421 VDFHMKFPTLPASDNFYLYAGVGTQLQDSNELPPEATGPNYESYSHRLSHGLIS 480  
QY 481 ASHVKALVSWTHRSADRTNTEIPNSITQIPLVKAFLNLSGAAVVRGPGTGGDIILRTN 540  
DB 481 ASHVKALVSWTHRSADRTNTEIPNSITQIPLVKAFLNLSGAAVVRGPGTGGDIILRTN 540  
QY 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
DB 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
QY 601 TPTTIGFTTFPSDSVQSTTICAWNPFSSGNEVYIDRIEFVPEVYVEAYEYDEKAQEKV 660  
DB 601 TPTTIGFTTFPSDLVQSTTICAWNPFSSGNEVYIDRIEFVPEVYVEAYEYDEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVSLSDEFYLDKRELFELVKYAKQHIERNM 719  
DB 661 TALFTSTNPRGLKTDVQYHIDQVSNLVSLSDEFYLDKRELFELVKYAKQHIERNM 719  
RESULT 4  
US-09-661-322A-42  
; Sequence 42, Application US/09661322A  
; Patent No. 6593293  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Ruper, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo  
; FILE REFERENCE: MECO201  
; CURRENT APPLICATION NUMBER: US/09/661,322A  
; CURRENT FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 42  
; LENGTH: 710  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (200)...(200)  
; OTHER INFORMATION: No. 6593293-Coding  
US-09-661-322A-42

Query Match 90.0%; Score 3368.5; DB 4; Length 710;  
Best Local Similarity 89.2%; Pred. No. 1.2e-301;  
Matches 641; Conservative 32; Mismatches 37; Indels 9; Gaps 1;  
QY 1 MRLKNDPKHQSLSSNAKVDKIATDSLKNETDIELKNNEDYLRMSHEHSDIPFVSASTI 60  
DB 1 MRLKNDPKHQSLSSNAKVDKIATDSLKNETDIELKNNEDYLRMSHEHSDIPFVSASTI 60  
QY 61 QTGIGTAGKILGTLPVPPAGQIASLVSFILGELWPKGKQWEIEMFMEHVEIINQKILTYA 120  
DB 61 QTGIGTAGKILGTLPVPPAGQIASLVSFILGELWPKGKQWEIEMFMEHVEIINQKILTYA 120  
QY 121 RNKALSDLRLGLDALAVYHESLESWVENNRNTRARSVVKNOYIALELMFVKLPSPFAVSG 180  
DB 121 RNKALSDLRLGLDALAVYHESLESWVENNRNTRARSVVKNOYIALELMFVKLPSPFAVSG 180  
QY 181 EHVPLLPPIYAQAANLHLLLRDASIFGKWLSDSEISTFYNRQSRKSEYSDHCWKYN 240  
DB 181 EHVPLLPPIYAQAANLHLLLRDASIFGKWLSDSEISTFYNRQSRKSEYSDHCWKYN 240  
QY 241 TGLNNLRGTNAKSWRVYNOFRDMLVLDLVALFPSYDTLVYPIKTTSQLTRVYTDAL 300  
DB 241 TGLNNLRGTNAKSWRVYNOFRDMLVLDLVALFPSYDTLVYPIKTTSQLTRVYTDAL 300  
QY 301 GTVHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYNNMW 360  
DB 301 GTVHPNPSFTSTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYNNMW 360  
QY 361 GGHRLSRPIGGALNTSTQSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPR 420  
DB 361 GGHKLEFRTIGTLNISTQSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPR 420  
QY 421 VDFHMKFPTLPASDNFYLYAGVGTQLQDSNELPPEATGPNYESYSHRLSHGLIS 480  
DB 421 VDFHMKFPTLPASDNFYLYAGVGTQLQDSNELPPEATGPNYESYSHRLSHGLIS 480  
QY 481 ASHVKALVSWTHRSADRTNTEIPNSITQIPLVKAFLNLSGAAVVRGPGTGGDIILRTN 540  
DB 481 ASHVKALVSWTHRSADRTNTEIPNSITQIPLVKAFLNLSGAAVVRGPGTGGDIILRTN 540  
QY 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
DB 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600

Db 532 TGTGDIRVNPPFAQRVIRYASTDLPHTSINGKAINQGNFSATMNRGDLDYK 591  
Qy 601 TFRIGTTPSPSDVOSTFTIGAWNFSNGNEVYIDRIEFVPEVTEAEVDEFEKAQEV 660  
Db 592 TFRVGTTPSPSDVOSTFTIGAWNFSNGNEVYIDRIEFVPEVTEAEVDEFEKAQEV 651  
Qy 661 TALTSTNPRGLKTDVXDYHIDQVSNLVSLSDFYLDKRELFEIYKAKQIHIERNM 719  
Db 652 TALTSTNPRGLKTDVXDYHIDQVSNLVSLSDFYLDKRELFEIYKAKQIHIERNM 710

RESULT 5

US-08-286-870A-4  
; Sequence 4, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENN, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PAUL N. KOKULIS  
; REGISTRATION NUMBER: 70608/220720  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 648 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-286-870A-4

Query Match 84.4%; Score 3160; DB 3; Length 648;  
Best Local Similarity 92.3%; Pred. No. 1.8e-282;  
Matches 598; Conservative 30; Mismatches 20; Indels 0; Gaps 0;  
Qy 1 MKLNPRKHQSLSSNAKVDKIATSLKNETDIELKNNMNEYLRMSHESIDPFVSASTI 60  
Db 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINNHEDCLKMSEVENVEPFVSASTI 60  
Qy 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGKSWEIFMEHVEEIIINOKILTYA 120  
Db 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGKQWEIIFMEHVEEIIINOKISTYA 120

Qy 121 RNKALSDLRGLGDLAVYTHESLESWENRNNTARSVVKNOYIALELMFYQKLPSPAVSG 180  
Db 121 RNKALTDLRGLGDLAVYHDSLESWGNRNNTARSVVKSQYIALELMFYQKLPSPAVSG 180  
Qy 181 EREVLLPIYAQAANLHLLLRDASIFGKEWGLSGASEISTFYNQVQVTRDYSCHCIKWYN 240  
Db 181 EREVLLPIYAQAANLHLLLRDASIFGKEWGLSGSSEISTFYNQVQVTRDYSCHCKWYS 240  
Qy 241 TGLNLRGNTNAKSWRYNQFRKDMTLMVLDLVALPFSYDTLVPYPIKTTSLTQVREYTDI 300  
Db 241 TGLNLRGNTNAESWRYNQFRDMTLMVLDLVALPFSYDTQMPYPIKTTAQLTREVYTDI 300  
Qy 301 GTVHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSWSNTQYNNMW 360  
Db 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW 360  
Qy 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLOQTSRDVYRTESLAGLNLELTQPVNGVPR 420  
Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLELTQPVNGVPR 420  
Qy 421 VDFHMKPEPTLPASDNFYILGYAGVGTQLODSENELPPTGQPNYESYSHRLSHIGLIS 480  
Db 421 VDFHMKFVTHPIASDNFYIPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
Qy 481 ASHVKALVSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
Db 481 ASHVKALVSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
Qy 541 TGTFGDIRVNINPPFAQRVIRYASTDLPHTSINGKAINQGNFSATMNRGDLDYK 600  
Db 541 TGTFGDIRVNINPPFAQRVIRYASTDLPHTSINGKAINQGNFSATMNRGDLDYK 600  
Qy 601 TFRIGTTPSPSDVOSTFTIGAWNFSNGNEVYIDRIEFVPEVTEAEVDEFEKAQEV 648  
Db 601 TFRVGTTPSPSDVOSTFTIGAWNFSNGNEVYIDRIEFVPEVTEAEVDEFEKAQEV 648

RESULT 6

US-08-286-870A-6  
; Sequence 6, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENN, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989

```
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-870A-6

Query Match 68.8%; Score 2573; DB 3; Length 535;
Best Local Similarity 91.0%; Pred. No. 2e-228;
Matches 487; Conservative 29; Mismatches 19; Indels 0; Gaps 0;

QY 1 MKLNPKHQSLSSNAKVDKIATDSLKNETDIELKNNMNEYDYLRMSEHESIDPFVSASTI 60
DB 1 MKLNQDKHQSPSSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEFPVSASTI 60
QY 61 QTGIGTAGKILGTGVPFAGQIASLYSIFILGELWPKGSQWEIPEHVEEILNOKILTYA 120
DB 61 QTGIGTAGKILGTGVPFAGQIASLYSIFILGELWPKGSQWEIPEHVEEILNOKISTYA 120
QY 121 RNKALSDRLGLDALAVYHESLESWENNRNTRARSVVKNOYIALELMFVKLPSPFVSG 180
DB 121 RNKALTDRLGLDALAVYHDSLESWGNRNTRARSVVKVKSQYIALELMFVKLPSPFVSG 180
QY 181 EYVPLPIYAAQANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYN 240
DB 181 EYVPLPIYAAQANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRAGDYSCHVKWYS 240
QY 241 TGLNLRGTNAKSWVRYNQPRKDMTLMVLDLVLPFSDYTLVPIKTTSQLTREVYTDAL 300
DB 241 TGLNLRGTNAESWVRYNQPRDMTLMVLDLVLPFSDYTMPIKTTAQLTREVYTDAL 300
QY 301 GTVHPNOAPASTTWYNNAPSAIEAAVIRSPHLLDFLEKVTIYSLLSWSNTQYNNMW 360
DB 301 GTVHPHPSFTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW 360
QY 361 GGHRLSPRTGGALNTSTQGSTNTSINPVLQFTSRDVRVYTESLAGLNLFLOTQVNGVPR 420
DB 361 GGHKLEPRTGGTLNISTQGSTNTSINPVLPTFTSRDVRVYTESLAGLNLFLOTQVNGVPR 420
QY 421 VDFHWKPTPIASDNFYLYGAGVGTQLODSENELPPETTGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFTVTHPIASDNFYLYGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGTGGDI 535
DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGTGGDI 535

RESULT 7
US-08-100-709-4
; Sequence 4, Application US/08100709
; Patent No. 5322687
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yeping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS clyt4 AND clyt5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panich Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
```

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; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,709
; FILING DATE: 19930729
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-100-709-4

Query Match 65.7%; Score 2459; DB 1; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.7e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKXPKHQSLSSNAKVDKIATDSLKNETDIELKNNMNEYDYLRMSEHESIDPFVSASTIQT 62
DB 20 VSNPSTQMNLSPDARI-----EDSLCVAEVNNDIPFVSASTVQT 58
QY 63 GTGIAGKILGTGVPFAGQIASLYSIFILGELWPKGSQWEIPEHVEEILNOKILTYARN 122
DB 59 GINIAGRILGLVGPVFPAGQIASLYSIFLVGELWPSGRDPWEIPLFLEHQILRQVNTNRN 118
QY 123 KALSRLRGDGLDALAVYHESLESWENNRNTRARSVVKNOYIALELMFVKLPSPFVSGEE 182
DB 119 TAIARLEGIRGVRYSQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRINEE 178
QY 183 VPLLPIYAAQANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYNTG 242
DB 179 VPLLAVYAAQANLHLLLRDASIFGSEWGMASDVNQYQEQIRYITEYSNHCQVWYNTG 238
QY 243 LNNLRGTNAKSWVRYNQPRKDMTLMVLDLVLPFSDYTLVPIKTTSQLTREVYTDALGT 302
DB 239 LNNLRGTNAESWVRYNQPRDRLTGLVLDVLPFSDYTRTPINTSAQLTREIYTDPIGR 298
QY 303 VHPNOAPASTTWYNNAPSAIEAAVIRSPHLLDFLEKVTIYSLLSWSNTQYNNMWG 362
DB 299 TWAPSGFASTWNNAPSAIEAAI FRPHLLDFPEQLTIYSASRRWSSTOHHMYWVG 358
QY 363 HRLESPIGALNTSTQGST-NTSINPVLQFTSRDVRVYTESLAGLNLFLOTQVNGVPRV 421
DB 359 HRLNRPRTGGTLNISTQGSTNTSINPVLQFTSRDVRVYTESNAGTNILFTTVPNGVPMW 418
QY 422 DFHWKPTPIASDNFYLYG-----YAGVGTQLODSENELPPETTGQPNYESYSHRLS 474
DB 419 RPNF-----INPQNIYERGATTSQPYQGVGQLDFDSETELPETTERPNYESYSHRLS 472
QY 475 HGLISASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGTGGD 534
DB 473 HGLIICNTLRAPVSWTHRSADRTNTIGNRITQIPLVKAENLHSGVTVVGPGTGGD 532
QY 535 ILRRTWTGFGDIRVNNINPFPFAQRVRIYASTTDLQFHTSINGKAINQGNFSATNWRG 594
DB 533 ILRRTWTGFGDIRLNLNINPLSQRYVRIRYASTTDLQFFTRINGTVNIGNFSRTNWRG 592
QY 595 ELDLYKFTFTIGTPTTFFSFDVQSTTICAMNPFSSGNEVYIDRIEFPVVEVTEAYDFE 654
DB 593 DNLEYSFRTAGFTSTPFNFLNAQSTFTLGAQFSN-QEVYIDRVFVPAEVTFAEAYDLE 651
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Tue Feb 15 10:07:56 2005

QY 655 KAQKVTALFTSTNPRGLKTDVYHIDQVSNLVESLSDBFYLDKRELFPEIVKYAKQIH 714  
DB 652 RAQKAVNALFTSTNPRGLKTDVYHIDQVSNLVESLSDBFYLDKRELFPEIVKYAKRLS 711  
QY 715 IERNM 719  
DB 712 DERNL 716  
RESULT 8  
US-08-176-865-4  
; Sequence 4, Application US/08176865  
; Patent No. 5616319  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yiping  
; APPLICANT: Jany, Christine S.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
; ADDRESSEE: Nadel  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/176.865  
; FILING DATE: 30-DEC-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/100,709  
; FILING DATE: 29-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Egoif, Christopher  
; REGISTRATION NUMBER: 27633  
; REFERENCE/DOCKET NUMBER: 7205-49  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-757-1590  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1229 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-176-865-4  
Query Match 65.7%; Score 2459; DB 1; Length 1229;  
Best Local Similarity 64.8%; Pred. No. 2.7e-217;  
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;  
QY 3 LKMPDKHQSLSSNAKVDKIATDSLKNETDIELKMNNDYLRMSEHESIDPFVSASTIQT 62  
DB 20 VSNPSTQMLSPDARI-----EDSLCVAENIDPFVSASTVQT 58  
QY 63 GIGTAGKILGTGVPAGQIASYFLTGLBWPKGKQWEIPEHVEEIIINOKILTYARN 122  
DB 59 GINIAGRIILGVLGVPAGQIASYFLVGLBWPKGKQWEIPEHVEEIIINOKILTYARN 118  
QY 123 KALSDLRGLDALVALVHESLESVVENRNNTARSVKNQVIALMLFMVKLPSFAVSGEE 182  
DB 119 TATARLEGLGRGYSYQQALETLDNRNDARSRIILERYVALELDITTAIFLPIRNEE 178  
QY 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISITFFYNRQVTRDYSDHCIKWNTG 242

DB 179 VPLLMVYAQAANLHLLLRDASIFGSEWGMASVVNQYQEQIRYTBESNHCQWNTG 238  
QY 243 LNNLRTGNAKSWRVNQKQKMDTLWLDLVALFSSYDTLVVPIKTTTSOLTREVTDAIGT 302  
DB 239 LNNLRTGNAKSWRVNQKQKMDTLWLDLVALFSSYDTLVVPIKTTTSOLTREVTDAIGT 298  
QY 303 VHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYLSLRSWSTQVNNMVG 362  
DB 299 TNAPSGFASTWNNNAPSFAIEAAVIRSPHLLDFLEKVTIYLSLRSWSTQVNNMVG 358  
QY 363 HRLSRPIGGALNTSTQGST-NTSINPVTLQFTSRDVTSTESLAGLNLFLTPQVNGVPRV 421  
DB 359 HRLNFRPIGGTTLNTSTQGLTNTSINPVTLQFTSRDVTSTESLAGLNLFLTPQVNGVPRV 418  
QY 422 DFHMKFPTLPIASDNFYVLG-----YAGVGTQLQDSSENELPPETTCQPNYESYSHRLS 474  
DB 419 RNF-----INPQNIYERGATTYSQPVGVGVLFDSETELPPETTERPNYESYSHRLS 472  
QY 475 HIGLISASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAPNLSSGAAVRGPGFTGCD 534  
DB 473 HIGLIGNTLRAPVYVSWTHRSADRTNTIEPNSITQIPLVKAPNLSSGAAVRGPGFTGCD 532  
QY 535 ILRRTNTGTFGDIRVNNINPPFAQRYRVRIRYASTTDLQFHTSINGKALNQGNFSATMNRG 594  
DB 533 ILRRTNTGTFGDIRVNNINPPFAQRYRVRIRYASTTDLQFHTSINGKALNQGNFSATMNRG 592  
QY 595 ELDLYKTFRTIGFTTTPFSFSDVQSTFTTGAMNFSNGEYIDRIEFVPEVETYEAYDPE 654  
DB 593 DNLEYRSFTAGSFIPFNFNAQSTFTLGAQFSN-QEYVIDRVEFVPAEYFEAYDLE 651  
QY 655 KAQKVTALFTSTNPRGLKTDVYHIDQVSNLVESLSDBFYLDKRELFPEIVKYAKQIH 714  
DB 652 RAQKAVNALFTSTNPRGLKTDVYHIDQVSNLVESLSDBFYLDKRELFPEIVKYAKRLS 711  
QY 715 IERNM 719  
DB 712 DERNL 716  
RESULT 9  
US-08-474-038-4  
; Sequence 4, Application US/08474038  
; Patent No. 5673343  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yiping  
; APPLICANT: Jany, Christine S.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
; ADDRESSEE: Nadel  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474.038  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/176.865  
; FILING DATE: 30-DEC-1993  
; APPLICATION NUMBER: US 08/100,709

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; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-474-038-4

Query Match 65.7%; Score 2459; DB 1; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.7e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKNPKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPPFVSASTIQT 62
DB 20 VSNPSTQMNLSPDARI-----EDSLCVAEVNNDPPFVSASTVQT 58
QY 63 GIGIAGKILGTGVPAGQIASYSLFGLWPKGKSQWEIPEHVEEIIINQKILTYARN 122
DB 59 GINIAGRILGVLGVPAGQIASYSLFGLWPKGKSQWEIPEHVEEIIINQKILTYARN 118
QY 123 KALSLDLRGDGLAVVHESLESVNNRNRTRSVKNOVIALELMFVKLPSPFVSGEE 182
DB 119 TAIARLEGGRGVRYSQQALETWLNDNRDARSIIILERYVALELDTTAPLFRINEE 178
QY 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNNRQVTRDYSKICIKWYNTG 242
DB 179 VPLLWVYAQAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEEYSNHCQVWYNTG 238
QY 243 LNNLRGTNAKSWRYNQPKDMTLMVLVLPSPYDTLVYPIKTTSQLTREVYTTAIGT 302
DB 239 LNNLRGTNAESWLRYNQFRDLTLGLVLDLVALFPSTDTTYPINTSAQLTREIYTDPIGR 298
QY 303 VHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRNSNTQYMMWVG 362
DB 299 TNAPSGFASTWNNFNAPSFAIEAIFRPPHLLDPPEQTIYSSASSRWSSTQHMWYVG 358

US-08-779-046-4
; Sequence 4, Application US/08779046
; Patent No. 5854053
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yeping
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESS: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,046
; FILING DATE: 06-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-779-046-4

Query Match 65.7%; Score 2459; DB 2; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.7e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKNPKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPPFVSASTIQT 62
DB 20 VSNPSTQMNLSPDARI-----EDSLCVAEVNNDPPFVSASTVQT 58
QY 63 GIGIAGKILGTGVPAGQIASYSLFGLWPKGKSQWEIPEHVEEIIINQKILTYARN 122
DB 59 GINIAGRILGVLGVPAGQIASYSLFGLWPKGKSQWEIPEHVEEIIINQKILTYARN 118
QY 123 KALSLDLRGDGLAVVHESLESVNNRNRTRSVKNOVIALELMFVKLPSPFVSGEE 182
DB 119 TAIARLEGGRGVRYSQQALETWLNDNRDARSIIILERYVALELDTTAPLFRINEE 178
QY 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNNRQVTRDYSKICIKWYNTG 242
DB 179 VPLLWVYAQAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEEYSNHCQVWYNTG 238
QY 243 LNNLRGTNAKSWRYNQPKDMTLMVLVLPSPYDTLVYPIKTTSQLTREVYTTAIGT 302
DB 239 LNNLRGTNAESWLRYNQFRDLTLGLVLDLVALFPSTDTTYPINTSAQLTREIYTDPIGR 298
QY 303 VHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRNSNTQYMMWVG 362
DB 299 TNAPSGFASTWNNFNAPSFAIEAIFRPPHLLDPPEQTIYSSASSRWSSTQHMWYVG 358

US-10-019-823b-59.rai
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-474-038-4

Query Match 65.7%; Score 2459; DB 1; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.7e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKNPKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPPFVSASTIQT 62
DB 20 VSNPSTQMNLSPDARI-----EDSLCVAEVNNDPPFVSASTVQT 58
QY 63 GIGIAGKILGTGVPAGQIASYSLFGLWPKGKSQWEIPEHVEEIIINQKILTYARN 122
DB 59 GINIAGRILGVLGVPAGQIASYSLFGLWPKGKSQWEIPEHVEEIIINQKILTYARN 118
QY 123 KALSLDLRGDGLAVVHESLESVNNRNRTRSVKNOVIALELMFVKLPSPFVSGEE 182
DB 119 TAIARLEGGRGVRYSQQALETWLNDNRDARSIIILERYVALELDTTAPLFRINEE 178
QY 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNNRQVTRDYSKICIKWYNTG 242
DB 179 VPLLWVYAQAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEEYSNHCQVWYNTG 238
QY 243 LNNLRGTNAKSWRYNQPKDMTLMVLVLPSPYDTLVYPIKTTSQLTREVYTTAIGT 302
DB 239 LNNLRGTNAESWLRYNQFRDLTLGLVLDLVALFPSTDTTYPINTSAQLTREIYTDPIGR 298
QY 303 VHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRNSNTQYMMWVG 362
DB 299 TNAPSGFASTWNNFNAPSFAIEAIFRPPHLLDPPEQTIYSSASSRWSSTQHMWYVG 358

US-10-019-823b-59.rai

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US-08-881-340-4

Query Match 65.7%; Score 2459; DB 2; Length 1229;  
Best Local Similarity 64.8%; Pred. No. 2.7e-217; Indels 36; Gaps 5;  
Matches 470; Conservative 91; Mismatches 128;

363 HRLSPRIGGALNTSTQGST-NTSINPVTLOFTSRDVRVYTESLAGNLFLTOPVNGVPRV 421  
359 HRLNFRPIGGTLNTSTQGLTNTSINPVTLOFTSRDVRVYTESNAGTNILFTTPVNGVPWA 418  
422 DFHWKFTPLPIASDNFYLG-----YAGVGTQLODSENELPPTGQPNYESYSHRLS 474  
419 RFNE-----INPQNIYERGATTYSQPYQGVIGLDFSETELPPTTERPNYESYSHRLS 472  
475 HIGLISASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 534  
473 HIGLIIGTLKAPVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 532  
535 ILRRTNTGTGDIRVNIINPPFAQRYRIRYASTTDLQFTSINGKAINOGNFSATWNRG 594  
533 ILRRTNTGTGDIRVNIINPPFAQRYRIRYASTTDLQFTSINGKAINOGNFSATWNRG 592  
595 EDLOYKFTRTIGFTTPFSFSDVQSTFTIGAWNFSGNEVYDRIEFPVPEVVEAYEYDFE 654  
593 DNLEYSRFTAGFTFPFNFLNAQSTFTLGAQSPFN-QEVYDRIEFPVPEVVEAYEYDFE 651  
655 KQAEKVYALFTSTNPRGLKTDVYDHYDQVSNLVESLDEFLYDKRELPEIKVYAKQIH 714  
652 RAQKAVNALFTSTNPRGLKTDVYDHYDQVSNLVESLDEFLYDKRELPEIKVYAKQIH 711  
715 IERNM 719  
712 DERNL 716

RESULT 11

US-08-881-340-4  
; Sequence 4, Application US/08881340  
; Patent No. 5942658  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yiping  
; APPLICANT: Jany, Christine S.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
; ADDRESSEE: Nadel  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,340  
; FILING DATE: 24-JUN-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/100,709  
; FILING DATE: 29-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Egolf, Christopher  
; REGISTRATION NUMBER: 27633  
; REFERENCE/DOCKET NUMBER: 7205-49  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-757-1590  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1229 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-881-340-4

Query Match 65.7%; Score 2459; DB 2; Length 1229;  
Best Local Similarity 64.8%; Pred. No. 2.7e-217; Indels 36; Gaps 5;  
Matches 470; Conservative 91; Mismatches 128;

3 LKNPDKHOSLSNAKVDKIATDSLKNETDIELKNNMDEYLRMSEHSIDPPFVSASTIQT 62  
20 VSNPSTQNLSPDARI-----EDSLCVAEVNNDIDPFVSASTVQT 58  
63 GIGIAGKILGTGVPPFAGQIASLYSIFILGELMPKQKQWEIFMEHVEIINOKILTVAEN 122  
59 GINIAGRILGVLGVPFAGQLASFYSLVGLWPGSRDPWEIFLVEHQIOLRQIQTENTRN 118  
123 KALSDRLGLGDALAYVHESLESVENNTRARSVWNOYIALEIMFVKQLSPFAVSGEE 182  
119 TAIARLEGGLRGYRYSQQALETWLDNRNDARSILERYVALELDITTAIFLRNEE 178  
183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSASELSTFYNQOVERTRDYSCHIKWYNTG 242  
179 VLLAVYAQAANLHLLLRDASLFGSEWGMASDVNOYQOIRYITEYSNHCQWYNTG 238  
243 LNNLRGTNAKSWRYNQFRKDWTLMLVDLVALFSDYDVLVPIKTTTSOLTREVYDAIGT 302  
239 LNNLRGTNAESWRYNQFRKDWTLMLVDLVALFSDYDVLVPIKTTTSOLTREVYDAIGT 298  
303 VHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYISLLSWNTQYNNMGG 362  
299 TNAPSGFASTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYISLLSWNTQYNNMGG 358  
363 HRLSPRIGGALNTSTQGST-NTSINPVTLOFTSRDVRVYTESLAGNLFLTOPVNGVPRV 421  
359 HRLNFRPIGGTLNTSTQGLTNTSINPVTLOFTSRDVRVYTESNAGTNILFTTPVNGVPWA 418  
422 DEHWKFTPLPIASDNFYLG-----YAGVGTQLODSENELPPTGQPNYESYSHRLS 474  
419 RFNE-----INPQNIYERGATTYSQPYQGVIGLDFSETELPPTTERPNYESYSHRLS 472  
475 HIGLISASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 534  
473 HIGLIIGTLKAPVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 532  
535 ILRRTNTGTGDIRVNIINPPFAQRYRIRYASTTDLQFTSINGKAINOGNFSATWNRG 594  
533 ILRRTNTGTGDIRVNIINPPFAQRYRIRYASTTDLQFTSINGKAINOGNFSATWNRG 592  
595 EDLOYKFTRTIGFTTPFSFSDVQSTFTIGAWNFSGNEVYDRIEFPVPEVVEAYEYDFE 654  
593 DNLEYSRFTAGFTFPFNFLNAQSTFTLGAQSPFN-QEVYDRIEFPVPEVVEAYEYDFE 651  
655 KQAEKVYALFTSTNPRGLKTDVYDHYDQVSNLVESLDEFLYDKRELPEIKVYAKQIH 714  
652 RAQKAVNALFTSTNPRGLKTDVYDHYDQVSNLVESLDEFLYDKRELPEIKVYAKQIH 711  
715 IERNM 719  
712 DERNL 716

RESULT 12

US-07-951-715A-7  
; Sequence 7, Application US/07951715A  
; Patent No. 5625136  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.



```
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-951-715A-7

Query Match 61.9%; Score 2314.5; DB 1; Length 1207;
Best Local Similarity 65.4%; Pred. No. 5.7e-204;
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;

Qy 40 EDYLRMSEHSDPVSASTQIGIGIAGKILGTGVFPAGQIASLYSFLGELWPKGKS 99
Db 10 EDSLCIAEGNNIDPVSASTVQTGINIAGRIAGLVGVPFAGQLASFYSLVGLWPRGRD 69
Qy 100 QWEIFMHEVEEIIKILTYARKKALSDLEGLDALAVHSESVENRNTARSVVK 159
Db 70 QWEIFLHEVEQLINQITENARTALRQGLSDSPRAYQOQSLDLENRDDARTSVLY 129
Qy 160 NOYIALFMVOKLFPVSGSEVPLPIYAQANLHLLLRDASIFGKEWGLSASEIST 219
Db 130 TQYIALEDFLNMPLFATNQEVPLLMVYAQANLHLLLRDASIFGSEFGLTSQEIQR 189
Qy 220 FYNQVERTRDSDHCIKWYNTGLNLRGNKSWRYNQFRKDMTLMVLDLVALPSPYD 279
Db 190 YBERQVERTRDSDYCVWNTGLNSLRGTNAASWRYNQFRDRLTLGLVLDLVALPSPYD 249
Qy 280 TLVYPIKTSQLTREYVTDGIVTHNQAFASITWNNNAPSATAEAAVIRSPHLLDEL 339
Db 250 TRTPYNTSAQLFREYVTDGIVTHNQAFASITWNNNAPSATAEAAVIRSPHLLDEL 307
Qy 340 EKVITYSLRSWNTOTMNMWGHRLSRPIGGALNTSTOGSTNTSINPVTLQFTGRDYY 399
Db 308 EKVITYSASRWNTKHTMYRGTHTQSRPIGGALNTSTIGATNTSINPVTLFASRDYY 367
Qy 400 RTESLAGLNF--LTQPVNGVPRVDFHWKPP--TLPIASDNFYLYGAGVGTQLQDSENEL 456

APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-951-715A-7

RESULT 13
US-08-459-448A-7
; Sequence 7, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
```

REGISTRATION NUMBER: 40403  
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8582  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-459-448A-7

Query Match 61.9%; Score 2314.5; DB 2; Length 1207;  
Best Local Similarity 65.4%; Pred. No. 5,7e-204;  
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;

QY 40 EDYLRMSEHSIDPFVSASTIQTGIGTAGKILGTGLGVPPFAGQIASLYSFLGELWPKGKS 99  
DB 10 EDSLCAIEGNNDIPFVSASTVQTGINIAGRILGLVGVPPFAGQIASLYSFLGELWPKG 69  
QY 100 QWEIFMEHVEEIIINQKILTYARNKALSDRLGLGDALAVYHESLESWVENRNNTRARSVK 159  
DB 70 QWEIFLEHVEQLINQITENARNALARLOGLGDSFRAYQOSLEDWLENDDARTSVLY 129  
QY 160 NOYIALELMFVKLPSPAVSGEEVPLPIYAQAANLHLLLRDASIFGKMWGLSASIST 219  
DB 130 TOYIALELDLFLNAPLFAIRNQEVPLLMVYAQAANLHLLLRDASIFGKMWGLSASIST 189  
QY 220 FYNQVETRDYSDHCIKWNTGLNLRGTNAKSWRYNQPRKDMTLMVLDLVALFPSYD 279  
DB 190 YFERQVETRDYSDHCIKWNTGLNLRGTNAKSWRYNQPRKDMTLMVLDLVALFPSYD 249  
QY 280 TLVYPIKTSQUTREVYTDALGTVHPNQAFSTWYNNNAPSFAIAAIVRSPLHLDPL 339  
DB 250 TRTYPINTSAQLTREYVTDALGTAVN--MASMWNWNNAPSFAIAAIVRSPLHLDPL 307  
QY 340 EKVTIYLLSRWNTQYNNMGHLESPRIGGALNTSTQGSTNTSINPVTLOFTSRDVI 399  
DB 308 EQLTIFSSASSRNSRTHRWYRGHTIQSRPIGGGLNTSTHGTATNTSINPVTLRASRDVI 367  
QY 400 RTESLAGMLF--LQPVNGVPRVDFHWKFP--TLPIASDNFYLYGYAGVGQLOQDSNEL 456  
DB 368 RTESYAGVLLWGLYLEPIHGVPTFRFNTPNQISDRGTANYSQPYESGLQLKXSETEL 427  
QY 457 PRTTQGPYNSYSHRLSHIGLISAHVKALVSWTHESADRTNTEPNSITQPLVKAF 516  
DB 428 PPETTERPNYESHRLSHIGLISAHVKALVSWTHESADRTNTEPNSITQPLVKAF 487  
QY 517 NLSSGAAVRGPQFTGGDLRLTNTGTGDIRVINPFPFAQRYRIRYASTTDLQPHTS 576  
DB 488 ELPOGTVVRGPGFTGGDLRLTNTGTGDIRVINPFPFAQRYRIRYASTTDLQPHTS 547  
QY 577 INKAINQGNFSAATMRGDELDTKPTRTGFTTPFSDFVQSTFTTIGAWNFGSGNEVYD 636  
DB 548 RGGTTVNNFRFLRTMNSGDELKYGNFVRRAFTPTFTQIQDIIRTS:QGLSGNGEVYD 607  
QY 637 RIEFVPEVTEYAEYDFEKAQKVTALFTSTNPRGLKTDVXDYHIDQVSNLVESLDEFY 696  
DB 608 KIEIIVTATFEAYDLEAQAQAVNALFTNTPRRLKTDVTDYHIDQVSNLVACLSDEF 667  
QY 697 LDEKRELFEIVKAKQIHIERNM 719  
DB 668 LDEKRELLEKVKYAKRLSDERNL 690

RESULT 14  
US-08-459-595A-7  
Sequence 7, Application US/08459595A  
Patent No. 6018104  
GENERAL INFORMATION:  
APPLICANT: Kozziel, Michael G.  
APPLICANT: Desai, Nalini M.

APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6018104artis Corporation  
STREET: Patent & Trademark Dept., 520 White Plains  
STREET: Rd., POB 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,595A  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: 40403  
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8582  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-459-595A-7

Query Match 61.9%; Score 2314.5; DB 3; Length 1207;  
Best Local Similarity 65.4%; Pred. No. 5,7e-204;  
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;

QY 40 EDYLRMSEHSIDPFVSASTIQTGIGTAGKILGTGLGVPPFAGQIASLYSFLGELWPKGKS 99  
DB 10 EDSLCAIEGNNDIPFVSASTVQTGINIAGRILGLVGVPPFAGQIASLYSFLGELWPKG 69  
QY 100 QWEIFMEHVEEIIINQKILTYARNKALSDRLGLGDALAVYHESLESWVENRNNTRARSVK 159  
DB 70 QWEIFLEHVEQLINQITENARNALARLOGLGDSFRAYQOSLEDWLENDDARTSVLY 129  
QY 160 NOYIALELMFVKLPSPAVSGEEVPLPIYAQAANLHLLLRDASIFGKMWGLSASIST 219  
DB 130 TOYIALELDLFLNAPLFAIRNQEVPLLMVYAQAANLHLLLRDASIFGKMWGLSASIST 189  
QY 220 FYNQVETRDYSDHCIKWNTGLNLRGTNAKSWRYNQPRKDMTLMVLDLVALFPSYD 279

Db 190 YYERQVTRDYSDYCVETWNTGLNSLRGTNAASWRYNQFRDLTLGVLDLVALPESYD 249  
Qy 280 TLVYPIKTSQLTREVYTDAGTVHPNQAFASFTWYNNAPSFSAEAAVIRSHLLDPL 339  
Db 250 TRTYPINTSAQLREVYTDAGTGVN--MASWYNNAPSFSAEAAVIRSHLLDPL 307  
Qy 340 EKVTIYLLSRWNTQYMMWGHRLSRPIGGALNTSTOGSTNTSINPVTLOFTSRDVI 399  
Db 308 EQLTIFSASSRWNTRHMTYWRGHTIQSRPIGGALNTSTHGATNTSINPVTLFASRDVI 367  
Qy 400 RTESLAGLNF--LTQPVNGVPRVDHKKFP-TLPIASDNFYVLGVAGVGTQLODSENEL 456  
Db 368 RTESYAGVLLWGIYLEPIHGVPTVRFNTNPQISDRGTANYSQPYESPLQLKDSSETL 427  
Qy 457 PPETTGQPNYESYSHRLSHIGLISASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAF 516  
Db 428 PPETTERPNYESYSHRLSHIGLILQSRVNVVSWTHRSADRNTTIGPNRITQIPWKAS 487  
Qy 517 NLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNNPPFAQRYVRIRYASTTDLQFHTS 576  
Db 488 ELPGQTTVVRGPGFTGGDILRRNTGTGDIRVNVGPLTQRYRIGFRYASTVDFDFVS 547  
Qy 577 INKAINQGNFSATMNRGDLKYKTRTIGFTTPPSFSDVQSTFTIGAMNFSNGEYVID 636  
Db 548 RGGTTVNNFRFLRTMNSGDELKYGNFVRRRAFTTPTFTQIDIIRTSIQGLSGNGEYVID 607  
Qy 637 RIBFPVPEVITYEAYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSEFY 696  
Db 608 KIEIIPVTATFEAYDLERAQEAVALFTNTNPRRLKTDVTDHYIDQVSNLVACLSDSEFC 667  
Qy 697 LDKRELFEIVYAKQIHBRNM 719  
Db 668 LDEKRELLEKVKYAKRLSDERNL 690

## RESULT 15

US-08-459-504B-7  
Sequence 7, Application US/08459504B  
Patent No. 6075185  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
APPLICANT: Desai, Nalini M.  
APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESS: No. 6075185artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,504B

## FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/459,595  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-459-504B-7

Query Match 61.9%; Score 2314.5; DB 3; Length 1207;

Best Local Similarity 65.4%; Pred. No. 5.7e-204;

Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;

Qy 40 EDYLRMSEHSDPPFVSASTIQTGIGIAGILGTGVPPAGQIASYFSLGLSLPKGKS 99

Db 10 EDSLCAIEGNIDPPFVSASTVQTGINIAGRILGLVGVPPAGQIASYFSLGLSLPRGRD 69

Qy 100 QWEIFMEHVEEIIINOKILTYARNKALSLRGLDALAVVHESLESVVENRNNTRASVVK 159

Db 70 QWEIFLHEVEQLINQOITENARNTALRQGLGDSFRAVQCSLEDELNRDDARTRSVLY 129

Qy 160 NOYIALELMFVOKLPSFAVSGBEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEIST 219

Db 130 TQYIALELDFLNAFLFAIRNQEVPMLVYAQAANLHLLLRDASIFGSEFGLTSQEIQR 189

Qy 220 FNRQVTRDYSDHCKIWKYNTGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALPESYD 279

Db 190 YYERQVTRDYSDYCVETWNTGLNSLRGTNAASWRYNQFRDLTLGVLDLVALPESYD 249

Qy 280 TLVYPIKTSQLTREVYTDAGTVHPNQAFASFTWYNNAPSFSAEAAVIRSHLLDPL 339

Db 250 TRTYPINTSAQLREVYTDAGTGVN--MASWYNNAPSFSAEAAVIRSHLLDPL 307

Qy 340 EKVTIYLLSRWNTQYMMWGHRLSRPIGGALNTSTOGSTNTSINPVTLOFTSRDVI 399

Db 308 EQLTIFSASSRWNTRHMTYWRGHTIQSRPIGGALNTSTHGATNTSINPVTLFASRDVI 367

Qy 400 RTESLAGLNF--LTQPVNGVPRVDHKKFP-TLPIASDNFYVLGVAGVGTQLODSENEL 456

Db 368 RTESYAGVLLWGIYLEPIHGVPTVRFNTNPQISDRGTANYSQPYESPLQLKDSSETL 427

Qy 457 PPETTGQPNYESYSHRLSHIGLISASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAF 516

Db 428 PPETTERPNYESYSHRLSHIGLILQSRVNVVSWTHRSADRNTTIGPNRITQIPWKAS 487

Qy 517 NLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNNPPFAQRYVRIRYASTTDLQFHTS 576

Db 488 ELPGQTTVVRGPGFTGGDILRRNTGTGDIRVNVGPLTQRYRIGFRYASTVDFDFVS 547

Qy 577 INKAINQGNFSATMNRGDLKYKTRTIGFTTPPSFSDVQSTFTIGAMNFSNGEYVID 636

Db 548 RGGTTVNNFRFLRTMNSGDELKYGNFVRRRAFTTPTFTQIDIIRTSIQGLSGNGEYVID 607

Qy 637 RIBFPVPEVITYEAYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSEFY 696

Db 608 KIEIIPVTATFEAYDLERAQEAVALFTNTNPRRLKTDVTDHYIDQVSNLVACLSDSEFC 667

Qy 697 LDEKRELFEIVKYAKQIHIERNM 719  
Db 668 LDEKRELLEKVKYAKRLSDERNL 690

Search completed: February 14, 2005, 20:59:11  
Job time : 24.3302 secs

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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:20:21 ; Search time 98.3514 Seconds  
(without alignments)  
2827.419 Million cell updates/sec

Title: US-10-019-823B-59

Perfect score: 3742

Sequence: 1 MLKRPDKHQLSSNAKVDK.....KRELFEIVKAKIHERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3742	100.0	719	4	AAB66912
2	3742	100.0	719	6	AAB66912 Insectici
3	3598	96.2	719	7	AAD74717 B. thurin
4	3546	94.8	719	2	AAB49089 Bacillus
5	3520	94.1	719	4	AAB66908 Insectici
6	3520	94.1	719	6	AAB66908 Insectici
7	3520	94.1	719	8	ADR89421
8	3516	94.0	719	4	AAB66910 Insectici
9	3516	94.0	719	6	AAB66910 Insectici
10	3511	93.8	719	4	AAB66911
11	3509	93.8	719	4	AAB66911 Insectici
12	3509	93.8	719	6	AAB66911 Insectici
13	3503	93.6	719	4	AAB66909 Insectici
14	3503	93.6	719	6	AAB66909 Insectici
15	3499	93.5	719	2	AAR08041
16	3488.5	93.2	718	6	AAB66907
17	3482.5	93.1	718	4	AAB66907 Insectici
18	3468.5	90.0	710	4	AAU02041
19	3311	88.5	719	3	ABB07073 Bacillus
20	3060	81.8	1217	4	AAU02092
21	2645	70.7	1208	8	AAU02093
22	2460	65.7	1230	8	ADK98484
23	2460	65.7	1230	8	ADK98489 B thuring
24	2460	65.7	1230	8	ADK98481 B thuring
25	2460	65.7	1230	8	ADK98491 B thuring

26	2460	65.7	1230	8	ADK98487
27	2459	65.7	1229	2	AAR54074
28	2459	65.7	1229	2	AAR54074 CryETs. 2
29	2459	65.7	1229	2	AAW35259 Bacillus
30	2459	65.7	1229	2	AAW17699 CryETs. 3
31	2459	65.7	1229	2	AAW87633 CryETs pr
32	2459	65.7	1229	2	AAW30923 B. thurin
33	2459	65.7	1229	8	ADK98479 B thuring
34	2322.5	62.1	1228	2	AAR50955 Bacillus
35	2317.5	61.9	1209	4	AAU02094
36	2308.5	61.7	1227	2	AAV31990 Chimeric
37	2243	59.9	1227	2	AAW44321 Bacillus
38	2243	59.9	1227	4	AAW44321 Bacillus
39	2234	59.7	1227	4	AAU02046 B. thurin
40	2233.5	59.7	488	2	AAW44322 Bacillus
41	2219	59.3	1186	4	AAW19947
42	2198.5	58.8	1221	4	AAV16796 Amino aci
43	2184.5	58.4	1221	4	AAU00420 B. thurin
44	2170.5	58.0	1228	4	AAW44628 Amino aci
45	2168.5	58.0	1228	4	AAU02039 B. thurin

#### ALIGNMENTS

RESULT 1  
AAB66912  
ID AAB66912 standard; protein; 719 AA.  
XX AC AAB66912;  
XX DT 12-APR-2001 (first entry)  
XX DE Insecticidal protein cryIb1.  
XX KW Insecticide; transgenic plant; insect-resistance.  
XX OS Paecilomyces sp.  
XX PN WO200100841-A1.  
XX PD 04-JAN-2001.  
XX PF 23-JUN-2000; 2000WO-GB002457.  
XX PR 29-JUN-1999; 99GB-00015215.  
XX PR 23-DEC-1999; 99GB-00030536.  
XX (ZENE ) ZENECA LTD.  
XX Griffin JL, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
XX Vincent JL, Lee MD;  
XX WPI; 2001-123015/13.  
XX Novel insecticidal protein obtained from species of Paecilomyces for  
XX controlling insects, and for insect-resistant transgenic plant  
XX production.  
XX Claim 14; Page 64-66; 72pp; English.  
XX The present invention relates to novel insecticidal proteins obtained  
XX from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
XX insecticidal proteins can be used to produce transgenic plants, which are  
XX insect-resistant. Also, the insecticidal proteins are useful for  
XX controlling insects by providing them at a locus where insects feed  
XX Sequence 719 AA;  
XX Query Match 100.0%; Score 3742; DB 4; Length 719;  
XX Best Local Similarity 100.0%; Pred. No. 2.1e-300;  
XX Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKLNPKHQSLSSNAKVDKIATDSLKNETDIELKNNNEDYLRMSEHSIDPFVSASTI	60	PI	Vincent JL, Viner R;
Db	1	MKLNPKHQSLSSNAKVDKIATDSLKNETDIELKNNNEDYLRMSEHSIDPFVSASTI	60	XX	WPI; 2003-175137/17.
Qy	61	QTGIGIAGKILGTGVPPAGQIASLYSFIILGELWPKGSQWEIFMEHVVEIINQKILTYA	120	XX	New insecticidal protein comprising an X-glycine motif at the amino-
Db	61	QTGIGIAGKILGTGVPPAGQIASLYSFIILGELWPKGSQWEIFMEHVVEIINQKILTYA	120	PT	terminus, useful as an active ingredient of a pesticide.
Qy	121	RNKALSDLRGLGDALAVYHESLESVENNRNTRRSVVKVQYIALELMFVKQLPSFAVSG	180	XX	Claim 12; Page 56-58; 67pp; English.
Db	121	RNKALSDLRGLGDALAVYHESLESVENNRNTRRSVVKVQYIALELMFVKQLPSFAVSG	180	CC	The invention relates to insecticidal protein comprising an X-glycine
Qy	181	EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNQVERTDYSDHCIKWYN	240	CC	motif at the amino-terminus. Polynucleotide or DNA constructs of the
Db	181	EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNQVERTDYSDHCIKWYN	240	CC	invention are useful for producing plants or plant parts that are
Qy	241	TGLNNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVTDAI	300	CC	resistant to insects. The protein or synergistic combination is useful as
Db	241	TGLNNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVTDAI	300	CC	an active ingredient of a pesticide or for controlling insects.
Qy	301	GTVHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW	360	CC	Antibodies raised to the insecticidal proteins can be used to identify
Db	301	GTVHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW	360	CC	other proteins with insecticidal activity. The present sequence is
Qy	361	GGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVYRTESLAGLNFLTPQVNGVPR	420	CC	Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This
Db	361	GGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVYRTESLAGLNFLTPQVNGVPR	420	CC	sequence is used in the invention
Qy	421	VDHFWKFTPLPIASDNFYILGAVGVTQLQDSENELPPETTGQPNYESYSHRSHIGLIS	480	XX	Sequence 719 AA;
Db	421	VDHFWKFTPLPIASDNFYILGAVGVTQLQDSENELPPETTGQPNYESYSHRSHIGLIS	480	Qy	Query Match 100.0%; Score 3742; DB 6; Length 719;
Qy	481	ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN	540	Db	Best Local Similarity 100.0%; Pred. No. 2.1e-300;
Db	481	ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN	540	Qy	Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	541	TGTFGDIRVINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK	600	Db	1 MKLNPKDQKQSLSSNAKVDKIATDSLKNETDIELKNNNEDYLRMSEHSIDPFVSASTI 60
Db	541	TGTFGDIRVINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK	600	Db	1 MKLNPKDQKQSLSSNAKVDKIATDSLKNETDIELKNNNEDYLRMSEHSIDPFVSASTI 60
Qy	601	TFRTIGFTTFFSDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVVEVYEAEDFEKAQEKV	660	Qy	61 QTGIGIAGKILGTGVPPAGQIASLYSFIILGELWPKGSQWEIFMEHVVEIINQKILTYA 120
Db	601	TFRTIGFTTFFSDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVVEVYEAEDFEKAQEKV	660	Db	61 QTGIGIAGKILGTGVPPAGQIASLYSFIILGELWPKGSQWEIFMEHVVEIINQKILTYA 120
Qy	661	TALFTSTNPRGLKTDVKDHYHDQVSNLVESLSDDEFYLDKRELFEIVKYAKQIHIERNM	719	Qy	121 RNKALSDLRGLGDALAVYHESLESVENNRNTRRSVVKVQYIALELMFVKQLPSFAVSG 180
Db	661	TALFTSTNPRGLKTDVKDHYHDQVSNLVESLSDDEFYLDKRELFEIVKYAKQIHIERNM	719	Db	121 RNKALSDLRGLGDALAVYHESLESVENNRNTRRSVVKVQYIALELMFVKQLPSFAVSG 180
RESULT 2					181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNQVERTDYSDHCIKWYN 240
ID	AAE36276 standard; protein; 719 AA.				181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNQVERTDYSDHCIKWYN 240
AC	AAE36276;				241 TGLNNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVTDAI 300
XX	26-JUN-2003 (first entry)				241 TGLNNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVTDAI 300
DT	B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIb1.				301 GTVHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW 360
XX	Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.				301 GTVHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW 360
XX	Bacillus thuringiensis.				361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVYRTESLAGLNFLTPQVNGVPR 420
KW	WO200298911-A2.				361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVYRTESLAGLNFLTPQVNGVPR 420
XX	12-DEC-2002.				421 VDFHFWKFTPLPIASDNFYILGAVGVTQLQDSENELPPETTGQPNYESYSHRSHIGLIS 480
PD	30-MAY-2002; 2002WO-GB0002666.				421 VDFHFWKFTPLPIASDNFYILGAVGVTQLQDSENELPPETTGQPNYESYSHRSHIGLIS 480
PF	07-JUN-2001; 2001GB-00013900.				481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
XX	(SYGN ) SYNGENTA LTD.				481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
XX					541 TGTFGDIRVINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
XX					541 TGTFGDIRVINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
XX					601 TFRTIGFTTFFSDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVVEVYEAEDFEKAQEKV 660
XX					601 TFRTIGFTTFFSDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVVEVYEAEDFEKAQEKV 660
XX					661 TALFTSTNPRGLKTDVKDHYHDQVSNLVESLSDDEFYLDKRELFEIVKYAKQIHIERNM 719
XX					661 TALFTSTNPRGLKTDVKDHYHDQVSNLVESLSDDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 3  
 ADM74717  
 ID ADM74717 standard; protein; 719 AA.  
 XX  
 AC ADM74717;  
 DT 03-JUN-2004 (first entry)  
 DE B. thuringiensis cryIIel SEQ ID NO:2.  
 XX  
 KW cryII; toxicity; lepidoptera; cryIaB; coleoptera; diptera;  
 cryIIel.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 PN CN1401772-A.  
 XX  
 PD 12-MAR-2003.  
 XX  
 PF 20-AUG-2001; 2001CN-00124163.  
 XX  
 PR 20-AUG-2001; 2001CN-00124163.  
 XX  
 PA (PLAN-) PLANT PROTECTION INST CHINESE ACAD AGRIC.  
 XX  
 PI Song F, Zhang J, Huang D;  
 XX  
 DR WPI; 2003-442339/42.  
 DR N-PSDB; ADM74716.  
 XX  
 PT Bacillus thuringiensis cryI gene, expression vector, nucleotide sequence  
 with high-toxicity to lepidoptera pests, encoded protein, primer  
 sequences and the shuttle vector pSX422b, useful as a pesticide.  
 XX  
 PS Example 3; SEQ ID NO 2; 29pp; Chinese.  
 XX  
 CC The invention relates to a novel Bacillus thuringiensis cryI gene, gene  
 combination, expression vector, nucleotide sequence of the B  
 thuringiensis cryI gene with high-toxicity to lepidoptera pests and the  
 amino acid sequence of the protein encoded by it, cooperative use of the  
 cryI gene with the expression product of cryIaB or cryIaA, primer  
 sequences for expressing the genes, and the constructed shuttle vector  
 pSX422b. The gene in combination with the cryIaB or cryIaA genes  
 displays high toxicity to the lepidoptera, coleoptera and diptera pests.  
 CC The present sequence represents the cryIIel protein.  
 XX  
 SQ Sequence 719 AA;  
 Query Match 96.2%; Score 3598; DB 7; Length 719;  
 Best Local Similarity 95.1%; Pred. No. 1.8e-288;  
 Matches 684; Conservative 23; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 MKLNKDPKQSLSSNAKVDAKIDTSKNETDIELKNNEEDYLRMSEHSIDPFVSASTI 60  
 DB 1 MKLNKDPKQSLSSNAKVDAKIDTSKNETDIELKNNEEDYLRMSEHSIDPFVSASTI 60  
 QY 61 QTGIGTAGKTLGTLPFPAGQIASLYSFTLGLWPKGSQWEIPMEHVETINQKILTYA 120  
 DB 61 QTGIGTAGKTLGTLPFPAGQIASLYSFTLGLWPKGSQWEIPMEHVETINQKILTYA 120  
 QY 121 RNKALDRLGLDALAVYHESLESSEVENNRNTRARSVVKNOYIALELMFVKQLPSFAVSG 180  
 DB 121 RNALADRLGLDALAVYHESLESSEWIKRNARATSVKKSQYIALELLFVKQLPSFAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSGASEISTPYNRQVTRDYSCHIKWYN 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASVFGKEWGLSGQISQISTPYNRQVTRDYSCHIKWYS 240  
 QY 241 TGLNLRGNTAKSWRYNQFRKDMTLMVLDLVALFSDYTLVYPIKTSQLTREVYTDAI 300  
 DB 241 TGLNLRGNTAKSWRYNQFRKDMTLMVLDLVALFSDYTLVYPIKTSQLTREVYTDAI 300

QY 301 GTVHPNQAPASTTWNNNAPSPSAEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQNMNMW 360  
 DB 301 GTVHPNASPASTTWNNNAPSPSAEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQNMNMW 360  
 QY 361 GGHRLSRPIGALANTSTOGSTNTSINPVTLOFTSRDVTYRTSLAGNLFLTOPVNGVPR 420  
 DB 361 GGHRLSFRITGGVLTSTOGSTNTSINPVTLPFTSRDVTYRTSLAGNLFLTOPVNGVPR 420  
 QY 421 VDFHMKFTPLPIASDNFFYLYGAGVGTQLQDSENELPPTTGPQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHMKFATLPIASDNFFYLYGAGVGTQLQDSENELPPTTGPQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDIILRTN 540  
 DB 481 ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDIILRTN 540  
 QY 541 TGTFGDIRVININPPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAITMNRGEULDYK 600  
 DB 541 TGTFGDIRVININPPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAITMNRGEULDYK 600  
 QY 601 TERTIGFTTFFSFDVQSTFTIGAMNFFSGNEVYIDRIEFVPVEVTYEAEDFEKAQEKV 660  
 DB 601 TERTVGFTTFFSFDVQSTFTIGAMNFFSGNEVYIDRIEFVPVEVTYEAEDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDDEFYLDKRELFEIVKAKQIHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDDEFYLDKRELFEIVKAKQIHIERNM 719  
 RESULT 4  
 AAW49089  
 ID AAW49089 standard; protein; 719 AA.  
 XX  
 AC AAW49089;  
 XX  
 DT 26-OCT-1998 (first entry)  
 XX  
 DE Bacillus thuringiensis isolate C-18 crystal II protein.  
 XX  
 KW Bacillus thuringiensis isolate C-18; BtC-18; Bt; crystal II; CryII;  
 sporulation; insecticidal activity; pest control; rootworm; agriculture.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 PN WO9830700-A1.  
 XX  
 PD 16-JUL-1998.  
 XX  
 PF 09-JAN-1998; 98WO-US000357.  
 XX  
 PR 10-JAN-1997; 97US-0035361P.  
 XX  
 PA (OSMA/) OSMAN Y A.  
 PA (MADK/) MADKOUR M A.  
 PA (BULL/) BULLA L A.  
 XX  
 PI Osman YA, Madkour MA, Bulla LA;  
 XX  
 DR WPI; 1998-399145/34.  
 DR N-PSDB; AAW32950.  
 XX  
 PT Bacillus thuringiensis strain with broad spectrum pesticidal activity -  
 useful as insecticidal agent, and proteins and nucleotide(s) isolated  
 from strain, useful as insecticides and to produce resistant plants.  
 XX  
 PS Disclosure; Fig 5; 50pp; English.  
 XX  
 CC The present sequence represents the Bacillus thuringiensis (Bt) isolate C  
 -18 (BtC-18) crystal II (CryII) protein. Bt is a bacterium which produces  
 crystalline inclusions during sporulation, composed primarily of a single  
 polypeptide. These crystal proteins (Cry, e.g. class CryII) exhibit highly  
 specific insecticidal activity, so that most Bt strains kill insects  
 belonging to only one order. The invention claims for a stable BtC-18

CC strain which produces at least three different types of crystal proteins  
CC and is therefore claimed to be capable of killing insects from at least  
CC three orders, thus providing a suitable alternative for broad-spectrum  
CC agricultural pest control. The isolated crystal proteins, for e.g. CryII  
CC protein, can also be applied to control pests (alone or with e.g. other  
CC insecticidal proteins) and is useful to produce antibodies to isolate  
CC similar proteins from other strains/organisms. The invention also  
CC provides a BtC-18 toxin protein which is active against rootworms. The  
CC Cry encoding nucleic acids are claimed to be useful for expressing the  
CC plant products, or in micro-organisms, which can be applied to protect  
CC agricultural crops. They are also useful to isolate nucleic acids  
CC encoding potentially pesticidal proteins from other strains/organisms by  
CC hybridisation  
XX  
XX Sequence 719 AA;

Query Match 94.8%; Score 3546; DB 2; Length 719;  
Best Local Similarity 95.0%; Pred. No. 3.5e-284; Indels 0; Gaps 0;  
Matches 683; Conservative 11; Mismatches 25;

QY 1 M K L N P D K H Q S L S N A K V D K I A T D S L K N E T D I E L K N M N E D Y L R M S E H S I D P F V S A S T I 60  
DB 1 M K L N P D K H Q S L S N A K V D K I A T D S L K N E T D I E L K N M N E D Y L R M S E H S I D P F V S A S T I 60

QY 61 Q T G I G I A K I L G T L G V P P A G Q I A S L Y S F I L G E L W P K G S Q W E I F M E H V E E I I N K I L T Y A 120  
DB 61 Q T G I G I A K I L G T L G V P P A G Q I A S L Y S F I L G E L W P K G S Q W E I F M E H V E E I I N K I L T Y A 120

QY 121 R N K A L S D L R G I G D A L A V Y H S E S L E S V E N R N T R A S V V K N Q Y I A L E M F V K L P S F A V S G 180  
DB 121 R N K A L T D L K G I G D A L A V Y H S E S L E S V E N R N T R A S V V K N Q Y I A L E M F V K L P S F A V S G 180

QY 181 E V P L L P I Y A Q A A N L H L L R D A S I F G K E W G L S A S E I S T F Y N Q R V E R T R D Y S D H C I K W Y N 240  
DB 181 E V P L L P I Y A Q A A N L H L L R D A S I F G K E W G L S A S E I S T F Y N Q R V E R T R D Y S D H C I K W Y N 240

QY 241 T G L N L R G T N A K S W R Y N Q R K D M T L M V L D L V A L P P S Y D T L V P I K T S Q L T R E V Y T D A I 300  
DB 241 T G L N L R A T N G S W R Y N Q R K D I E L M V L D L V R P P S D T L V P I K T S Q L T R E V Y T D A I 300

QY 301 G T V H P N Q A P A S T T W Y N N N A P S F A I E A A V I R S P H L L D F L E K V T I Y S L L S R W S N T Q Y N M W 360  
DB 301 G T V D P N Q A L R S T T W Y N N N A P S F A I E A A V I R S P H L L D F L E K V T I Y S L L S R W S N T Q Y N M W 360

QY 361 G G H R L E S R P I G A L N T S T O G S T N T S I N P V T L Q F T S R D Y R T E S L A G L N L F L T Q P V N G V P R 420  
DB 361 G G H R L E S R P I G A L N T S T O G S T N T S I N P V T L Q F T S R D Y R T E S L A G L N L F L T Q P V N G V P R 420

QY 421 V D P H K F P T L P I A S D N F Y I L G V A G V G T Q L Q D S E N E L P P E T T Q P N Y E S Y S H R L S H I G L I S 480  
DB 421 V D P H K F P T L P I A S D N F Y I L G V A G V G T Q L Q D S E N E L P P E T T Q P N Y E S Y S H R L S H I G L I S 480

QY 481 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G G D I L R T N 540  
DB 481 G S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G G H I L R T K 540

QY 541 T C F T G I R V N I N P P E A Q R Y R V R Y A S T T D L Q P H T S I N K A I N O G N F S A T M N R G E D L D Y K 600  
DB 541 S G T F G H I R V N I N P P E A Q R Y R V R Y A S T T D L Q P H T S I N K A I N O G N F S A T M N R G E D L D Y K 600

QY 601 T F R T I G T T P F S D V Q S T F T I G A M N F S S G N E Y I D R I E F V P V E V T Y E A Y E F P E K A Q E K V 660  
DB 601 T F R T V G T T T F S D V Q S T F T I G A M N F S S G N E Y I G R I E F V P V E V T Y E A Y E F P E K A Q E K V 660

QY 661 T A L F T S N P R G L K T D V K D Y H I D Q V S N I V E S L S D E L Y D K R E L F E I V K Y A K O I H I E R N M 719  
DB 661 T A L F T S N P R G L K T D V K D Y H I D Q V S N I V E S L S D E L Y D K R E L F E I V K Y A K O I H I E R N M 719

RESULT 5  
AAB66908  
ID AAB66908 standard; protein; 719 AA.

XX AAB66908;  
AC 12-APR-2001 (first entry)  
XX Insecticidal protein cryIIa2.  
XX Insecticide; transgenic plant; insect-resistance.  
XX Paecilomyces sp.  
XX WO200100841-A1.  
XX 04-JAN-2001.  
XX 23-JUN-2000; 2000WO-GB002457.  
XX 29-JUN-1999; 99GB-00015215.  
XX 23-DEC-1999; 99GB-00030536.  
XX (ZENE ) ZENECA LTD.  
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
XX Vincent JL, Lee MD;  
XX WPI; 2001-123015/13.  
XX Novel insecticidal protein obtained from species of Paecilomyces for  
XX controlling insects, and for insect-resistant transgenic plant  
XX production.  
XX Claim 14; Page 55-57; 72pp; English.  
XX The present invention relates to novel insecticidal proteins obtained  
XX from Paecilomyces sp. (see AAB66901 and AAB66913). The  
XX insecticidal proteins can be used to produce transgenic plants, which are  
XX insect-resistant. Also, the insecticidal proteins are useful for  
XX controlling insects by providing them at a locus where insects feed  
XX Sequence 719 AA;

Query Match 94.1%; Score 3520; DB 4; Length 719;  
Best Local Similarity 92.9%; Pred. No. 5e-282;  
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

QY 1 M K L N P D K H Q S L S N A K V D K I A T D S L K N E T D I E L K N M N E D Y L R M S E H S I D P F V S A S T I 60  
DB 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I H E D C L K M S E Y E N V E F V S A S T I 60

QY 61 Q T G I G I A K I L G T L G V P P A G Q I A S L Y S F I L G E L W P K G S Q W E I F M E H V E E I I N K I L T Y A 120  
DB 61 Q T G I G I A K I L G T L G V P P A G Q A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N K I S T Y A 120

QY 121 R N K A L S D L R G I G D A L A V Y H S E S L E S V E N R N T R A S V V K N Q Y I A L E M F V K L P S F A V S G 180  
DB 121 R N K A L T D L K G I G D A L A V Y H S E S L E S V G N R N T R A S V V K S Q Y I A L E M F V K L P S F A V S G 180

QY 181 E V P L L P I Y A Q A A N L H L L R D A S I F G K E W G L S A S E I S T F Y N Q R V E R T R D Y S D H C I K W Y N 240  
DB 181 E V P L L P I Y A Q A A N L H L L R D A S I F G K E W G L S S E I S T F Y N Q R V E A G D Y S D H C K W Y S 240

QY 241 T G L N L R G T N A K S W R Y N Q R K D M T L M V L D L V A L P P S Y D T L V P I K T S Q L T R E V Y T D A I 300  
DB 241 T G L N L R G T N A E S W R Y N Q R F R D M T L M V L D L V A L P P S Y D T Q M Y P I K T A Q L T R E V Y T D A I 300

QY 301 G T V H P N Q A P A S T T W Y N N N A P S F A I E A A V I R S P H L L D F L E K V T I Y S L L S R W S N T Q Y N M W 360  
DB 301 G T V H P H S F T S T T W Y N N N A P S F A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y N M W 360

QY 361 G G H R L E S P I G A L N T S T O G S T N T S I N P V T L Q F T S R D Y R T E S L A G L N L F L T Q P V N G V P R 420  
DB 361 G G H K L E P T I G T L N I S T O G S T N T S I N P V T L P F T S R D Y R T E S L A G L N L F L T Q P V N G V P R 420



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QY 421 VDFHWKFTPLPIASDNFYVLGVAGVGTQLQDSNELPPETTGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFTVTHPIASDNFYVPGVAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAENLSSGAAVVRGPGTGGDILRRTN 540
DB 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAENLSSGAAVVRGPGTGGDILRRTN 540
QY 541 TGTFGDIRVINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSAATMRGDLDYK 600
DB 541 TGTFGDIRVINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSAATMRGDLDYK 600
QY 601 TERTIGFTTFFSFDVQSTFTIGAMNFFSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
DB 601 TERTIGFTTFFSFDVQSTFTIGAMNFFSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 6
AAE36272
ID AAE36272 standard; protein; 719 AA.
XX
AC AAE36272;
DT 26-JUN-2003 (first entry)
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.
XX
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX
OS Bacillus thuringiensis.
XX
PN WO200298911-A2.
PD 12-DEC-2002.
XX
PP 30-MAY-2002; 2002WO-GB0002666.
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN ) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX
PS Claim 12; Page 44-47; 67pp; English.
XX
CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.
XX
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is
XX
CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
XX
SQ Sequence 719 AA;

Query Match 94.1%; Score 3520; DB 6; Length 719;
Best Local Similarity 92.9%; Pred.No.5e-282;
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKLKNPKDKHQSSNAKVDTATDSLKNETDELKNNEDYLRMSEHSIDPFVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDTISDSLKNETDIELQINHEDCLKMSEYENVPFVSASTI 60
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## RESULT 7

ADR89421

ID ADR89421 standard; protein; 719 AA.

XX

AC ADR89421;

XX

DT 18-NOV-2004 (first entry)

XX

DE cryIIa.

XX

KW delta-endotoxin; delta-endotoxin associate polypeptide;

KW expression cassette; transformation; transgenic; plant; bacteria;

KW lepidoptera; coleoptera; pest; pesticide; resistance;

KW pesticidal activity.

XX

OS Bacillus thuringiensis.

XX

PN WO2004074462-A2.

XX

PD 02-SEP-2004.

XX

PF 20-FEB-2004; 2004WO-US005829.

XX

PR 20-FEB-2003; 2003US-0448632P.

XX

PR 20-FEB-2003; 2003US-0448633P.

XX

PR 20-FEB-2003; 2003US-0448797P.

XX

PR 20-FEB-2003; 2003US-0448806P.

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PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
PR
XX (ATHE-) ATHENIX CORP.
PA
XX Carozzi N, Hargiss T, Kozziel MG, Duck NB, Carr B;
XX WPI; 2004-635574/61.
XX
XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
XX and polypeptides, useful for killing lepidopteran or coleopteran pests or
XX for producing organisms with pesticide resistance.
XX
XX Example 6; SEQ ID NO 33; 178pp; English.
XX
XX This sequence represents a delta-endotoxin crystal protein. This protein
XX was included in the scope of the invention as a comparison to the delta-
XX endotoxins of the invention. Some of the delta-endotoxin coding sequences
XX of the invention have alternative start codons, producing more than one
XX protein from a single open reading frame. The nucleic acid sequences of
XX the invention are useful in DNA constructs or expression cassettes for
XX transformation and expression in plants and bacteria. The nucleic acids
XX and corresponding polypeptides are useful for killing lepidopteran or
XX coleopteran pests. Compositions containing the delta-endotoxins of the
XX invention, and methods for their production, are useful for the
XX production of organisms with pesticide resistance, specifically bacteria
XX and plants. These organisms are useful for generating altered or improved
XX delta-endotoxin or delta-endotoxin-associated proteins that have
XX pesticidal activity, or for detecting the presence of delta-endotoxin or
XX delta-endotoxin-associated proteins or nucleic acids in products or
XX organisms.
XX
XX Sequence 719 AA;
XX
XX Query Match 94.1%; Score 3520; DB 8; Length 719;
XX Best Local Similarity 92.9%; Pred. No. 5e-282;
XX Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;
XX
QY 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSHESIDPFVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECKMSEYENVEPFVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQIASLYSFTLGLWPKGSQWEIFMEHVEEIIINQKILTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQIASLYSFTLGLWPKGSQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALSDRLGLDALAVHYHESLESWVENNTRARSVVKQYIALELMFVKQLPSFVSG 180
DB 121 RNKALTDLGLDALAVHYHDSLESWVGNNTRARSVVKQYIALELMFVKQLPSFVSG 180
QY 181 EEPVLLPIYAQAANTHLLLRDASIFGKEWGLSASEISFYNNQVERDYSDHCICKWYN 240
DB 181 EEPVLLPIYAQAANTHLLLRDASIFGKEWGLSSSEISFYNNQVERAGDYSDHCVKWYS 240
QY 241 TGLNNLRGTNAKSWRYNFRKDMTLMVLVDLVALFSPSYDTLVPYIKTTSQLTREYVTDI 300
DB 241 TGLNNLRGTNAESWRYNQFRDWTLMVLVDLVALFSPSYDTMYPYIKTTAQLTREYVTDI 300
QY 301 GTVHPNOAFSTWYNNAPSFSAIEAAYRSRPHLDLEKVTIYSLLSRWNTQVMNMW 360
DB 301 GTVHPNPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNTQVMNMW 360
QY 361 GGHLESRPIGGALNTSTQGSTNTSINPVTLOFTSRDYRTESLAGLNLFLTQPNVGVR 420
DB 361 GGHLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTQPNVGVR 420
QY 421 VDFHWKFTPLPIASDNFYIYGAGVGTQLODSENELPPTTGGQPNYESYSHRLSHIGLIS 480
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DB 421 VDFHWKFTPLPIASDNFYIYGAGVGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIENSTOIPLVKAFNLSSGAAVVRGPGFTGGDILARTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIENSTOIPLVKAFNLSSGAAVVRGPGFTGGDILARTN 540
QY 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDIIDYK 600
DB 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATWNRGEDIIDYK 600
QY 601 TFRITGFTTSPFSVDQSTFTIGAWNFSSGNEVVIDRIEFVPEVTVYEAEDFEKAQEKV 660
DB 601 TFRITGFTTSPFSFLDVQSTFTIGAWNFSSGNEVVIDRIEFVPEVTVYEAEDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVDKDYHIDQVNLVESLSDFYLDKRELFELVKYAKQIHIERNM 719
DB 661 TALFTSTNPRGLKTDVDKDYHIDQVNLVESLSDFYLDKRELFELVKYAKQIHIERNM 719
XX
XX RESULT 8
XX AAB66910 standard; protein; 719 AA.
XX
XX AAB66910;
XX
XX 12-APR-2001 (first entry)
XX
XX Insecticidal protein cryIIa4.
XX
XX Insecticide; transgenic plant; insect-resistance.
XX
XX Paecilomyces sp.
XX
XX WO200100841-A1.
XX
XX 04-JAN-2001.
XX
XX 23-JUN-2000; 2000WO-GB002457.
XX
XX 29-JUN-1999; 99GB-00015215.
XX 23-DEC-1999; 99GB-00030536.
XX
XX (ZENE ) ZENECA LTD.
XX
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
XX Vincent JL, Lee MD;
XX
XX WPI; 2001-123015/13.
XX
XX Novel insecticidal protein obtained from species of Paecilomyces for
XX controlling insects, and for insect-resistant transgenic plant
XX production.
XX
XX Claim 14; Page 60-62; 72pp; English.
XX
XX The present invention relates to novel insecticidal proteins obtained
XX from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
XX insecticidal proteins can be used to produce transgenic plants, which are
XX insect-resistant. Also, the insecticidal proteins are useful for
XX controlling insects by providing them at a locus where insects feed
XX
XX Sequence 719 AA;
XX
XX Query Match 94.0%; Score 3516; DB 4; Length 719;
XX Best Local Similarity 92.8%; Pred. No. 1.1e-281; Indels 0; Gaps 0;
XX Matches 667; Conservative 31; Mismatches 21;
XX
QY 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSHESIDPFVSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECKMSEYENVEPFVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQIASLYSFTLGLWPKGSQWEIFMEHVEEIIINQKILTYA 120
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Db 61 QTGIGTAGKILGTGVPPAGQVASYLSPILGELWPKGKQWEIFMHEVBEIIINQKISTYA 120  
QY 121 RNKALDRLGIGDALAVYHESLESVENNTRARSVKNOYIALELMFVKLPSPFAVSG 180  
Db 121 RNKALDRLGIGDALAVYHESLESVENNTRARSVKNOYIALELMFVKLPSPFAVSG 180  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNNQVRTRDYSRHCWKYN 240  
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNNQVRTRDYSRHCWKYS 240  
QY 241 TGLNNLRGNTNAKSWVRNQPRKDMTLMVLDFVALFSPYDTLVPIKTTSQLTREVYTDAL 300  
Db 241 TGLNNLRGNTNAKSWVRNQPRKDMTLMVLDFVALFSPYDTLVPIKTTSQLTREVYTDAL 300  
QY 301 GTVHPNQAFSTTWNNNAPSPFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYNNMW 360  
Db 301 GTVHPHPSFTSTTWNNNAPSPFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW 360  
QY 361 GGHRLSPRIGGALNTSTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFTQPVNGVPR 420  
Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFTQPVNGVPR 420  
QY 421 VDFHWKFPPTLPASDNFYLYGAGVGTQLODSENELPPETTGQPNYESYSHRLSHIGLIS 480  
Db 421 VDFHWKFPVTHPIASDNFYLYGAGVGTQLODSENELPPETTGQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLKAFNLSSGAAVVRGPGTGGDILRRTN 540  
Db 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLKAFNLSSGAAVVRGPGTGGDILRRTN 540  
QY 541 TGTFGDIRVINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSAATMNRGEDLDYK 600  
Db 541 TGTFGDIRVINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSAATMNRGEDLDYK 600  
QY 601 TFRITGFTTFFPSFSDVQSTFTIGAMNFFSGNEVYIDRIEFPVPEVTEYAEYDEFEKAQEKV 660  
Db 601 TFRITGFTTFFPSFSDVQSTFTIGAMNFFSGNEVYIDRIEFPVPEVTEYAEYDEFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFPEIVKAKQIHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFPEIVKAKQIHIERNM 719

## RESULT 9

AAE36274

ID AAE36274 standard; protein; 719 AA.

XX AAE36274;

XX 26-JUN-2003 (first entry)

XX B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.

XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

XX Bacillus thuringiensis.

XX WO200298911-A2.

XX 12-DEC-2002.

XX 30-MAY-2002; 2002WO-00013900.

XX 07-JUN-2001; 2001GB-00013900.

XX (SYGN ) SYNGENTA LTD.

XX Vincent JL, Viner R;

XX WPI; 2003-175137/17.

XX New insecticidal protein comprising an X-glycine motif at the amino-

terminus, useful as an active ingredient of a pesticide.

Claim 12; Page 50-53; 67pp; English.

The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

Sequence 719 AA;

XX

Query Match

Best Local Similarity 94.0%; Score 3516; DB 6; Length 719;

Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

QY 1 MKLKNPKDQKSSNAKVDKIATDSLKNETDIELKMNNEDEYLRMSEHESIDPFVSASTI 60

Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKMSEYENVEFPVSASTI 60

QY 61 QTGIGTAGKILGTGVPPAGQVASYLSPILGELWPKGKQWEIFMHEVBEIIINQKISTYA 120

Db 61 QTGIGTAGKILGTGVPPAGQVASYLSPILGELWPKGKQWEIFMHEVBEIIINQKISTYA 120

QY 121 RNKALDRLGIGDALAVYHESLESVENNTRARSVKNOYIALELMFVKLPSPFAVSG 180

Db 121 RNKALDRLGIGDALAVYHESLESVENNTRARSVKNOYIALELMFVKLPSPFAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNNQVRTRDYSRHCWKYN 240

Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNNQVRTRDYSRHCWKYS 240

QY 241 TGLNNLRGNTNAKSWVRNQPRKDMTLMVLDFVALFSPYDTLVPIKTTSQLTREVYTDAL 300

Db 241 TGLNNLRGNTNAKSWVRNQPRKDMTLMVLDFVALFSPYDTLVPIKTTSQLTREVYTDAL 300

QY 301 GTVHPNQAFSTTWNNNAPSPFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYNNMW 360

Db 301 GTVHPHPSFTSTTWNNNAPSPFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYNNMW 360

QY 361 GGHRLSPRIGGALNTSTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFTQPVNGVPR 420

Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFTQPVNGVPR 420

QY 421 VDFHWKFPPTLPASDNFYLYGAGVGTQLODSENELPPETTGQPNYESYSHRLSHIGLIS 480

Db 421 VDFHWKFPVTHPIASDNFYLYGAGVGTQLODSENELPPETTGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLKAFNLSSGAAVVRGPGTGGDILRRTN 540

Db 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLKAFNLSSGAAVVRGPGTGGDILRRTN 540

QY 541 TGTFGDIRVINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSAATMNRGEDLDYK 600

Db 541 TGTFGDIRVINPPFAQRYRVRIRYASTTDLQPHTSINGKAINQGNFSAATMNRGEDLDYK 600

QY 601 TFRITGFTTFFPSFSDVQSTFTIGAMNFFSGNEVYIDRIEFPVPEVTEYAEYDEFEKAQEKV 660

Db 601 TFRITGFTTFFPSFSDVQSTFTIGAMNFFSGNEVYIDRIEFPVPEVTEYAEYDEFEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFPEIVKAKQIHIERNM 719

Db 661 TALFTSTNPRGLKTDVKDHYDQVSNLVSLSDEFYLDKRELFPEIVKAKQIHIERNM 719

## RESULT 10

AAU02095

ID AAU02095 standard; protein; 719 AA.

XX

[illegible]

RESULT 11  
AAB66911

ID	Standard; protein; 719 AA.
1	1
2	2
3	3
4	4
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6	6
7	7
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90	90
91	91
92	92
93	93
94	94
95	95
96	96
97	97
98	98
99	99
100	100

AA  
AC

12-APR-2001 (first entry)

Insecticidal protein cvrIIa5.

XX | Insecticide: transgenic plant: insect-resistance.

XX CC need to be removed on

XX  
W0300300841-27

XX 04 JAN 2007

	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100					
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

[illegible]

PR | 23-DEC-1999; 99GB-00030536.

PA (ZENE) ZENECALTD.

PI	Griffin J, Carlile AJ, Mackay EA, Warner SAJ,
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XX

XX Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PT production.

PS Claim 14; Page 62-64; 72pp; English.

CC The present invention relates to novel insecticidal proteins obtained  
CC from *Paecliomys* sp. (see AAB66899 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
CC

Sequence 719 AA:

AC	AAU02095;		
XX	07-SEP-2001 (first entry)		
XX	Bacillus thuringiensis partial mutant CryIIa.		
XX	Crystal protein; CryIIa; CryIIa; moth; butterfly; Colorado potato beetle;		
XX	mutant; mutein.		
XX	Bacillus thuringiensis.		
XX	Key	Location/Qualifiers	
XX	Peptide	1. 19	
XX	Protein	/label= Signal_peptide	
XX		20. 719	
XX		/label= Mature_CryIIa	
XX	EP1099760-A1.		
XX	16-MAY-2001.		
XX	09-NOV-1999;	99EP-00203723.	
XX	09-NOV-1999;	99EP-00203723.	
XX	(CFRO-) CFRO-DLO CENT PLANTENVERDEDELINGS REPROD.		
XX	De Maagd RA, Bosch HJ;		
XX	WPI; 2001-337141/36.		
XX	N-PSDB; AAS04855.		

New hybrid *Bacillus thuringiensis* hybrid toxins comprising structural domains derived from at least 2 different crystal proteins, such as CryIIa and CryIIb, and having insecticidal activity, useful for combating insects.

XX  
ps Example: Page 30-32: 43pp: English.

XX CC The sequence is *B. thuringiensis* (Bt) crystal protein CryIIa, the DNA  
CC encoding which was mutated to allow cloning of domain III or domains I  
CC and II, to make the hybrid protoxins of the invention. The hybrid toxins  
CC of the invention, having structural domains I, II and III in this order  
CC starting from the N-terminal derived from at least 2 different crystal  
CC proteins, are useful for protecting plants against pest insects, e.g.  
CC moths, butterflies and Colorado potato beetle or for combating insects

Sequence 719 AA; SO

Query Match	93.8%;	Score 3511;	DB 4;	Length 719;
Best Local Similarity	92.8%;	Pred. No. 2.8e-281;		
Matches	667.	Mismatches 31;	Indels 0;	Gaps 0;
Conservative				

QY	1	MKLKQPDKHQSLSNAKVDKIATDSLKNETDTELKNNMNEEDYLRMSHESIDPFPVSASTI	60
Db	1	MKLKQDQKHQSFSNAKVDKISTDSLKNETDTELQNIHNECDLCKMSEYENVEPFPVSASTI	60
QY	61	QTGIGTAGKILGTGLVPPFAGQATASYSFTLGBELWPKGKSOWEIMFMEHVEEIIINOILFYA	120
Db	61	QTGIGTAGKILGTGLVPPFAGQAVASYSFTLGBELWPKGKNQWEIMFMEHVEEIIINOISFYA	120
QY	121	RNKALSDLRGLGDALAYIHESIWSVWENRNNTRASVVKNOVIALLELMFVKQLPSFVSG	180
Db	121	RNKALTDLRGLGDALAYIHDSLESWGVRNNTRASVVKSOVIALLELMFVKQLPSFVSG	180
QY	181	EEVPLLPITYAQAANLHLLLRDASIFGKQWGLSASEISTIFYNROVERTEDSDHCICKWYN	240
Db	181	EEVPLLPITYAQAANLHLLLRDASIFGKQWGLSSSEISTIFYNROVERAGDYSYHCWKVYS	240
QY	241	TGLNNLRGTNAKSWRYNOFRKDMTLMVLDDLVALFPSYDTLVYPYIKTTSQLTREVYTDAI	300
Db	241	TGLNNLRGTNAESWRYNOFRDMTLMVLDDLVALFPSYDTQWYPIKTTAQLTREVYTDAI	300

```
Query Match 93.8%; Score 3509; DB 4; Length 719;
Best Local Similarity 92.5%; Pred. No. 4.1e-281;
Matches 665; Conservative 33; Mismatches 21; Indels 0; Gaps 0;

QY 1 MCLKNPKHQSSNAKVDKIATDSLKNKNTDIELKMNEDYLRMSEHSIDPFVSASTI 60
DB 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNKNTDIELQNHEDCLKMSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQASLYSFILGELMPKQKQWEIFMEHVEEIIINQKILTVA 120
DB 61 QTGIGIAGKILGTGVPFAGQASLYSFILGELMPKQKQWEIFMEHVEEIIINQKILTVA 120
QY 121 RNKALSDLRGLDALAVYHESLESVWENNRNTRARSVVRVRSQVIALELMFVKLPSFAVSG 180
DB 121 RNKALSDLRGLDALAVYHESLESVWENNRNTRARSVVRVRSQVIALELMFVKLPSFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASISIFYNRQVTRDYSDHCHIKWYN 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASISIFYNRQVTRDYSDHCHIKWYS 240
QY 241 TGLNLRGTNAKSWRYNOFRDMLVLDLVALPSPYDTLVYPIKTTSQLTREVTDAI 300
DB 241 TGLNLRGTNAKSWRYNOFRDMLVLDLVALPSPYDTLVYPIKTTSQLTREVTDAI 300
QY 301 GTVHPNQAFSTTWNNAAPSFAIEAAVIRSPHLLDFLEKVTIYLLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNW 360
QY 361 GGHRLSPRIGALNTSTOGSNTSINPVTLOFTSRDVRTESLAGLNLFLTOPVNGVPR 420
DB 361 GGHKLEFRTIGTGLNISTOGSNTSINPVTLPFTSRDVRTESLAGLNLFLTOPVNGVPR 420
QY 421 VDFHMKFPTLPASDNFYVLGAGVGTQLQDSNELPPEATGQPNYESYSHRLSHLGLIS 480
DB 421 VDFHMKFVTHP TASDNFYYPGAGIGTQLQDSNELPPEATGQPNYESYSHRLSHLGLIS 480
QY 481 ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVINPPFAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGEBLDYK 600
DB 541 TGTFGDIRVINPPFAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGEBLDYK 600
QY 601 TERTTGFTTSPFSVDQSTFTIGAMNFFSGNEVYIDRIEFVPEVTEYAEYDEPEKAQKV 660
DB 601 TERTVGFTTFFFLDVQSTFTIGAMNFFSGNEVYIDRIEFVPEVTEYAEYDEPEKAQKV 660

RESULT 12
AAE36275
ID AAE36275 standard; protein; 719 AA.
XX
AC AAE36275;
XX
DT 26-JUN-2003 (first entry)
XX
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa5.
XX
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX
OS Bacillus thuringiensis.
XX
PN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
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PR 07-JUN-2001; 2001GB-00013900.
XX (SYGN ) SYNGENTA LTD.
XX Vincent JL, Viner R;
XX WPI; 2003-175137/17.
XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX Claim 12; Page 53-56; 67pp; English.
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.
XX Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
XX Sequence 719 AA;
XX
Query Match 93.8%; Score 3509; DB 6; Length 719;
Best Local Similarity 92.5%; Pred. No. 4.1e-281;
Matches 665; Conservative 33; Mismatches 21; Indels 0; Gaps 0;

QY 1 MCLKNPKHQSSNAKVDKIATDSLKNKNTDIELKMNEDYLRMSEHSIDPFVSASTI 60
DB 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNKNTDIELQNHEDCLKMSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQASLYSFILGELMPKQKQWEIFMEHVEEIIINQKILTVA 120
DB 61 QTGIGIAGKILGTGVPFAGQASLYSFILGELMPKQKQWEIFMEHVEEIIINQKILTVA 120
QY 121 RNKALSDLRGLDALAVYHESLESVWENNRNTRARSVVRVRSQVIALELMFVKLPSFAVSG 180
DB 121 RNKALSDLRGLDALAVYHESLESVWENNRNTRARSVVRVRSQVIALELMFVKLPSFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASISIFYNRQVTRDYSDHCHIKWYN 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASISIFYNRQVTRDYSDHCHIKWYS 240
QY 241 TGLNLRGTNAKSWRYNOFRDMLVLDLVALPSPYDTLVYPIKTTSQLTREVTDAI 300
DB 241 TGLNLRGTNAKSWRYNOFRDMLVLDLVALPSPYDTLVYPIKTTSQLTREVTDAI 300
QY 301 GTVHPNQAFSTTWNNAAPSFAIEAAVIRSPHLLDFLEKVTIYLLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNW 360
QY 361 GGHRLSPRIGALNTSTOGSNTSINPVTLOFTSRDVRTESLAGLNLFLTOPVNGVPR 420
DB 361 GGHKLEFRTIGTGLNISTOGSNTSINPVTLPFTSRDVRTESLAGLNLFLTOPVNGVPR 420
QY 421 VDFHMKFPTLPASDNFYVLGAGVGTQLQDSNELPPEATGQPNYESYSHRLSHLGLIS 480
DB 421 VDFHMKFVTHP TASDNFYYPGAGIGTQLQDSNELPPEATGQPNYESYSHRLSHLGLIS 480
QY 481 ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVINPPFAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGEBLDYK 600
DB 541 TGTFGDIRVINPPFAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATMNRGEBLDYK 600
QY 601 TERTTGFTTSPFSVDQSTFTIGAMNFFSGNEVYIDRIEFVPEVTEYAEYDEPEKAQKV 660
DB 601 TERTVGFTTFFFLDVQSTFTIGAMNFFSGNEVYIDRIEFVPEVTEYAEYDEPEKAQKV 660
```

QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNM 719

RESULT 13  
AAB66909 standard; protein; 719 AA.  
AC AAB66909;  
XX 12-APR-2001 (first entry)  
DT Insecticidal protein cryIIa3.  
XX Insecticide; transgenic plant; insect-resistance.  
XX Paecilomyces sp.  
XX WO200100841-A1.  
PN 04-JAN-2001.  
PD 23-JUN-2000; 2000WO-GB002457.  
PF 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX (ZENE ) ZENECA LTD.  
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX WPI; 2001-123015/13.  
XX Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PT production.  
XX Claim 14; Page 57-59; 72pp; English.  
XX The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX Sequence 719 AA;  
SQ

Query Match 93.6%; Score 3503; DB 4; Length 719;  
Best Local Similarity 92.5%; Pred. No. 1.3e-280;  
Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;

QY 1 MKLNKPDKQKSSNAKVADKIDATSLKNETDIELKNNEDYLRMSEHESIDPFVSASTI 60  
DB 1 MKLNKQDKHQSFSSNAKVADKIDATSLKNETDIELQINHEDELCKMSEYNEVFFVSASTI 60  
QY 61 QTGIGTAGKILGTLYGVPFAGQIASLYSFLIGELWPKGQSWELFMEHVEEIIINQKILTYA 120  
DB 61 QTGIGTAGKILGTLYGVPFAGQVASLYSFLIGELWPKGQSWELFMEHVEEIIINQKISTYA 120  
QY 121 RNKALSDRLGIDALAVYHESLSWENRNNTARSVYKNQYIALBELFVQKLPSPAVSG 180  
DB 121 RNKALTDLKGIDALAVYHESLSWGNRNNTARSVYKVSQYIALBELFVQKLPSPAVSG 180  
QY 181 EEPVLLPIYAQANLHLLLRDASIFCKEWGLSASELSTFYNNQVTRDYSDHCKIKWN 240  
DB 181 EEPVLLPIYAQANLHLLLRDASIFCKEWGLSSSELSTFYNNQVTRAGDYSHCVKWN 240  
QY 241 TGLNLRGTNAKSWRVYNNQFRKDMTLMVLDLVALFPSTYDLTVYPKITSQLTREVYTDI 300  
DB 241 TGLNLRGTNAESWYRVYNNQFRDMTLMVLDLVALFPSTYDMYPIKTAQLTREVYTDI 300

QY 301 GTVHPNOAFASFTWYNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYLLSRWSNTQYNNMW 360  
DB 301 GTVHPNPSFTTWNWNNAPSFSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYNNMW 360  
QY 361 GGHLESRPITGGALNTSTQSTNTSINPVTLOQTSRDVYTESLAGNLFLTOPVNGVPR 420  
DB 361 GGHKLEFRITGGTLNISTQSTNTSINPVTLPFTSRDVYTESLAGNLFLTOPVNGVPR 420  
QY 421 VDFHWKPTPLIASDNFYLYGAGVGTQLOQSENELPETTGQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFVTHEIASDNFYLYGAGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILARTN 540  
DB 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILARTN 540  
QY 541 TGTGDIRVNIINPPPAQRYRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDLDYK 600  
DB 541 TGTGDIRVNIINPPPAQRYRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDLDYK 600  
QY 601 TERTIGFTTTPFSFSDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
DB 601 TERTIGFTTTPFSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNM 719

## RESULT 14

AAE36273  
ID AAE36273 standard; protein; 719 AA.

XX AAE36273;

XX 26-JUN-2003 (first entry)

DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.

XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

XX Bacillus thuringiensis.

XX WO200298911-A2.

XX 12-DEC-2002.

XX 30-MAY-2002; 2002WO-GB002666.

XX 07-JUN-2001; 2001GB-00013900.

XX (SYGN ) SYNGENTA LTD.

XX Vincent JL, Viner R;

XX WPI; 2003-175137/17.

XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

XX Claim 12; Page 47-50; 67pp; English.

XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.

XX Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

XX Sequence 719 AA;

XX	09-MAY-1989;	89GB-00010624.			
XX	09-MAY-1989;	89GB-00010624.			
XX	(ICIL ) IMPERIAL CHEM IND PLC.				
PI	Blenk RG, Ely S, Tailor RH, Tippet JM;				
XX	WPI; 1990-361486/48.				
DR	N-PSDB; AAQ06636.				
XX	Bacillus thuringiensis strains - used for producing an endotoxin for protecting plants against insects, partic. Lepidoptera and Coleoptera.				
PS	Claim 5; Fig 5-10; 66pp; English.				
XX	The sequence carried on pJH12 which was isolated from B. thurin- gienais strains JHCC4835 and JHCC 4353 (NCIB 40091 and 40090 resp.). The DNA can be used to produce transformants E.coli strain MC12022/pJH12 (NCIB 40278, or bacteriophage EMBL4 vector (NCIB 40279) or E.coli strain BL21/pJH11 (NCIB 40275). The delta-endo- toxin produced by the transformants can be used in formulations for combatting Lepidoptera and Coleoptera pests. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)				
XX	Sequence 719 AA;				
QY	Query Match	93.5%;	Score 3499;	DB 2;	Length 719;
DB	Best Local Similarity	92.5%;	Pred. No. 2.8e-280;		
QY	Matches 665;	Conservative 31;	Mismatches 23;	Indels 0;	Gaps 0;
QY	1	MKLKDPKHQSLSNAKVDKIATDSLKNETDIELKNNEDYLRMSHESIDPFVSASTI	60		
DB	1	MKLKQDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMESENVPEPFVSASTI	60		
QY	61	QTGIGIAGKILGTGVFPAGQIASLYSIFILGELWPKGKSQWEIFMEHVEEIIINOKILTYA	120		
DB	61	QTGIGIAGKILGTGVFPAGQVASLYSIFILGELWPKGKNQWEIFMEHVEEIIINOKISTYA	120		
QY	121	RNKALSDLRGLDALAVYHESLESVENNRNTRARSVVKNQYIALSLMFVQKLPSPAVSG	180		
DB	121	RNKALTDLKGLDALAVYHDSLESWGNRNNTRARSVVKSYIALSLMFVQKLPSPAVSG	180		
QY	181	EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYN	240		
DB	181	EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCWKYS	240		
QY	241	TGLNNLRGTNAKSWRYNQFRKDMTLMVLDPVALPFSYDTLVVPIKTTSQLTREVTDAI	300		
DB	241	TGLNNLRGTNAESWRYNQFRDMTLMVLDPVALPFSYDTQWPIKTTAQLTREVTDAI	300		
QY	301	GTVHPNQAFSTTWNNAAPSFAEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW	360		
DB	301	GTVHPHPSFTSTTWNNAAPSFAEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW	360		
QY	361	GGHRLSRPIGGALNTSTOGSTNTSINPVTLOFTSRDVTYRTESLAGNLFLTPQVNGVPR	420		
DB	361	GGHKLFRFTIGTGLNISTOGSTNTSINPVTLPFTSRDVTYRTESLAGNLFLTPQVNGVPR	420		
QY	421	VDFHWKFTPLPIASDNFYVLGYAGVGTQLQDSENELPPTTGPQNYESYSHRLSHIGLIS	480		
DB	421	VDFHWKFVTHPIASDNFYYPGVAGIGTQLQDSENELPPEATGPQNYESYSHRLSHIGLIS	480		
QY	481	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540		
DB	481	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540		
QY	541	TGTFGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK	600		
DB	541	TGTFGDIRVNIINPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK	600		
QY	601	TPRTIGFTTFFSDVQSTFTTICAMNFFSSGNEVYIDRIEFVPVEVTEAYEDFEKAQEKV	660		
DB	601	TPRTVGFTTFFSLDVQSTFTTICAMNFFSSGNEVYIDRIEFVPVEVTEAYEDFEKAQEKV	660		
QY	661	TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFETIVKYAKQTHIERNM	719		
DB	661	TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFETIVKYANELHIERNM	719		
XX	RESULT 15				
XX	AAR08041				
ID	AAR08041	standard; protein; 719 AA.			
XX					
AC	AAR08041;				
XX					
DT	24-OCT-2003 (revised)				
DT	25-MAR-2003 (revised)				
DT	27-FEB-1991 (first entry)				
XX					
DE	81 kD endotoxin deduced from DNA carried on pJH12.				
XX					
KW	Crystal; insecticide; toxin; delta endotoxin.				
XX					
OS	Bacillus thuringiensis; JHCC 4353 and 4835.				
XX					
PN	W09013651-A.				
XX					
PD	15-NOV-1990.				

Tue Feb 15 10:07:56 2005

Db	601	TEXTVGFTTFSLDVQSTFTIGAWNFSGNEVIIDRIEFVPVEVTEAEYDEKQEKV 660
Qy	661	TALFTSTNPRGLKTDVKDYHIDQVSNLVESSLDEFYLDKRELFELVKYAKQIHIERNM 719
Db	661	TALFTSTNPRGLKTDVKDYHIDQVSNLVESSLDEFYLDKRELFELVKYAKQIHIERNM 719

Search completed: February 14, 2005, 20:50:40  
Job time : 101.351 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 20:11:42 ; Search time 81.1112 Seconds  
(without alignments)  
4539.261 Million cell updates/sec

Title: US-10-019-823B-59  
Perfect score: 3742  
Sequence: 1 MKLKNPKHQSLSSNAKVK.....KRELFEIVKYAKQIHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3742	100.0	719	1 C1IB_BACTE	Q45709 bacillus th
2	3598	96.2	719	2 Q9F0P8	Q9f0p8 bacillus th
3	3546	94.8	719	1 C1IC_BACTU	Q87404 bacillus th
4	3520	94.1	719	1 C1IA_BACTK	Q45752 bacillus th
5	3520	94.1	719	2 Q6X181	Q6x181 bacillus th
6	3515	93.9	719	2 Q93NJ5	Q93nj5 bacillus th
7	3514	93.9	719	2 Q85796	Q85796 bacillus th
8	3510	93.8	719	2 Q8KY61	Q8ky61 bacillus th
9	3311	88.5	719	1 C1ID_BACTU	Q9xd11 bacillus th
10	2459	65.7	1229	1 C1IB_BACTU	Q45739 bacillus th
11	2459	65.7	1233	1 C1BC_BACTM	Q45774 bacillus th
12	2322.5	62.1	1228	2 Q93T75	Q93t75 bacillus th
13	2321.5	62.0	1228	1 C1BA_BACTK	P05517 bacillus th
14	2313.5	61.8	1228	2 Q93NM5	Q93nm5 bacillus th
15	2243	59.9	849	2 Q6PYW8	Q6pyw8 bacillus th
16	2243	59.9	1227	1 C1BE_BACTU	Q85805 bacillus th
17	2129	56.9	1231	2 Q8KNY2	Q8kny2 bacillus th
18	2116	56.5	1231	1 C1BD_BACTZ	Q92a25 bacillus th
19	1963	52.5	1215	1 C1KA_BACTM	Q45715 bacillus th
20	1817	48.6	381	2 Q45740	Q45740 bacillus th
21	1670	44.6	1144	2 Q8KZL7	Q8kz17 bacillus th
22	1657.5	44.3	1157	1 C8AA_BACUK	Q45704 bacillus th
23	1507	40.3	1157	1 C9CA_BACTO	Q45733 bacillus th
24	1503.5	40.2	1166	1 C1GA_BACTM	Q45746 bacillus th
25	1497.5	40.0	1169	2 C1FB_BACTM	Q66377 bacillus th
26	1491.5	39.9	1174	2 Q45749	Q45749 bacillus th
27	1484.5	39.7	1169	1 C8BA_BACUK	Q45705 bacillus th
28	1480.5	39.6	1155	1 C1AB_BACTK	P06578 bacillus th
29	1480.5	39.6	1155	2 Q7B9S8	Q7b9s8 bacillus th
30	1480.5	39.6	1155	2 Q9F296	Q9f296 bacillus th
31	1475.5	39.4	1156	2 Q6GUA7	Q6gua7 bacillus th

RESULT 1

ID	C1IB_BACTE	STANDARD;	PRT;	719 AA.
AC	Q45709;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Pesticidal crystal protein cryIIb (Insecticidal delta-endotoxin)			
DE	CryII(b) (Crystalline entomocidal protoxin) (81 kDa crystal protein).			
GN	Name=cryIIb; Synonyms=cryII(b), cryV, cryV465;			
OS	Bacillus thuringiensis (subsp. entomocidus).			
OC	Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1436;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BP465;			
RC	MEDLINE=95314293; PubMed=7793960;			
RA	Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;			
RT	"Distribution of cryV-type insecticidal protein genes in Bacillus			
RT	thuringiensis and cloning of cryV-type genes from Bacillus			
RT	thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.			
RT	entomocidus";			
RL	Appl. Environ. Microbiol. 61:2402-2407(1995)			
CC	-!- FUNCTION: Promotes colloidal osmotic lysis by binding to the midgut			
CC	epithelial cells of certain coleopteran and lepidopteran species.			
CC	Active on Plutella xylostella but not on Bombyx mori.			
CC	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during			
CC	sporulation and is accumulated both as an inclusion and as part of			
CC	the spore coat.			
CC	-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-			
CC	terminus.			
CC	-!- SIMILARITY: Belongs to the delta endotoxin family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	EMBL; U07642; AAA82114.1; -			
DR	PIR; I40590; I40590.			
DR	HSSP; P02965; 1CIV.			
DR	InterPro; IPR001178; Endotoxin.			
DR	InterPro; IPR005638; endotoxin_C.			
DR	InterPro; IPR005639; endotoxin_N.			
DR	InterPro; IPR008979; Gal_bind_like.			
DR	Pfam; PF03944; Endotoxin_C; 1.			
DR	Pfam; PF00555; Endotoxin_M; 1.			
DR	Pfam; PF03945; Endotoxin_N; 1.			
KW	Sporulation; Toxin.			
SEQUENCE	719 AA; 81295 MW; E8210ABEA97688E CRC64;			

32	1473.5	39.4	1118	2	Q9AM83	Q9am83 bacillus th
33	1470.5	39.3	793	2	Q6PYW7	Q6pyw7 bacillus th
34	1470.5	39.3	1177	2	Q6EIX3	Q6eix3 bacillus th
35	1468.5	39.2	1155	2	Q93T21	Q93t21 bacillus th
36	1468	39.2	1167	1	C1JA_BACTU	Q45738 bacillus th
37	1463.5	39.1	1181	1	C1AE_BACTL	Q03748 bacillus th
38	1459	39.0	1180	2	Q9S5V8	Q9s5v8 bacillus th
39	1457	38.9	1176	2	Q7WZT9	Q7wzt9 bacillus th
40	1451	38.8	1176	2	Q45736	Q45736 bacillus th
41	1447	38.7	1176	1	C1AA_BACTK	P02965 bacillus th
42	1447	38.7	1176	2	Q9RC30	Q9rc30 bacillus th
43	1436.5	38.4	1179	1	C1AD_BACTA	Q03744 bacillus th
44	1419.5	37.9	1118	2	Q9AM82	Q9am82 bacillus th
45	1416	37.8	1169	2	Q8GHE8	Q8ghe8 bacillus th



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ID CLIC_BACTU STANDARD; PRT; 719 AA.
AC 087404;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIc (Insecticidal delta-endotoxin
DE Pesticidal crystal protein cryIIc (Insecticidal delta-endotoxin
DE CryII(c) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name:cryIIc; Synonyms:cryII(c);
OS Bacillus thuringiensis.
OG Plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C18 / Egypt;
RA Osman Y.A., Madkour M.A., Bulla L.A. Jr.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION. Promotes colloidomotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -1- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -1- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -1- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF056933; AAC62933.1; -.
DR HSSP; P02965; IC1Y.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C_1.
DR Pfam; PF00555; Endotoxin_M_1.
DR Pfam; PF03945; Endotoxin_N_1.
DR Plasmid; Sporulation; Toxin.
KW Plasmid; Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81210 MW; 8370B3F06B905DFF CRC64;

Query Match 94.8%; Score 3546; DB 1; Length 719;
Best Local Similarity 95.0%; Pred. No. 4.8e-236;
Matches 683; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

QY 1 MKLNPKKHQSLSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI 60
DB 1 MKLNPKKHQTLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI 60
QY 61 QTGIGIAGKILGTGVFPAGQIASLVSFILGELWPKGQWEIFMEHVEIINQKILTYA 120
DB 61 QTGIGIAGKILGTGVFPAGQIASLVSFILGELWPKGQWEIFMEHVEIINQKISTYA 120
QY 121 RNKALSDRLGLDALVYHESLSSESWENRNTARSVVKQNYALELMFVKLPFAVSG 180
DB 121 RNKALTDRLGLDALVYHESLSSESWGNRNTARSVVKQNYALELMFVKLPFAVSG 180
QY 181 EEVPLPIYAAQANLHLLLRDASIFGKESGLSASEISTFYNQVTRDYSDHCWKYN 240
DB 181 EEVPLPIYAAQANLHLLLRDASIFEKNGGLSASEISTFYNQVTRDYSHCVKNN 240
QY 241 TGLNNLRGTNAKSWRYNQFRKQMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYDAI 300
DB 241 TGLNNLRATNGQSWRYNQFRKQIELMVLDLVRFPSYDTLVYPIKTTSQLTREVYDAI 300
QY 301 GTVHPNQAFSTTWNNAAPSFAIEAAVIRSHPLDLFLEKVTIYSLLSWSNTQYNNMW 360
DB 301 GTVDPNQALRSTTWNNAAPSFAIEAAVIRSHPLDLFLEKVTIYSLLSWSNTQYNNMW 360

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## RESULT 4

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CLIA_BACTK STANDARD; PRT; 719 AA.
ID CLIA_BACTK STANDARD; PRT; 719 AA.
AC Q45752; P71092; Q45750; Q45751; Q45756;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIa (Insecticidal delta-endotoxin
DE CryII(a) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name:cryIIa; Synonyms:cGcryv, cryII(a), cryV, cryVI;
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSIR732;
RX MEDLINE=93298009; PubMed=8517758;
RA Gleave A.P., Williams R., Hedges R.J.;
RT "Screening by polymerase chain reaction of Bacillus thuringiensis
RT serotypes for the presence of cryV-like insecticidal protein genes and
RT characterization of a cryV gene cloned from B. thuringiensis subsp.
RT kurstaki."
RL Appl. Environ. Microbiol. 59:1683-1687(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=JHCC4835;
RX MEDLINE=92269582; PubMed=1598820;
RA Tailor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;
RT "Identification and characterization of a novel Bacillus thuringiensis
RT delta-endotoxin entomocidal to coleopteran and lepidopteran larvae."
RL Mol. Microbiol. 6:1211-1217(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-1;
RX MEDLINE=95314293; PubMed=7793960;
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;
RT "Distribution of cryV-type insecticidal protein genes in Bacillus
RT thuringiensis and cloning of cryV-type genes from Bacillus
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
RT entomocidus."
RL Appl. Environ. Microbiol. 61:2402-2407(1995).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=AB88;
RX MEDLINE=96178985; PubMed=8606196;
RA Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,
RA Craig J.A., Koziel M.G., Estruch J.J.;

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RT "Cloning of a cryV-type insecticidal protein gene from *Bacillus*  
 RT *thuringiensis*: the cryV-encoded protein is expressed early in  
 RT stationary phase." ;  
 RL J. Bacteriol. 178:2141-2144(1996).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=61;  
 RA Selvaandian A., Bhatnagar R.K.;  
 RA "Isolation, cloning and expression of cryV gene." ;  
 RL submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Promotes colloidomotic lysis by binding to the midgut  
 CC epithelial cells of certain coleopteran and lepidopteran species.  
 CC Active on *Plutella xylostella* and *Bombyx mori*.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; N98544; AAA22354.1; -;  
 DR EMBL; X62821; CAA44633.1; -;  
 DR EMBL; L36338; AAC6999.1; -;  
 DR EMBL; L49391; AAB00958.1; -;  
 DR EMBL; Y08920; CAA70124.1; -;  
 DR PIR; I39815; I39815.  
 DR PIR; S25383; S25383.  
 DR HSSP; P02965; ICIV.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal bind like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 DR Sporulation; Toxin.  
 KW Sporecoat; Toxin.  
 FT 159 K -> R (in strain 61).  
 FT 233 D -> Y (in strain JHCC4835 and strain HD-  
 FT VARIANT 1).  
 FT 443 A -> V (in strain AB88).  
 FT 711 KQ -> NE (in strain HD-1 and strain 61).  
 FT 712 KQ -> NE (in strain HD-1 and strain 61).  
 SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;  
 Query Match 94.1%; Score 3520; DB 1; Length 719;  
 Best Local Similarity 92.9%; Pred. No. 3e-234;  
 Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 MRLKNPKGHOSLSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSHESIDPFSVASTI 60  
 DB 1 MRLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECLKMSYENVEPFSVASTI 60  
 QY 61 QTGIGIAGKILGTGVFPAGQASLYSFIIGELMPKKSQWEIFMEHVEEIIINOKILTVA 120  
 DB 61 QTGIGIAGKILGTGVFPAGQASLYSFIIGELMPKKSQWEIFMEHVEEIIINOKILTVA 120  
 QY 121 RNKALSDLRGDGLAVVHSESVENNRNTRARSVVKNQYIALELMFVQKLPSPAVSG 180  
 DB 121 RNKALTDLKGLDALAVVHDSLESVGNRNTRARSVVKSQYIALELMFVQKLPSPAVSG 180  
 QY 181 BEVPLLPYQAANLHLLLDASIFGKWLCSASEISTYFNQVETRYSDHCICKWYN 240  
 DB 181 BEVPLLPYQAANLHLLLDASIFGKWLCSASEISTYFNQVETRYSDHCICKWYN 240  
 QY 241 TGLNNLRGTNAESWVRYNQFRDWTMLVLDLVALPFSYDTQMYPIKTTAQLTREVTDAI 300

DB 241 TGLNNLRGTNAESWVRYNQFRDWTMLVLDLVALPFSYDTQMYPIKTTAQLTREVTDAI 300  
 QY 301 GTVHPNQAFSTTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW 360  
 DB 301 GTVHPNPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMW 360  
 QY 361 GCHLEGRPIGGALNTSTQGSTNTSINPVTLOFTSRDVRVYTESLAGLNLFLOPVGVP 420  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLOPVGVP 420  
 QY 421 VDFHWKFTPLIASDNFYLYGAGVQLODSENELPPTTGPQNVESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFTVTHPIASDNFYLYGAGVQLODSENELPPTTGPQNVESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYVTHRSADRTNIEPNSITQIPLVAFNLSGAAVVRGPGFTGGDILRTN 540  
 DB 481 ASHVKALVYVTHRSADRTNIEPNSITQIPLVAFNLSGAAVVRGPGFTGGDILRTN 540  
 QY 541 TGTFGDIRVNPPPAQRYRVRIRYASTTDOFTHSINGKAINQGNFSATNRCEDLYK 600  
 DB 541 TGTFGDIRVNPPPAQRYRVRIRYASTTDOFTHSINGKAINQGNFSATNRCEDLYK 600  
 QY 601 TERTTGFTTSPFSVQSTFTIGAWNFSNGNEVYIDRIEFVPEVYVEAEYDFFKAQSKV 660  
 DB 601 TERTVGFTTSPFSVQSTFTIGAWNFSNGNEVYIDRIEFVPEVYVEAEYDFFKAQSKV 660  
 QY 661 TALFTSTNPRGLTKDVKDYHIDQVSNLVESLSDEFYLDKELFEIVKAKQLHIERNN 719  
 DB 661 TALFTSTNPRGLTKDVKDYHIDQVSNLVESLSDEFYLDKELFEIVKAKQLHIERNN 719  
 RESULT 5  
 QX181 PRELIMINARY; PRT; 719 AA.  
 ID QX181  
 AC QX181;  
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
 DE CryII.  
 GN Names=cryII;  
 OS *Bacillus thuringiensis*.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;  
 RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AY262167; AAP86782.1; -;  
 DR GO; GO:0005102; F:receptor binding; IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal bind like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;  
 Query Match 94.1%; Score 3520; DB 2; Length 719;  
 Best Local Similarity 92.9%; Pred. No. 3e-234;  
 Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 MRLKNPKGHOSLSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSHESIDPFSVASTI 60  
 DB 1 MRLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECLKMSYENVEPFSVASTI 60  
 QY 61 QTGIGIAGKILGTGVFPAGQASLYSFIIGELMPKKSQWEIFMEHVEEIIINOKILTVA 120  
 DB 61 QTGIGIAGKILGTGVFPAGQASLYSFIIGELMPKKSQWEIFMEHVEEIIINOKILTVA 120  
 QY 121 RNKALSDLRGDGLAVVHSESVENNRNTRARSVVKNQYIALELMFVQKLPSPAVSG 180

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Db 121 RNKALTDLGLGDALAVYHDSLESWGNNRNRARSVKSQYIALSLMFVQKLPSPAVSG 180
Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISITFYNRQVTERTDYSDHCKIKWN 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISITFYNRQVTERTDYSDHCKIKWN 240
Qy 241 TGLNNLRGTNAKSWRYNQFRDMTLMVLDLVALPFSYDTLVYPIKTTQLTREVTDAI 300
Db 241 TGLNNLRGTNAKSWRYNQFRDMTLMVLDLVALPFSYDTLVYPIKTTQLTREVTDAI 300
Qy 301 GTVHPNQAFSTTWYNNAPSPSAIEAAVIRSPHLLDFLEKVTIYSLLRWSNTQTMNMW 360
Db 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVIRSPHLLDFLEKVTIYSLLRWSNTQTMNMW 360
Qy 361 GGHRLSRPIGGALNTSTOGSTNTSINPVTLOFTSRDVTYRTESLAGLNLFLTOPVNGVPR 420
Db 361 GGHKLEFRITGTLNISTOGSTNTSINPVTLOFTSRDVTYRTESLAGLNLFLTOPVNGVPR 420
Qy 421 VDFHMKFPTLPASDNFYLYGAGVGTQLQDSENELPPETGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHMKFVTHPIASDNFYLYGAGVGTQLQDSENELPPETGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGCDILRRTN 540
Db 481 ASHVKALVSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGCDILRRTN 540
Qy 541 TGFPGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 541 TGFPGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Qy 601 TFRFTGFTTFFPSFDVQSTFTIGAMNFFSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
Db 601 TFRFTGFTTFFPSFDVQSTFTIGAMNFFSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
Qy 661 TALFTSTNPRGLTKDVKDHYDOVSNLVESLSDEFYLDKRELFEIVKAKQIHIERNM 719
Db 661 TALFTSTNPRGLTKDVKDHYDOVSNLVESLSDEFYLDKRELFEIVKAKQIHIERNM 719
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## RESULT 6

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Q93NJ5 PRELIMINARY; PRT; 719 AA.
ID Q93NJ5
AC Q93NJ5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Crylia.
GN Names=Crylia;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]_
SEQUENCE FROM N.A.
RP Song F., Zhang J., Gu A., Huang D., Li G.;
RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF373207; AAK66742.1; -.
DR HSSP: P02965; 1CIY.
DR GO: GO:0005102; Fireceptor binding; IEA.
DR GO: GO:0006952; P:defense response; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR0011178; Endotoxin.
DR InterPro: IPR005638; endotoxin_C.
DR InterPro: IPR005639; endotoxin_N.
DR InterPro: IPR008979; Gal_bind_like.
DR Pfam: PF03944; Endotoxin_C_1.
DR Pfam: PF00555; Endotoxin_M; 1.
DR Pfam: PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81225 MW; C629DF2C4827241 CRC64;
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Query Match 93.9%; Score 3515; DB 2; Length 719;  
Best Local Similarity 92.8%; Pred. No. 6,7e-234;  
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

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Qy 1 MKLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKMNNEIDYLRMSEHESIDPFVSASTI 60
Db 1 MKLKNQDKHQSFSSNAKVDKIATDSLKNETDIELQINHEDECLKMSEYENVEFPVSASTI 60
Qy 61 QTGIGIAGKILGTGVPFAGQIASLYSIFILGELWPKGKQWEIFMEHVEEIIINOKILTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQIASLYSIFILGELWPKGKQWEIFMEHVEEIIINOKILTYA 120
Qy 121 RNKALSDLRGLGDALAVHESLESWVENNRNRARSVKSQYIALSLMFVQKLPSPAVSG 180
Db 121 RNKALTDLKGLGDALAVHDSLESWGNNRNRARSVKSQYIALSLMFVQKLPSPAVSG 180
Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISITFYNRQVTERTDYSDHCKIKWN 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASEISITFYNRQVTERTDYSDHCKIKWN 240
Qy 241 TGLNNLRGTNAKSWRYNQFRDMTLMVLDLVALPFSYDTLVYPIKTTQLTREVTDAI 300
Db 241 TGLNNLRGTNAKSWRYNQFRDMTLMVLDLVALPFSYDTLVYPIKTTQLTREVTDAI 300
Qy 301 GTVHPNQAFSTTWYNNAPSPSAIEAAVIRSPHLLDFLEKVTIYSLLRWSNTQTMNMW 360
Db 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVIRSPHLLDFLEKVTIYSLLRWSNTQTMNMW 360
Qy 361 GGHRLSRPIGGALNTSTOGSTNTSINPVTLOFTSRDVTYRTESLAGLNLFLTOPVNGVPR 420
Db 361 GGHKLEFRITGTLNISTOGSTNTSINPVTLOFTSRDVTYRTESLAGLNLFLTOPVNGVPR 420
Qy 421 VDFHMKFPTLPASDNFYLYGAGVGTQLQDSENELPPETGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHMKFVTHPIASDNFYLYGAGVGTQLQDSENELPPETGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGCDILRRTN 540
Db 481 ASHVKALVSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGCDILRRTN 540
Qy 541 TGFPGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 541 TGFPGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Qy 601 TFRFTGFTTFFPSFDVQSTFTIGAMNFFSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
Db 601 TFRFTGFTTFFPSFDVQSTFTIGAMNFFSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
Qy 661 TALFTSTNPRGLTKDVKDHYDOVSNLVESLSDEFYLDKRELFEIVKAKQIHIERNM 719
Db 661 TALFTSTNPRGLTKDVKDHYDOVSNLVESLSDEFYLDKRELFEIVKAKQIHIERNM 719
```

## RESULT 7

```
O85796 PRELIMINARY; PRT; 719 AA.
ID O85796
AC O85796;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Insecticidal protein.
GN Name=cryVI01;
OS Bacillus thuringiensis (subsp. kurstaki).
OG Plasmid large plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]_
SEQUENCE FROM N.A.
RP STRAIN=SI01;
RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF076953; AAC26910.1; -.
DR HSSP: P02965; 1CIY.
DR GO: GO:0005102; Fireceptor binding; IEA.
DR GO: GO:0006952; P:defense response; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
```

```
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Plasmid.
SQ SEQUENCE 719 AA; 81230 MW; 42746D478359BBA7 CRC64;

Query Match 93.9%; Score 3514; DB 2; Length 719;
Best Local Similarity 92.8%; Pred. No. 7.8e-234;
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MKLNPKDQHSLSSNAKVDTSLKNETDIELKNNEDYLRMSEHESIDPVSASTI 60
Db 1 MKLNPKDQHSLSSNAKVDTSLKNETDIELKNNEDYLRMSEHESIDPVSASTI 60
Qy 61 QTGIGIAGKILGTGVPPAGQIASLYSFLGELWPKGKQWEIFMEHVEEIIINQKILTYA 120
Db 61 QTGIGIAGKILGTGVPPAGQIASLYSFLGELWPKGKQWEIFMEHVEEIIINQKILTYA 120
Qy 121 RNKALSDLRGDGLAVVHESLESWENNRNTRARSVVKNQYIALELMFVKLPSPAVSG 180
Db 121 RNKALSDLRGDGLAVVHESLESWENNRNTRARSVVKNQYIALELMFVKLPSPAVSG 180
Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKEMGLSASEISTFYNRQVTRDYSDHCIKWYN 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEMGLSASEISTFYNRQVTRDYSDHCIKWYN 240
Qy 241 TGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPYDTLVYPIKTTSQLTREVTDAI 300
Db 241 TGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPYDTLVYPIKTTSQLTREVTDAI 300
Qy 301 GTVHPNQAFSTTWNNAAPSFAIEAAVIRSHPLDLEKVTIYSLSRWSNTQYNNMW 360
Db 301 GTVHPNQAFSTTWNNAAPSFAIEAAVIRSHPLDLEKVTIYSLSRWSNTQYNNMW 360
Qy 361 GGHRLSRPIGGALNTSQGSTNTSINPVTLOFTSRDVRTESLAGNLFLTQPVNGVPR 420
Db 361 GGHRLSRPIGGALNTSQGSTNTSINPVTLOFTSRDVRTESLAGNLFLTQPVNGVPR 420
Qy 421 VDFHWKFPPTLPASDNFYLYGAVGTQLODSENELPPEATTGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFPPTLPASDNFYLYGAVGTQLODSENELPPEATTGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVNIAPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTFGDIRVNIAPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TFRFTGFTTTPFSFSDVQSTFTTIGAWNFSGNEVIYDRIEFVPEVVEYAEYDPEKAQEKV 660
Db 601 TFRFTGFTTTPFSFSDVQSTFTTIGAWNFSGNEVIYDRIEFVPEVVEYAEYDPEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 8
Q8KY61 PRELIMINARY; PRT; 719 AA.
AC Q8KY61;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cry.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
```

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OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Porcar M., Martinez C., Caballero P.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF278797; AAW73516.1; -.
DR PIR; B42459; B42459.
DR HSSP; P02965; 1CIY.
DR GO; GO:005102; F:receptor binding; IEA.
DR GO; GO:006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin_C.
DR InterPro; IPR005638; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;

Query Match 93.8%; Score 3510; DB 23; Length 719;
Best Local Similarity 92.8%; Pred. No. 1.5e-233;
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MKLNPKDQHSLSSNAKVDTSLKNETDIELKNNEDYLRMSEHESIDPVSASTI 60
Db 1 MKLNPKDQHSLSSNAKVDTSLKNETDIELKNNEDYLRMSEHESIDPVSASTI 60
Qy 61 QTGIGIAGKILGTGVPPAGQIASLYSFLGELWPKGKQWEIFMEHVEEIIINQKILTYA 120
Db 61 QTGIGIAGKILGTGVPPAGQIASLYSFLGELWPKGKQWEIFMEHVEEIIINQKILTYA 120
Qy 121 RNKALSDLRGDGLAVVHESLESWENNRNTRARSVVKNQYIALELMFVKLPSPAVSG 180
Db 121 RNKALSDLRGDGLAVVHESLESWENNRNTRARSVVKNQYIALELMFVKLPSPAVSG 180
Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKEMGLSASEISTFYNRQVTRDYSDHCIKWYN 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEMGLSASEISTFYNRQVTRDYSDHCIKWYN 240
Qy 241 TGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPYDTLVYPIKTTSQLTREVTDAI 300
Db 241 TGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPYDTLVYPIKTTSQLTREVTDAI 300
Qy 301 GTVHPNQAFSTTWNNAAPSFAIEAAVIRSHPLDLEKVTIYSLSRWSNTQYNNMW 360
Db 301 GTVHPNQAFSTTWNNAAPSFAIEAAVIRSHPLDLEKVTIYSLSRWSNTQYNNMW 360
Qy 361 GGHRLSRPIGGALNTSQGSTNTSINPVTLOFTSRDVRTESLAGNLFLTQPVNGVPR 420
Db 361 GGHRLSRPIGGALNTSQGSTNTSINPVTLOFTSRDVRTESLAGNLFLTQPVNGVPR 420
Qy 421 VDFHWKFPPTLPASDNFYLYGAVGTQLODSENELPPEATTGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFPPTLPASDNFYLYGAVGTQLODSENELPPEATTGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVNIAPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTFGDIRVNIAPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TFRFTGFTTTPFSFSDVQSTFTTIGAWNFSGNEVIYDRIEFVPEVVEYAEYDPEKAQEKV 660
Db 601 TFRFTGFTTTPFSFSDVQSTFTTIGAWNFSGNEVIYDRIEFVPEVVEYAEYDPEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
```

[illegible]



```

DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;

Query Match 65.7%; Score 2459; DB 1; Length 1233;
Best Local Similarity 64.8%; Pred. No. 1.2e-160;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

Qy 3 LKMPDKHQSSNAKVADKIATDSLKNETDIELKMNNDYLRMSEHSIDPFVSASTIQT 62
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
20 VSNPSTQNLSPDARI-----EDSLCVAEVANNIDPFVSASTVQT 58
Qy 63 GIGTAGKILGTGVPPAGQIASLYSFTLGLWPKGSKQWEIFMEHVEEIIKILTYARN 122
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
59 GINTAGRLGVLPVPPAGQIASLYSFTLGLWPKGSKQWEIFMEHVEEIIKILTYARN 118
Qy 123 KALSDRLGLGDALAVHESLESWVENRNNTRARVWKNQYIALELMPVQKLPSFAVSGEE 182
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
119 TAIARLEGLGRGYSYQQALETWLDNNDARSIIILERYVALELDITTAIPLPRINEE 178
Qy 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNNQVTRTDYSDHCIKWTNG 242
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
179 VPLLMVYAQAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTBESNHCVCQWYNTG 238
Qy 243 LNNLRGTNAKSWRYNQFRKDMTLWLDLVALRPSYDTLVVPIKTTSQLTRVYTDAGT 302
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
239 LNNLRGTNAKSWRYNQFRKDMTLWLDLVALRPSYDTLVVPIKTTSQLTRVYTDAGT 298
Qy 303 VHPNQAFSTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWGNTQTMNMGW 362
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
299 TNAPSGFASWNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWGNTQTMNMGW 358
Qy 363 HRLSPRIGGALNTSTQGST-NTSINPVTLOFTSRDYRTESLAGLNLFTQPVNGVPRV 421
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
359 HRLNFRPIGGTLNTSTQGLTNNTSINPVTLOFTSRDYRTESLAGLNLFTQPVNGVPRV 418
Qy 422 DFHWKFTPLDASDNFYVLG-----YAGVGTQLODSENELPETTPGQNYESYSHRLS 474
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
419 RFNF-----INPQNIYERGATTYSQPYQGVGIQLFDSLETLPETTERPNYESYSHRLS 472

Name=cryIbC; Synonyms=cryIB(c), cryIBc;
Bacillus thuringiensis (subsp. morrisoni).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1441;
[]]
SEQUENCE FROM N.A.
Bishop A.H., Bone E.J., Ellar D.J.;
"Cloning of novel Bacillus thuringiensis delta-endotoxin.";
Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
-i- FUNCTION: Promotes colloidomotic lysis by binding to the midgut
epithelial cells of insects.
-i- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
the spore coat.
-i- MISCELLANEOUS: Toxin segment of the protein is located in the N-
terminus.
-i- SIMILARITY: Belongs to the delta endotoxin family.
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or send an email to license@isb-sib.ch).
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EMBL; Z46442; CAA86568.1; -.
HSP; P02965; IC1Y.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin_C.
InterPro; IPR005639; endotoxin_N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PF03944; Endotoxin_C; 1.
Pfam; PF00555; Endotoxin_M; 1.
Pfam; PF03945; Endotoxin_N; 1.
Sporulation; Toxin.
SQ SEQUENCE 1233 AA; 140451 MW; 7318382413529F21 CRC64;

Query Match 65.7%; Score 2459; DB 1; Length 1233;
Best Local Similarity 64.8%; Pred. No. 1.2e-160;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

Qy 3 LKMPDKHQSSNAKVADKIATDSLKNETDIELKMNNDYLRMSEHSIDPFVSASTIQT 62
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
20 VSNPSTQNLSPDARI-----EDSLCVAEVANNIDPFVSASTVQT 58
Qy 63 GIGTAGKILGTGVPPAGQIASLYSFTLGLWPKGSKQWEIFMEHVEEIIKILTYARN 122
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
59 GINTAGRLGVLPVPPAGQIASLYSFTLGLWPKGSKQWEIFMEHVEEIIKILTYARN 118
Qy 123 KALSDRLGLGDALAVHESLESWVENRNNTRARVWKNQYIALELMPVQKLPSFAVSGEE 182
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
119 TAIARLEGLGRGYSYQQALETWLDNNDARSIIILERYVALELDITTAIPLPRINEE 178
Qy 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNNQVTRTDYSDHCIKWTNG 242
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
179 VPLLMVYAQAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTBESNHCVCQWYNTG 238
Qy 243 LNNLRGTNAKSWRYNQFRKDMTLWLDLVALRPSYDTLVVPIKTTSQLTRVYTDAGT 302
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
239 LNNLRGTNAKSWRYNQFRKDMTLWLDLVALRPSYDTLVVPIKTTSQLTRVYTDAGT 298
Qy 303 VHPNQAFSTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWGNTQTMNMGW 362
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
299 TNAPSGFASWNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWGNTQTMNMGW 358
Qy 363 HRLSPRIGGALNTSTQGST-NTSINPVTLOFTSRDYRTESLAGLNLFTQPVNGVPRV 421
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
359 HRLNFRPIGGTLNTSTQGLTNNTSINPVTLOFTSRDYRTESLAGLNLFTQPVNGVPRV 418
Qy 422 DFHWKFTPLDASDNFYVLG-----YAGVGTQLODSENELPETTPGQNYESYSHRLS 474
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
419 RFNF-----INPQNIYERGATTYSQPYQGVGIQLFDSLETLPETTERPNYESYSHRLS 472

RESULT 11
C1BC_BACTM STANDARD; PRT; 1233 AA.
AC Q45774;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIbC (Insecticidal delta-endotoxin
DE CryIb(c)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).

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QY 475 HIGLISASHVYKALVYSWTHRSADRTNTIBPNSITQIPLVKAFLNLSGAAVVRGPGFTGSD 534
D 473 HIGLIIIGNTLRAPVYSWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTVVGSGPGFTGSD 532
QY 535 ILARTWTGFGDIRVNNPFAQRYRVIRYASTDLOFHTSINGKAINOGNFSATMNRG 594
D 533 ILARTWTGFGDIRLNLNPLSQRYRVIRYASTDLOFHTSINGKAINOGNFSATMNRG 592
QY 595 EDLDYKTFRTIGTTPFSQSDVQSTTIGAMNFSNGNEVYIDRIEFPVVEVYEAAYDPE 654
D 593 DNLKYSFRTAGSTPFLNQAQSTTLGAQSPSN-QEVIDRVEFPVPAEVTPEABYDLE 651
QY 655 KAEQKVYALFTSTNPRGLKTDVYHIDQVSNLVSLEDFYLDKRELFYKAKQIH 714
D 652 RAQKAVNALFTSTNPRGLKTDVYHIDQVSNMVACLSDEFCLDKRELFYKAKRLS 711
QY 715 IERNM 719
D 712 DERNL 716

RESULT 12
Q93T75 PRELIMINARY; PRT; 1228 AA.
AC Q93T75;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Delta-endotoxin CryIBa2.
GN Names=CryIBa2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAK51084.1;
DR HSSP; P07130; IDLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin.C.
DR InterPro; IPR005639; endotoxin.N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139520 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match 62.1%; Score 2322.5; DB 2; Length 1228;
Best Local Similarity 63.6%; Pred. No. 3.2e-151;
Matches 453; Conservative 80; Mismatches 162; Indels 17; Gaps 4;

QY 23 TDSLKNETDI-----ELKNNMEDYLRMSHEHSIDPFVASTIQTGIGTAGKI 70
D 2 TSNRKNEEINAVSNHSAQMDLLPARIEDSLCIAEGNNIDPFVASTVQTGINTAGRI 61
QY 71 LGTLGVPPFAGQIASFLIGELWPKGQWEIFMEHVEEINOKILTYARNKALSDLRG 130
D 62 LGVLGVPPFAGQIASFSLVGLWLPGRDQWEIFLEHVEQLINQITENARNALALQ 121
QY 131 LGDALAVYTHSLSWENRNNTRARSVKVQNYIALELMFVKQLPSPAVSGEEVPLPIYA 190
D 122 LGDSFRAYQOQSLDLENRDDARTSVLHFTQYIALELDFLNAMPFAIRNQEVPLMWYA 181
QY 191 QAAHLHLLLRDASIFGKEWGLSASEISTPYNQRVTRDYSRHCCKWNTGLNLRGTN 250
D 182 QAAHLHLLLRDASLFGSEFGLTSQBIQRYRQVTRDYSQVCEWYNTGLNSLRGTN 241

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QY 251 AKSWRVYQFRKDMTLMVLDAVALPSPSYDTLVYPIKTTSQLTREYVYDAIGTVHPNOAFA 310
D 242 AASWRYVQFRDLTLGLVLDLVALPSPSYDTLVYPIKTTSQLTREYVYDAIGTVHPNOAFA 299
QY 311 STTWYNNAPSAEAAVIRSPHLLDLEKVTIYSLLSRWNTQTMNMGHRLSRPI 370
D 300 SMWYNNAPSAEAAVIRSPHLLDLEKVTIYSLLSRWNTQTMNMGHRLSRPI 359
QY 371 CGALNTSTGCGSTNTSINPVTLOFTSRDVYRTESLAGNLNF--LTQPVNGVPRVDFHWKFP 428
D 360 GGLNTSTHGANTSTINPVTLRFASRDVYRTESYAGVLLWGLYLEPIHGVPVTRFNTNP 419
QY 429 -TLPIASDNFYLYAGVGTQLODSENELPPTTGPQNPYESYSHRLSHGLISASHVKAL 487
D 420 QNISDRGTANYQSPYESPGLQKDSLELPTETTERPNYESYSHRLSHGLIILQSRVNP 479
QY 488 VYSWTHRSADRTNTTTPNSITQIPLVKAFLNLSGAAVVRGPGFTGDIILRRNTGTGDI 547
D 480 VYSWTHRSADRTNTTTPNSITQIPLVKAFLNLSGAAVVRGPGFTGDIILRRNTGTGDI 539
QY 548 RVNINPPFAQRYRVIRYASTDLOFHTSINGKAINOGNFSATMNRGEDLDYKTFRTIGF 607
D 540 RVTVNGPLTORIRIGFRYASTVDFFVSRGGTTVNNFRLTMNSGDELKYNFVRRAF 599
QY 608 TTPFSQSDVQSTTIGAMNFSNGNEVYIDRIEFPVVEVYEAAYDPEKAEKVYALFTST 667
D 600 TTPFTFTQDIIRTSIQGLSGNGEVYIDKIIIPVATFAEYDLERAQEAVALFTNT 659
QY 668 NPGRLKTDVYHIDQVSNLVSLEDFYLDKRELFYKAKQIHIERNM 719
D 660 NPRLKTDVYHIDQVSNLVSLEDFYLDKRELFYKAKQIHIERNM 711

RESULT 13
CIBA_BACTK STANDARD; PRT; 1228 AA.
AC P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-PEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein crylBa (Insecticidal delta-endotoxin
DE CrylB(a) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=crylBa; Synonyms=cryA4, crylB(a);
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1436;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
RX MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from
RT Bacillus thuringiensis subsp. thuringiensis.";
RL Nucleic Acids Res. 16:2723-2723 (1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

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CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----

DR EMBL; X05711; CAA29898.1; -;  
DR EMBL; X95704; CAA65003.1; -;  
DR PIR; S00873; S00873.  
DR HSSP; P07130; 1DLC.  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR008979; Gal bind Like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
KW Sporulation; Toxin.  
FT VARIANT 150 150 Y -> H (in strain HD-110).  
SQ SEQUENCE 1228 AA; 139647 MW; C8E3A19FB5D98575 CRC64;

Query Match 62.0%; Score 2321.5; DB 1; Length 1228;  
Best Local Similarity 63.6%; Pred. No. 3.7e-151; Indels 17; Gaps 4;  
Matches 453; Conservative 80; Mismatches 162;

QY 23 TDSLKNETDI-----ELKNNMNEYLRMSEHESIDPFVSASTIQTGIGIAGKI 70  
DB 2 TSNKKNENEIINAVSNHSAQMDLLDPARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61  
QY 71 LGTLGVPPAGQIASYLSFILGELMPKGSQWEIEMHVEEIIINOKILTIVARNKALSDLRG 130  
DB 62 LGVLGVPPAGQLASFSYFLVGLMPGRDQWEIFLEHVEQLINQOITENARNTALARLOG 121  
QY 131 LGDALAVHESLESVENRNTRARSVVKNOVIALELMFVKQLPSFVSGEVEPLPIYA 190  
DB 122 LGDSFRAYQQSLEDWLNDRDARTRSVLYTQYIALELDFINAMPLFAIRNQEVPLLMVYA 181  
QY 191 QAAHLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCICKWYNTGLNLRGTN 250  
DB 182 QAAHLHLLLRDASLFGSEFGLTSQEIQRYERQVTRDYSDYCVWEYNTGLNLRGTN 241  
QY 251 AKSWRVNQFRKDMTLMVLVALPSYDTLVYPIKTTSQLTREVYTDATGTVHPNQAF 310  
DB 242 AASWRYNQFRDLTLGVLDLVALPSYDTRTYPIINTSAQLTREVYTDATGTVN -MA 299  
QY 311 STTWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMGGHRLSRPI 370  
DB 300 SMWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMGGHRLSRPI 359  
QY 371 GGALNTSQGSTNTSINPVTLQFTSRDYRTESLAGLNF -LTOPVNGVPRVDFHWKFP 428  
DB 360 GGGLNTSTHGATNTSINPVTLRFASRDVYRTESYAGVLLMGYLEPIHGVPTVRFNFTNP 419  
QY 429 -TLPIASDNFYLYGAVGTQLQDSNELPPTTGPQNYESYSHRLSHIGLISASHVKAL 487  
DB 420 QNISDRGTANYSQYSPESGLQKDSSETLPPTTERPNYESYSHRLSHIGLILQSRVNP 479  
QY 488 VYSWTHRSADRTNTIENSIQIPLKAFNLSSGAAVVRGPGFTGGDILRNTTGTGDI 547  
DB 480 VYSWTHRSADRTNTIGENRITQIPMKVASELPQGTIVVRGPGFTGGDILRNTTGTGDI 539  
QY 548 RVNINPPAQRYVRIRYASTTDLQFTSINGKAINQGNFSATMRGDELDYKFTTIGF 607  
DB 540 RVTVNGPLTQRYRIGFRYASTVDFDFVSRGGTIVNFRFLRTMNSGDELKYNFVRAP 599  
QY 608 TTPFSDVOSTFTIGAWNFSSGNEVYIDRIEIPVPEVTEYAEYDPEKAQKVTLFTST 667  
DB 600 TTFPTTQIQDITRTSQISGNGEYIDKIEIIPVATFAYEYDLERAQEAVALFTNT 659  
QY 668 NPRELKTVDKXDHIDQVSNLVSLSDEFYLDKRELFEIVYKAKQHIERNM 719  
DB 660 NPRELKTVDYDHIIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 711

Q93NM5 PRELIMINARY; PRT; 1228 AA.  
AC Q93NM5  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Cry1Ba.  
GN Name=crv1Ba;  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zhang J., Song F., Huang D.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DDJ databases.  
DR EMBL; AF368257; AAK63251.1; -;  
DR HSSP; P07130; 1DLC.  
DR GO; GO:0005102; F:receptor binding; IEA.  
DR GO; GO:0006952; P:defense response; IEA.  
DR GO; GO:0009405; P:pathogenesis; IEA.  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR008979; Gal bind Like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
SQ SEQUENCE 1228 AA; 139665 MW; E86D9842341FB439 CRC64;

Query Match 61.8%; Score 2313.5; DB 2; Length 1228;  
Best Local Similarity 63.5%; Pred. No. 1.3e-150;  
Matches 452; Conservative 80; Mismatches 163; Indels 17; Gaps 4;

QY 23 TDSLKNETDI-----ELKNNMNEYLRMSEHESIDPFVSASTIQTGIGIAGKI 70  
DB 2 TSNKKNENEIINAVSNHSAQMDLLDPARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61  
QY 71 LGTLGVPPAGQIASYLSFILGELMPKGSQWEIEMHVEEIIINOKILTIVARNKALSDLRG 130  
DB 62 LGVLGVPPAGQLASFSYFLVGLMPGRDQWEIFLEHVEQLINQOITENARNTALARLOG 121  
QY 131 LGDALAVHESLESVENRNTRARSVVKNOVIALELMFVKQLPSFVSGEVEPLPIYA 190  
DB 122 LGDSFRAYQQSLEDWLNDRDARTRSVLYTQYIALELDFINAMPLFAIRNQEVPLLMVYA 181  
QY 191 QAAHLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCICKWYNTGLNLRGTN 250  
DB 182 QAAHLHLLLRDASLFGSEFGLTSQEIQRYERQVTRDYSDYCVWEYNTGLNLRGTN 241  
QY 251 AKSWRVNQFRKDMTLMVLVALPSYDTLVYPIKTTSQLTREVYTDATGTVHPNQAF 310  
DB 242 AASWRYNQFRDLTLGVLDLVALPSYDTRTYPIINTSAQLTREVYTDATGTVN -MA 299  
QY 311 STTWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMGGHRLSRPI 370  
DB 300 SMWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMGGHRLSRPI 359  
QY 371 GGALNTSQGSTNTSINPVTLQFTSRDYRTESLAGLNF -LTOPVNGVPRVDFHWKFP 428  
DB 360 GGGLNTSTHGATNTSINPVTLRFASRDVYRTESYAGVLLMGYLEPIHGVPTVRFNFTNP 419  
QY 429 -TLPIASDNFYLYGAVGTQLQDSNELPPTTGPQNYESYSHRLSHIGLISASHVKAL 487  
DB 420 QNISDRGTANYSQYSPESGLQKDSSETLPPTTERPNYESYSHRLSHIGLILQSRVNP 479  
QY 488 VYSWTHRSADRTNTIENSIQIPLKAFNLSSGAAVVRGPGFTGGDILRNTTGTGDI 547  
DB 480 VYSWTHRSADRTNTIGENRITQIPMKVASELPQGTIVVRGPGFTGGDILRNTTGTGDI 539  
QY 548 RVNINPPAQRYVRIRYASTTDLQFTSINGKAINQGNFSATMRGDELDYKFTTIGF 607  
DB 540 RVTVNGPLTQRYRIGFRYASTVDFDFVSRGGTIVNFRFLRTMNSGDELKYNFVRAP 599



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2005, 17:22:50 ; Search time 70.6029 Seconds  
(without alignments)  
3350.901 Million cell updates/sec

Title: US-10-019-823B-59

Perfect score: 3742

Sequence: 1 MLLKNPKHQSLSSNAKVDK.....KRELFEIVKYAKQIHIERNM 719

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
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13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
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16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	3520	94.1	719	16	US-10-782-020-10
2	3520	94.1	719	16	US-10-782-141-8
3	3368.5	90.0	710	15	US-10-428-961-42
4	2324.5	62.1	1228	16	US-10-809-953-10
5	2314.5	61.9	1207	10	US-09-988-462-7
6	2234	59.7	1227	15	US-10-428-961-63
7	2219	59.3	1186	9	US-09-826-660-23
8	2170.5	58.0	1228	15	US-10-428-961-38
9	2170.5	58.0	1228	15	US-10-614-524-2
10	1982	53.0	643	9	US-09-826-660-25
11	1734.5	46.4	1167	14	US-10-089-678-1
12	1683.5	45.0	653	15	US-10-428-961-6
13	1657.5	44.3	1157	16	US-10-782-141-16

14	1514	40.5	1206	13	US-10-032-717-2	Sequence 2, Appli
15	1514	40.5	1206	14	US-10-414-637-2	Sequence 2, Appli
16	1514	40.5	1206	15	US-10-606-320-2	Sequence 2, Appli
17	1500.5	40.1	1156	14	US-10-099-285-72	Sequence 28, Appl
18	1500.5	40.1	1156	15	US-10-428-961-28	Sequence 28, Appl
19	1494	39.9	1210	13	US-10-032-717-4	Sequence 4, Appli
20	1494	39.9	1210	14	US-10-414-637-4	Sequence 4, Appli
21	1494	39.9	1210	15	US-10-606-320-4	Sequence 4, Appli
22	1480.5	39.6	1155	9	US-09-756-643-2	Sequence 2, Appli
23	1480.5	39.6	1155	10	US-09-988-462-9	Sequence 9, Appli
24	1480.5	39.6	1155	15	US-10-136-998A-2	Sequence 2, Appli
25	1480.5	39.6	1181	10	US-09-988-462-11	Sequence 11, Appl
26	1480.5	39.6	1181	10	US-09-988-462-13	Sequence 13, Appl
27	1480.5	39.6	1181	10	US-09-988-462-15	Sequence 15, Appl
28	1480.5	39.6	1181	10	US-09-988-462-17	Sequence 17, Appl
29	1480.5	39.6	1181	10	US-09-988-462-28	Sequence 28, Appl
30	1480.5	39.6	1181	15	US-10-136-998A-4	Sequence 4, Appli
31	1480.5	39.6	1181	15	US-10-136-998A-8	Sequence 8, Appli
32	1480.5	39.6	1181	15	US-10-136-998A-10	Sequence 10, Appl
33	1480.5	39.6	1181	15	US-10-136-998A-12	Sequence 12, Appl
34	1475.5	39.4	1177	14	US-10-035-060-6	Sequence 6, Appli
35	1472.5	39.4	1177	14	US-10-102-469-24	Sequence 24, Appl
36	1470.5	39.3	1177	14	US-10-035-060-2	Sequence 2, Appli
37	1470.5	39.3	1177	14	US-10-782-141-6	Sequence 6, Appli
38	1447	38.7	1176	16	US-10-035-060-8	Sequence 8, Appli
39	1436.5	38.4	1176	11	US-09-837-961-2	Sequence 2, Appli
40	1436.5	38.4	1176	16	US-10-825-751-2	Sequence 2, Appli
41	1391	37.2	1167	15	US-10-428-961-40	Sequence 40, Appl
42	1386.5	37.1	1177	9	US-09-873-873-26	Sequence 26, Appl
43	1386.5	37.1	1177	10	US-09-916-956A-26	Sequence 26, Appl
44	1386.5	37.1	1177	10	US-09-997-314-26	Sequence 26, Appl
45	1386.5	37.1	1177	14	US-10-365-645-26	Sequence 26, Appl

#### ALIGNMENTS

RESULT 1  
US-10-782-020-10  
; Sequence 10, Application US/10782020  
; Publication No. US20040197916A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargies, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and  
; FILE REFERENCE: Methods for Its Use  
; FILE REFERENCE: 045600/274139  
; CURRENT APPLICATION NUMBER: US/10782,020  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,810  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-020-10

Query Match 94.1%; Score 3520; DB 16; Length 719;  
Best Local Similarity 92.9%; Pred. No. 4.7e-287;  
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MLLKNPKHQSLSSNAKVDKIATDSLKNETDIELKNNEDYLRMSHESIDPFVSASTI 60

Db 1 MLLKNQDKHQSFSSNAKVDKISTDSLKNETDIELKNNEDYLRMSHESIDPFVSASTI 60

Qy 61 QTGIGIAGKILGTGVPPAGQIASLYSFLGELPKGKSOHEIFMEHVEEIIINQILTYA 120

Db 61 QTGIGIAGKILGTGVPPAGQVASLYSFLGELPKGKQKQWEIFMEHVEEIIINQILTYA 120





Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Launis, Karen L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Syngenta Biotechnology, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/988,462  
FILING DATE: 20-NO. US20030046726A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/547,422  
FILING DATE: 11-APR-2000  
APPLICATION NUMBER: US 08/459,504  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-188051  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-988-462-7  
Query Match 61.9%; Score 2314.5; DB 10; Length 1207;  
Best Local Similarity 65.4%; Pred. No. 3.3e-185;  
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;  
QY 40 EDYLRMSEHSDIPFVSASTIQIGIAGKILGTLPVFPAGQIASLYSIFILGELMPKGS 99  
DB 10 EDSLCIAEGNIDIPFVSASTIQIGIAGKILGTLPVFPAGQIASLYSIFILGELMPKGRD 69  
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DB 70 QWEIFLHVQLINQITENARTALRQLGLGDSFRAYQOQSLDLEWLRDARTRSVLY 129  
QY 160 NOVIALELMFVKQLPSPFVSGEEVPLLPYVQAANLHLLLRDASIFGKEWGLSASEIST 219  
DB 130 TVQVIALELDFLNAMPLFAIRNQEVPLLVYVQAANLHLLLRDASIFGSEFGLTSQEIQR 189  
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250 TRTYPINTSAQLTRVYTDAGTVHPNQAFSTTWNNAFSAIEAAVIRSPHLLDFL 307  
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DB 428 PPTTERPNYESYSHLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAF 487  
QY 517 NLSSGAADVVRGPGFTGGDILRRTNTGTGDIRVNIINPPFAQYRVIRVASTDIDQFHTS 576  
DB 488 ELPOGTTVVVRGPGFTGGDILRRTNTGTGDIRVNIINPPFAQYRVIRVASTDIDQFHTS 547  
QY 577 INKAINQGNFSATMNRGSDLDYKIPRTIGFTTSPFSVDQSTFTTIGAMNFGSGNEVYID 636  
DB 548 RGGTTVNNFRFLRTMNSGDELKYGNFVRRAFTTFTTQIIDIIRTSIOGLSGNGEVYID 607  
QY 637 RIEFVPEVVTYAEYDFEKAQKVTALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFY 696  
DB 608 KIEIIPVATFEAYDLEAQAENALFTNTNPRRLKTDVYHIDQVSNLVESLSDEFY 667  
QY 697 LDEKRELFEIVKYAKQIHIERNN 719  
DB 668 LDEKRELLEKVKYAKRLSDERNL 690  
RESULT 6  
US-10-428-961-63  
; Sequence 63, Application US/10428961  
; Publication No. US20030237111A1  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Wei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Rupar, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)  
; FILE REFERENCE: MECO201--1  
; CURRENT APPLICATION NUMBER: US/10/428,961  
; CURRENT FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: 09/661,322  
; PRIOR FILING DATE: 2000-09-13  
; PRIOR APPLICATION NUMBER: 60/153,995  
; PRIOR FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 63  
; LENGTH: 1227  
; TYPE: PPT  
; ORGANISM: Bacillus thuringiensis  
US-10-428-961-63  
Query Match 59.7%; Score 2234; DB 15; Length 1227;  
Best Local Similarity 60.8%; Pred. No. 2e-178;  
Matches 434; Conservative 100; Mismatches 162; Indels 18; Gaps 3;  
QY 23 TDSLKNETDI----ELKMNK-----EDYLRMSEHSDIPFVSASTIQIGIG 65  
DB 2 TSNRKNENETINALSIPAVSNHSAQMNISTDARIEDSLCIAEGNIDIPFVSASTIQIGIN 61  
QY 66 TAGKILGTLPVFPAGQIASLYSIFILGELMPKGSQWEIFMEHVEEIIQKILTYVARNKAL 125  
DB 62 INGRILGLVLPVFPAGQIASLYSIFILGELMPKGRDQWEIFLHVQLINQITENARTALRQL 121  
QY 126 SDRLGLGDALAVTHESLESWENNTTRARSVVKVNYALFMFVKQLPSPFVSGEEVPL 185





Query Match		58.0%; Score 2170.5; DB 15; Length 1228;
Best Local Similarity		60.5%; Pred. No. 4.5e-173;
Matches 435; Conservative		98; Mismatches 171; Indels 15; Gaps 8;
12 LSSNAK-----VDKIATDSLKN-ETDIELK-NMNNEDYLRMSHESIDPFVSASTIQTGI		64
1 LTSNRKNEINEINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI		60
65 GIAGKILGTGVFPAGQIASLYSIFILGELWPKGSQWEIFMEHVEEIIINQILTYARNKA		124
61 NIAGRILGVLPAGQIASFYSLFVGLWPRGRDQWEIFLEHVEQLINQOITENARNTA		120
125 LSDLRGLGDALAVYHESLESVENNTRARSVVKNQYIALELMFVQKLPSPFAVSGEVP		184
121 LARLQGLGDSFRAYQOQSLDLENRDARTSRVLYTYQYIALELDFLNAFLPFAIRNQEVP		180
185 LPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNNQVTRDYSDHCIKWYNTGLN		244
181 LLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVETRDYSDYCVWYNTGLN		240
245 NLRGTAASWRYNQFRDMLVLDLVALPSPYDTRTPINTSAQLTREYVTDAGTGVH		304
241 SLRGTAASWRYNQFRDMLVLDLVALPSPYDTRTPINTSAQLTREYVTDAGTGVH		300
305 PNQAFASWRYNQFRDMLVLDLVALPSPYDTRTPINTSAQLTREYVTDAGTGVH		364
301 VN--MASMNNWYNNAPSFSAIEAIVIRSPHLLDFLEKVTIYSLLSRWSTNTQYNNMNGGHR		358
365 LESRPIGALNTSTOGSTNTSINPVLQFTSRDVRTESLAGLNLF--LTQPVNGVPRVD		422
359 IQSRPIGGGLNTSTHGSTNTSINPVLQFTSRDVRTESLAGLNLF--LTQPVNGVPRVD		418
423 FHWKFP--TLPTASDNFYLYAGVGTQLODSENELPPTTQPNYESYSHRLSHIGLIS		480
419 FNRNPQNTFERGTAN--YSQPYESPGQLQKQDSELPPTTQPNYESYSHRLSHIGLIS		477
481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRTN		540
478 QSRVHVVPVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRTN		537
541 TGTGDIRVNIINPPFAQRVVRIRYASTDLOFHTSINGKAINQGNFSAATMNRGEDLDYK		600
538 NGSVLSMGLNFNTSLQRYRVRVYAAASQTMVLRTVTVGGSTTFDQGPSTMSANESLSQ		597
601 TFRITGFTTFFSDVQSTFTIGANFSSGNEVVDRIEFVPEVVEYAEYDFEKAQEKV		660
598 SFRFAEPFVGISASGSQ--TAGISISNNAGROTFFHDKIEFIPITATFEAYDLERAQAV		656
661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM		719
657 NALFTNTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM		715

RESULT 10  
US-10-614-524-2  
Sequence 25, Application US/09826660  
Patent No. US20010026940A1  
GENERAL INFORMATION:  
APPLICANT: Cardineau, Guy A.  
APPLICANT: Stelman, Steven J.  
APPLICANT: Narva, Kenneth E.  
TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins  
FILE REFERENCE: MA-714XC2D1  
CURRENT APPLICATION NUMBER: US/09/826,660  
PRIORITY FILING DATE: 2001-04-05

US-10-614-524-2  
Sequence 2, Application US/10614524  
Publication No. US20040016020A1  
GENERAL INFORMATION:  
APPLICANT: Arnaut, Greta  
APPLICANT: Boets, Annemie  
APPLICANT: Damme, Nicole  
APPLICANT: Mathieu, Eva  
APPLICANT: Vanneste, Stijn  
APPLICANT: Van Rie, Jeroen  
TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.  
FILE REFERENCE: NEWBTSUS2  
CURRENT APPLICATION NUMBER: US/10/614,524  
PRIORITY FILING DATE: 2003-07-08  
PRIORITY FILING DATE: 2000-12-19  
PRIORITY FILING DATE: 1999-12-28



US-10-428-961-6  
; Sequence 6, Application US/10428961  
; Publication No. US20030237111A1  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Ruper, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)  
; FILE REFERENCE: MECO201-1  
; CURRENT APPLICATION NUMBER: US/10/428,961  
; PRIORITY FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: 09/661,322  
; PRIORITY FILING DATE: 2000-09-13  
; PRIOR APPLICATION NUMBER: 60/153,995  
; PRIORITY FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 653  
; TYPE: PRN  
; ORGANISM: Bacillus thuringiensis  
US-10-428-961-6  
  
Query Match 45.0%; Score 1683.5; DB 15; Length 653;  
Best Local Similarity 51.3%; Pred. No. 1.7e-132;  
Matches 345; Conservative 111; Mismatches 169; Indels 47; Gaps 15;  
  
QY 13 SSNAKDKIATDSLKN--ETDIELKMNEDYLRMSHESIDPPVSASTITQTGIGIAGK 69  
DB 2 NENEINALSIPAVSHNSQMDLSL-DARIEDSLCIAEGNNINPLVSASTVQTGINAGR 60  
  
QY 70 ILGLTGVPPAGIASLYFILGELMPKGSQWEIPEWHEVEIINOKIITYARNKALSRLR 129  
DB 61 ILGLVGPAGIAGLSPYSLVGLWPSGRDPWEIPEWHEVEIINOKIITYARNKALSRLR 120  
  
QY 130 GLGDALAVHESLESVENNTRARSVVKNQVYALFELMFVQKLPSPFAVSGEEVPLPIY 189  
DB 121 GLGRGYSYQOALWLDNRNDRSIIILERYVALEDDITTAIFLFRINEVEVPLLMVY 180  
  
QY 190 AQAAHLHLLLRDASIFGKSWGLSASEISFTFNQVQRTDYSDHCIKWYNTGLNLRGT 249  
DB 181 AQAAHLHLLLRDASIFGSEWGWASSDVNQYQOEQIRYEEYNSHCVQWYNTGLNLRGT 240  
  
QY 250 NAKSWRYNQFRKDMTLMVLVDLVALPPSYDTLPIYPIKTSQTLTREYTDATGTVHPNQAF 309  
DB 241 NAKSWRYNQFRDLTLGLVLDLVALPPSYDTLPIYPIKTSQTLTREYTDATGTVHPNQAF 300  
  
QY 310 ASTTWYNNAPSAEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYMMWGHRLGRP 369  
DB 301 ASTWYNNAPSAEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYMMWGHRLGRP 360  
  
QY 370 IGGALNTSGST-NTSINPVTIQF-TSRDVRITESLAGLNLFLTOPVNGVPRVDFPHKF 427  
DB 361 IGGALNTSGST-NTSINPVTIQF-TSRDVRITESLAGLNLFLTOPVNGVPRVDFPHKF 418  
  
QY 428 PTL-----PIASDN-FYVLGAVGTQLQDSENELPPTGQPNYESYHRLSHIG-- 477  
DB 419 ITLRIFKEAPLPTVNRIRLGENYLIQKLNHYQK-----QQNDQIMNHIVIDISYR 470  
  
QY 478 LISASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSCAAVVRGPGFTGDIILR 537  
DB 471 LIIGTLURAPVSWTHRSADRTNTEPNSITQIPLVKAFNLSCAAVVRGPGFTGDIILR 529  
  
QY 538 -RINTGTGTF---GIRVNNIN-PFPAQRYRVRIRVASTTDLQFHTSINGKAINQGNFATWN 592  
DB 530 LNRNNGNIQNGYIEVPIQTSSTRYRVRVRVASVTSIELNVNLGNSIFTNLTLPATAA 589  
  
QY 593 RGEDLDYKTRTGTFTFPFSFDSQSTFT-----IGAWNFSGNEVYIDRIEFVPEVT 646  
DB 590 SLDNLQ-----SGDFGYEINNFTSATGNIVGARNFSAEVIIDRIEFVPEVT 640

QY 647 YEAAYDFEKAQE 658  
DB 641 FEVEYDLERAQK 652  
  
RESULT 13  
US-10-782-141-16  
; Sequence 16, Application US/10782141  
; Publication No. US20040197917A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274143  
; CURRENT APPLICATION NUMBER: US/10/782,141  
; CURRENT FILING DATE: 2004-02-20  
; PRIOR APPLICATION NUMBER: 60/448,632  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 1157  
; TYPE: PRN  
; ORGANISM: Bacillus thuringiensis  
US-10-782-141-16  
  
Query Match 44.3%; Score 1657.5; DB 16; Length 1157;  
Best Local Similarity 48.9%; Pred. No. 6.4e-130;  
Matches 368; Conservative 107; Mismatches 228; Indels 49; Gaps 19;  
  
QY 1 MKNLPKQHSLSNAKVDKIATDS---LKNETDIELKMNEDYLRMSEHE-----S 50  
DB 1 MSPNNQNEYELIATPST-SVSDSNRYPPANETPDALQNNYKDYLKMSGGENPELFCN 59  
  
QY 51 IDPFVSASTITQTGIGIAGKILGTGVPPAGIAGLSPYSLVGLWPSGRDPWEIPEWHEVE 109  
DB 60 PETIISSTIQTGIGIAGKILGTGVPPAGIAGLSPYSLVGLWPSGRDPWEIPEWHEVE 119  
  
QY 110 EIIINOKILTIVARNKALSRLRGLGDALAVHESLESVENNTRARSVVKNQVYALFELMF 169  
DB 120 ELVDQKIEKYVKDALKALAEKGLGNALDYQOOSLEWLENRNDARTSVSNQFALDLP 179  
  
QY 170 VOKLPSPFAVSGEEVPLPIYAAQANLHLLLRDASIFGKSWGLSASEISFTFNQVQRTDY 229  
DB 180 VSSIPSPFAVSGEEVPLPIYAAQANLHLLLRDASIFGKSWGLSASEISFTFNQVQRTDY 239  
  
QY 230 DYSRHCIKWYNTGLNLRGTNAKSWRYNQFRKDMTLMVLVDLVALPPSYDTLPIKTS 289  
DB 240 EYSDYCVKWKYKIGLDKLGKGTTSKSWLVYHQFRRENTLLVLDLVALFPNYDTHMYP 299  
  
QY 290 QLTREYVTDATG-TVHPNQAFSTTWYNNAPSAEAAVIRSPHLLDFLEKVTIYSL 348  
DB 300 QLTREYVTDATG-TVHPNQAFSTTWYNNAPSAEAAVIRSPHLLDFLEKVTIYSL 356  
  
QY 349 SR-----WSTQYMMWGHRLGRPPIGALNTST--QGSTNTSINPVTIQFSTRDVRITES 402  
DB 357 SRGGITLNDAYINYSWGHRLGRPPIGALNTST--QGSTNTSINPVTIQFSTRDVRITES 414  
  
QY 403 SLAGLNLFLTOPVNGVPRVDFPHW-KPPLTPASDNFYVLGAVGTQLQ-----DSENE 455  
DB 415 STVANLANVYQKAYGVPGSWFHMKRGKGT-----SSTTAYL-YSKHTALQCGTQVYESSDE 469  
  
QY 456 LPPEITGQPNYESYHRLSHI-----GLISASHVKALVSWTHRSADRTNTEPNSI 507  
DB 470 IFLDRT-VFVAESYSHRLSHITSHFSKNG--SAYGSPFVFWHTTSADLNNIYSDKI 526  
  
QY 508 TQIPLVKAFNLSSGAAVVRGPGFTGDIILRNTGTGDIRVNNINPFPAPQRYRVRIRVAS 567

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Db 527 TQIPAVKGMVLYLGGVVQVGGFTGGDILKRTNPSILGTFPAVTNGSLSQRVRIIRYAS 586
Qy 568 TTDLOFHTSINGKAINQGNFATMNRGDLKYKTRITGFTTPPSFSDVQSTFTIGAWNF 627
Db 587 TTDPEF-TLYLGDITIEKRNKTMONGASLTVEYFKPASFITDQFRETQDKILLSMGDF 645
Qy 628 SSGHEVYIDRIEFVPEVVEYAEVDYFKAQKVALFTSTNPRGLKTDVVDYHIDQVSLN 687
Db 646 SSGQEVYIDRIEFVPEVVEYAEVDYFKAQKVALFTSTNPRGLKTDVVDYHIDQVSLN 704
Qy 688 VESLSDFYLDKRELFEIVKAKQIHIERNM 719
Db 705 VECLSDLLYPNEKRLFLDFAVREAKRLSGARNL 736

RESULT 14
US-10-032-717-2
; Sequence 2, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-032-717-2
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Query Match 40.5%; Score 1514; DB 13; Length 1206;
Best Local Similarity 44.1%; Pred. No. 8.3e-118;
Matches 338; Conservative 126; Mismatches 226; Indels 76; Gaps 22;

Qy 1 MKNPNPKHQSLSSNAKVDKIATDS----LKNETDIELKNNNEDYLRMSHESID---- 52
Db 1 MSPNNQNEYIIDATPST-SVNSDNRYPFPANETNALQNMDDYKDYLKMSAGNASEYPGS 59

Qy 53 PFVSAS---TIQTGIGIAGKILGTGVFPAGQIASLYSFIILGELWPKG-KSQWEIFMEHV 108
Db 60 PEVLVSGQDAKAADIIVGKLLSGLVFPVGPVIVSLYTLQDILWLPSEKQWEIFMEQV 119

Qy 109 EEINQKILTYARNKALSDRLGDLALAVYHESLESWVENNTRARVVKVQYIALELM 168
Db 120 EEINQKIAEYARNKALSEGLGNQYLYLTALAEWEENPGSRALDRVRNREILDSL 179

Qy 169 FVQKLPSFVSGEVEVPLPIYQAQANLHLLLRDASIFGKEWGLSASISITFYNOVERT 228
Db 180 PTQWPSFRVTNFEVFFLTVYMAANLHLLLRDASIFGKEWGLSASISITFYNOVERT 239

Qy 229 RYSDHCIKYNTGLNNLRNNAKSWRYNFRKDMTLMVLDLVALFPSTYDLYVPIKTT 288
Db 240 AEYSDHCVKVETGLAKLGTSAKOWDYNOFRREMTLAVLDVVALFPNRYDRIYPMETK 299

Qy 289 SOLTREYVTDAGTVHPNQAFSTWYNNNAAPSFAIEAAVIRSPHLDFLEKVIYSL 348
Db 300 AQLTREYVTDPLGAVNVS---SIGSWY-DKAPSGVIESSVIRPPHVPDYITGLTVYTS 355

Qy 349 SPMNSTQYMMWGGHLESRRPIGGLATNTSTOGSTNTSINPV-TLQFTSRDYRTESLAGL 407
Db 356 RSISAYIRHWAGHQISYHRVSRGSLQYMGYGTNQNLHJSTSTFDFTNYDIKTLSDAV 415
```

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Qy 408 NLFLTQP-----VNGVPRVDFHW-----KEPTL-----PIASDNFYLYGAGVGTQLDSE 453
Db 416 LLDIVYPCYTYIFGMEVEFFVMVQNLNRTKILKYNEVSKD-----IIASTRUSE 466
Qy 454 NELPETTGQPNYESYSHRLSHIGLISAS-HVKAL--VYSWTHRSADRTNTEPNSITQI 510
Db 467 LELPETSDQPNYESYSHRLCHITISIPATGNTTGLVPVSWTHRSADLNNIYSDKITQI 526
Qy 511 PLVKAFNLSSGAAVVRGPGFTGGDILR-RTNTGTFGDI---RVNINPPFAQRYRIRIYA 566
Db 527 PAVKCDNLFPVVPVVGPGHTGGDLLQVNRSTGSGVGLTFLARYGLALEKAGKYRVLRYA 586
Qy 567 STTDLOFHTSINGKAINQGNFATMNRGDLKYKTRITGFTTPPSFSDVQSTFTIGAWNF 627
Db 587 TTDPEF-TLYLGDITIEKRNKTMONGASLTVEYFKPASFITDQFRETQDKILLSMGDF 645
Qy 615 -DVOSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEVDYFKAQKVALFTSTNPRGLK 673
Db 642 EDPNSTLS-----GIVVDRIEFIPVDETYEAEQDLEAKKAVNALFTNTKD-GLR 691
Qy 674 TDVVDYHIDQVSLVESLSDFYLDKRELFEIVKAKQIHIERNM 719
Db 692 PGVTDYEVNQANLVCECLSDLLYPNEKRLFLDFAVREAKRLSGARNL 737

RESULT 15
US-10-414-637-2
; Sequence 2, Application US/10414637
; Publication No. US20030177528A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/414,637
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-414-637-2
```

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Query Match 40.5%; Score 1514; DB 14; Length 1206;
Best Local Similarity 44.1%; Pred. No. 8.3e-118;
Matches 338; Conservative 126; Mismatches 226; Indels 76; Gaps 22;

Qy 1 MKNPNPKHQSLSSNAKVDKIATDS----LKNETDIELKNNNEDYLRMSHESID---- 52
Db 1 MSPNNQNEYIIDATPST-SVNSDNRYPFPANETNALQNMDDYKDYLKMSAGNASEYPGS 59

Qy 53 PFVSAS---TIQTGIGIAGKILGTGVFPAGQIASLYSFIILGELWPKG-KSQWEIFMEHV 108
Db 60 PEVLVSGQDAKAADIIVGKLLSGLVFPVGPVIVSLYTLQDILWLPSEKQWEIFMEQV 119

Qy 109 EEINQKILTYARNKALSDRLGDLALAVYHESLESWVENNTRARVVKVQYIALELM 168
Db 120 EEINQKIAEYARNKALSEGLGNQYLYLTALAEWEENPGSRALDRVRNREILDSL 179

Qy 169 FVQKLPSFVSGEVEVPLPIYQAQANLHLLLRDASIFGKEWGLSASISITFYNOVERT 228
Db 180 PTQWPSFRVTNFEVFFLTVYMAANLHLLLRDASIFGKEWGLSASISITFYNOVERT 239
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Qy 229 RDYSDHCIKWNTGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPDYDTLVPIKTT 288
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
240 AEYSDHCVKWYETGLAKLKGTSKQWVDYQFREMILAVLDVVALFPNYDTRTPMETK 299
Qy 289 SOLTREVYTDAGTVHPNQAFSTWYNNAPSAEAAVIRSPHLLDFLEKVTIYSL 348
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
300 AOLTREVYTDPLGAVNVS--SIGSWY--DKAPSGFVIESSVIRPPHVPDYITGLTVY 355
Qy 349 SRWENTQYMNWGGHRLSRRIGGALNTSTQGSTNTSINPV-TLQFTSRDVYRTESLAGL 407
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
356 RSISARVIRHWAGHQISYHRVSRGSLNQMYGTNQNLHSTSTFDFNYDIYKTLSDAV 415
Qy 408 NLFLTQP-----VNGVPRVDFHW-----KPFTL---PIASDNFYILGYAGVGTQLODSE 453
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
416 LLDIVYPGYTVIFFGMPVEPFVFNQNLNTRKTLKYNVSKD-----IIASTRDS 466
Qy 454 NELPRTTGPQNYESYSHLSHIGLISAS-HVKAL--VYSWTHESADETNTIEPNSITOI 510
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
467 LELPETSDDQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKITOI 526
Qy 511 PLVKAFNLSSGAAVVRGPGFTGGDILR-RTNTGTFGDI---RVNINPPFAQYRVIRIYA 566
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
527 PAVKCDNLFPVPVVKGFHGGDLLOYNRSTGSGVGTFLFARYGLALEKACKYRVRLEYA 586
Qy 567 STTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFR-----TIGFTTPEFS- 614
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
587 TDADIVLH--VNDAGI---QMPKTMNPGEDLTSKTFKVADAITTLNLTATDSSLAKHNLG 641
Qy 615 -DVQSTFTIGAWNPFSSGNEVYDRIEFVVPVEVYEAEDFEKAQEKYTALETSTNPRCLK 673
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
642 EDPNSTLS-----GIVYVDRIEFIPVDETVEAEQDLEAKKAVNALFTNTKD-GLR 691
Qy 674 TDVKDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQIHIERNM 719
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
692 PGVTDYEVNQANLVNVECLSDDLYPNEKRLLPDAVREAKRLSEARNL 737

```

Search completed: March 9, 2005, 18:08:26  
Job time : 73.6029 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 9, 2005, 17:18:14 ; Search time 23.1512 Seconds  
(without alignments)  
2318.356 Million cell updates/sec

Title: US-10-019-823B-59  
Perfect score: 3742  
Sequence: 1 MKLKNPKHQSLSSNAKVDK.....KRELFEIVKYAKQHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pap:\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pap:\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pap:\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pap:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pap:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3546	94.8	719	2	US-09-003-217-2
2	3541	94.6	719	3	US-09-218-942-2
3	3516	94.0	719	3	US-08-286-870A-8
4	3368.5	90.0	710	4	US-09-661-322A-42
5	3160	84.4	648	3	US-08-286-870A-4
6	2573	68.8	535	3	US-08-286-870A-6
7	2459	65.7	1229	1	US-08-100-709-4
8	2459	65.7	1229	1	US-08-176-865-4
9	2459	65.7	1229	1	US-08-474-038-4
10	2459	65.7	1229	2	US-08-779-046-4
11	2459	65.7	1229	2	US-08-881-340-4
12	2314.5	61.9	1207	1	US-07-951-715A-7
13	2314.5	61.9	1207	2	US-08-459-448A-7
14	2314.5	61.9	1207	3	US-08-459-595A-7
15	2314.5	61.9	1207	3	US-08-459-504B-7
16	2314.5	61.9	1207	3	US-08-459-444-7
17	2314.5	61.9	1207	3	US-09-053-549-8
18	2314.5	61.9	1207	3	US-09-547-432-7
19	2314.5	61.9	1207	4	US-09-988-462-7
20	2308.5	61.7	1227	3	US-09-053-549-2
21	2243	59.9	1227	1	US-08-448-170-8
22	2243	59.9	1227	3	US-08-961-803-9
23	2234	59.7	1227	4	US-09-661-322A-63
24	2233.5	59.7	488	1	US-08-448-170-10
25	2233.5	59.7	488	3	US-08-961-803-10
26	2219	59.3	1186	3	US-09-178-252-23
27	2219	59.3	1186	4	US-09-826-660-23

28	2168.5	58.0	1228	4	US-09-661-322A-38	Sequence 38, Appl
29	1982	53.0	643	3	US-09-178-252-25	Sequence 25, Appl
30	1982	53.0	643	4	US-09-826-660-25	Sequence 25, Appl
31	1813	48.5	380	5	PCT-US91-02560-4	Sequence 4, Appl
32	1683.5	45.0	653	4	US-09-661-322A-6	Sequence 6, Appl
33	1657.5	44.3	1157	1	US-07-876-280-30	Sequence 30, Appl
34	1657.5	44.3	1157	1	US-07-812-180A-2	Sequence 2, Appl
35	1657.5	44.3	1157	1	US-08-315-468-2	Sequence 2, Appl
36	1657.5	44.3	1157	3	US-07-941-650A-2	Sequence 2, Appl
37	1519.5	40.6	1176	1	US-08-257-999-2	Sequence 2, Appl
38	1507	40.3	1157	2	US-08-532-547-5	Sequence 5, Appl
39	1507	40.3	1157	2	US-08-379-656B-5	Sequence 5, Appl
40	1507	40.3	1157	3	US-08-458-838-5	Sequence 5, Appl
41	1507	40.3	1157	3	US-09-019-809-5	Sequence 5, Appl
42	1507	40.3	1157	4	US-09-471-177-5	Sequence 5, Appl
43	1507	40.3	1157	4	US-09-220-806-5	Sequence 5, Appl
44	1506.5	40.3	1168	1	US-08-291-368-4	Sequence 4, Appl
45	1506.5	40.3	1168	2	US-08-962-190-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1  
US-09-003-217-2  
; Sequence 2, Application US/09003217  
; Patent No. 5986177  
; GENERAL INFORMATION:  
; APPLICANT: Osman, Yehia A.  
; APPLICANT: Madkour, Magdy A.  
; APPLICANT: Bulla, Lee A.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH  
; TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)  
; STREET: 3605 Glenwood Ave. Suite 310  
; CITY: Raleigh  
; STATE: NC  
; COUNTRY: US  
; ZIP: 27622  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/003,217  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: 5718-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919 420 2202  
; TELEFAX: 919 881 3175  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-003-217-2

Query Match 94.8%; Score 3546; DB 2; Length 719;  
Best Local Similarity 95.0%; Pred. No. 6.1e-316;  
Matches 683; Conservative 11; Mismatches 25; Indels 0; Gaps 0;  
Qy 1 MKLKNPKHQSLSSNAKVDKIATSLKNETDIELKNNMNEVDYLRMSEHSDPPFVSASTI 60  
Db 1 MKLKNPKHQSLSSNAKVDKIATSLKNETDIELKNNMNEVDYLRMSEHSDPPFVSASTI 60

QY 61 QTGIGIAGKILGTGLVPPAGQIASLYSIFILGELWPKGKSQWEIFMEHVEEIIINQKILTYA 120  
 DB 61 QTGIGIAGKILGTGLVPPAGQIASLYSIFILGELWPKGKSQWEIFMEHVEEIIINQKILTYA 120  
 QY 121 RNKALSDLRGLGDALAVYHESLESWENNRNTRARSVVKNQYIALELMFVKQLPSPFAVSG 180  
 DB 121 RNKALSDLRGLGDALAVYHESLESWENNRNTRARSVVKNQYIALELMFVKQLPSPFAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLDASIFGKEMGLSASEISTFYNRQVTRDYSDHCIIKWN 240  
 DB 181 BEVPLLPPIYAQAANLHLLLDASIFGKEMGLSASEISTFYNRQVTRDYSDHCIIKWN 240  
 QY 241 TGLNLRGTNAKSWVRYNQFRKDMVLDLVALFPSSYDITLVPYIKTTSQLTREVYTDAI 300  
 DB 241 TGLNLRGTNAKSWVRYNQFRKDMVLDLVALFPSSYDITLVPYIKTTSQLTREVYTDAI 300  
 QY 301 GTVHPNOAFASSTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW 360  
 DB 301 GTVHPNOAFASSTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW 360  
 QY 361 GGHRLSPICGALNTSTQSTNTSINPVTLOFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420  
 DB 361 GGHRLSPICGALNTSTQSTNTSINPVTLOFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420  
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 DB 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLODSENELPETTGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTK 540  
 DB 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTK 540  
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 DB 541 TGTGCDIRVNINPPPAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDLDYK 600  
 QY 601 TFRITGFTTSPFSQVSTFTIGAWNFSSGNEVYIDRIEFVPEVYVTEAEYDFFKAQEKV 660  
 DB 601 TFRITGFTTSPFSQVSTFTIGAWNFSSGNEVYIDRIEFVPEVYVTEAEYDFFKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFELFVYKAKQIHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFELFVYKAKQIHIERNM 719

RESULT 2  
 US-09-218-942-2  
 ; Sequence 2, Application US/09218942  
 ; Patent No. 6232439  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Osman, Yehia  
 ; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum  
 ; FILE REFERENCE: CryII  
 ; CURRENT APPLICATION NUMBER: US/09/218,942  
 ; EARLIER FILING DATE: 1998-12-22  
 ; EARLIER APPLICATION NUMBER: 60/035,361  
 ; EARLIER FILING DATE: 1997-01-10  
 ; EARLIER APPLICATION NUMBER: 09/003,217  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-09-218-942-2  
 Query Match 94.6%; Score 3541; DB 3; Length 719;  
 Best Local Similarity 95.0%; Pred. No. 1.4e-317;  
 Matches 683; Conservative 11; Mismatches 25; Indels 0; Gaps 0;  
 QY 1 MFLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSHESIDPFVSASTI 60

DB 1 MFLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSHESIDPFVSASTI 60  
 QY 61 QTGIGIAGKILGTGLVPPAGQIASLYSIFILGELWPKGKSQWEIFMEHVEEIIINQKILTYA 120  
 DB 61 QTGIGIAGKILGTGLVPPAGQIASLYSIFILGELWPKGKSQWEIFMEHVEEIIINQKILTYA 120  
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 DB 121 RNKALSDLRGLGDALAVYHESLESWENNRNTRARSVVKNQYIALELMFVKQLPSPFAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLDASIFGKEMGLSASEISTFYNRQVTRDYSDHCIIKWN 240  
 DB 181 BEVPLLPPIYAQAANLHLLLDASIFGKEMGLSASEISTFYNRQVTRDYSDHCIIKWN 240  
 QY 241 TGLNLRGTNAKSWVRYNQFRKDMVLDLVALFPSSYDITLVPYIKTTSQLTREVYTDAI 300  
 DB 241 TGLNLRGTNAKSWVRYNQFRKDMVLDLVALFPSSYDITLVPYIKTTSQLTREVYTDAI 300  
 QY 301 GTVHPNOAFASSTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW 360  
 DB 301 GTVHPNOAFASSTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW 360  
 QY 361 GGHRLSPICGALNTSTQSTNTSINPVTLOFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420  
 DB 361 GGHRLSPICGALNTSTQSTNTSINPVTLOFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLODSENELPETTGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLODSENELPETTGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTK 540  
 DB 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTK 540  
 QY 541 TGTGCDIRVNINPPPAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDLDYK 600  
 DB 541 TGTGCDIRVNINPPPAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDLDYK 600  
 QY 601 TFRITGFTTSPFSQVSTFTIGAWNFSSGNEVYIDRIEFVPEVYVTEAEYDFFKAQEKV 660  
 DB 601 TFRITGFTTSPFSQVSTFTIGAWNFSSGNEVYIDRIEFVPEVYVTEAEYDFFKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFELFVYKAKQIHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFELFVYKAKQIHIERNM 719

RESULT 3  
 US-08-286-870A-8  
 ; Sequence 8, Application US/08286870A  
 ; Patent No. 6063605  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ELY, S  
 ; APPLICANT: TAILOR, RH  
 ; APPLICANT: TIPPETT, JM  
 ; APPLICANT: BLENN, RG  
 ; TITLE OF INVENTION: BACTERIAL GENES  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
 ; ADDRESSEE: Intellectual Property Group of  
 ; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
 ; STREET: 1100 New York Avenue, N.W.  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005-3918  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30



CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286.870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PAUL N. KOKULIS  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 70608/220720  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-286-870A-8

Query Match 94.0%; Score 3516; DB 3; Length 719;  
Best Local Similarity 92.8%; Pred. No. 3e-315;  
Matches 667; Conservative 32; Mismatches 20; Indels 0; Gaps 0;  
  
Qy 1 M K L N P D K H Q S L S N A K V D K I A T D S L K N E T D I E L K M N N E D Y L R M S E H S I D P P F V S A S T I 60  
Db 1 M K L N Q D R H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P P F V S A S T I 60  
  
Qy 61 Q T G I G I A C K I L G T L G V P P A G O I A S I Y S F I L G E L W P K G S O W E I F M E H V E E I I N O K I L T Y A 120  
Db 61 Q T G I G I A C K I L G T L G V P P A G O I A S I Y S F I L G E L W P K G N Q W E I F M E H V E E I I N O K I S I Y A 120  
  
Qy 121 R N K A L S D L R G L G D A L A V Y H S E S L E S V E N N R N T R A S V V K N Q Y I A L E L M F V Q K L P S F A V S G 180  
Db 121 R N K A L T D L K G L G D A L A V Y H S L E S V E N N R N T R A S V V K S O V I A L E L M F V Q K L P S F A V S G 180  
  
Qy 181 E E V P L L P T I Y A Q A A N L H L L L R D A S I F G K W G L S A S E I S T F Y N Q R V E R T R D Y S D H C I K W Y N 240  
Db 181 E E V P L L P T I Y A Q A A N L H L L L R D A S I F G K W G L S S E I S T F Y N Q R V E R A G D Y S D H C V K W Y S 240  
  
Qy 241 T G L N L R G T N A K S W R Y N Q F R D M T L M V L D I A L V A L P P S Y D T L V P I K T T S Q L T R E V Y T D A I 300  
Db 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D I A L V A L P P S Y D T Q M P I K T T A Q T R E V Y T D A I 300  
  
Qy 301 G T V H P N O A F A S T T W Y N N N A P S F A I E A A V I R S P H L L D F L E K V T I Y S L L S R W S N T Q Y M N M W 360  
Db 301 G T V H P H P S F T S T T W Y N N N A P S F A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360  
  
Qy 361 G G H R L E S R P I G G A L N T S T Q G S T N T S I N P V T L Q F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
Db 361 G G H K L E F R T I G G T L N T S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
  
Qy 421 V D F H W K F P T L P I A S D N F Y I L G Y A G V G T O L Q D S E N E L P P E T T G O P N Y E S Y S H R L S H I G L I S 480  
Db 421 V D F H W K F V T H P I A S D N F Y I P G Y A G I G T Q L Q D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
  
Qy 481 A S H V K A L V Y S W T H S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G G D I L R R T N 540  
Db 481 A S H V K A L V Y S W T H S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G G D I L R R T N 540  
  
Qy 541 T G T F G D I R V N I N P P P A Q R Y R V I R Y A S T D T L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
Db 541 T G T F G D I R V N I N P P P A Q R Y R V I R Y A S T D T L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
  
Qy 601 T F R T I G F T T P S F S D Q S T F T I G A W N F S S G N E V I I D R I E F V P V E V T Y E A Y D F E K A Q E K V 660  
Db 601 T F R T V G F T T P S F L D V Q S T F T I G A W N F S S G N E V I I D R I E F V P V E V T Y E A Y D F E K A Q E K V 660

Qy 661 T A L F T S T N P R G L K T D V D Y H I D Q V S N L V E S L S D R F Y L D E K R E L F E I V K A Q I H I E R N M 719  
Db 661 T A L F T S T N P R G L K T D V D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q I H I E R N M 719  
  
RESULT 4  
US-09-661-322A-42  
; Sequence 42, Application US/09661322A  
; Patent No. 6593293  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Ruper, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo  
; FILE REFERENCE: MECO201  
; CURRENT APPLICATION NUMBER: US/09/661.322A  
; CURRENT FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 42  
; LENGTH: 710  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (200)-(200)  
; OTHER INFORMATION: No. 6593293-Coding  
US-09-661-322A-42

Query Match 90.0%; Score 3368.5; DB 4; Length 710;  
Best Local Similarity 89.2%; Pred. No. 1.2e-301;  
Matches 641; Conservative 32; Mismatches 37; Indels 9; Gaps 1;  
  
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Db 1 M K S K N Q N H Q S L S N A T V D K N F T G S L E N T N T E L Q N F N ----- H E G I E P F V S V S T I 51  
  
Qy 61 Q T G I G I A C K I L G T L G V P P A G O I A S I Y S F I L G E L W P K G S O W E I F M E H V E E I I N O K I L T Y A 120  
Db 52 Q T G I G I A C K I L G N L G V P P A G V A S I Y S F I L G E L W P K G S O W E I F M E H V E E I I N O K I S I Y A 111  
  
Qy 121 R N K A L S D L R G L G D A L A V Y H S E S L E S V E N N R N T R A S V V K N Q Y I A L E L M F V Q K L P S F A V S G 180  
Db 112 R N K A L A D L K G L G D A L A V Y H S E S L E S W I E N R N T R S V V K S O Y I T I L E L M F V Q S L P S F A V S G 171  
  
Qy 181 E E V P L L P T I Y A Q A A N L H L L L R D A S I F G K W G L S A S E I S T F Y N Q R V E R T R D Y S D H C I K W Y N 240  
Db 172 E E V P L L P T I Y A Q A A N L H L L L R D A S I F G K W G L S D S E I S T F Y N Q S G K S K E Y S D H C V K W Y N 231  
  
Qy 241 T G L N L R G T N A K S W R Y N Q F R D M T L M V L D I A L V A L P P S Y D T L V P I K T T S Q L T R E V Y T D A I 300  
Db 232 T G L N R L M G N N A E S W R Y N Q F R D M T L M V L D I A L V A L P P S Y D T Q M P I K T T A Q T R E V Y T D A I 291  
  
Qy 301 G T V H P N O A F A S T T W Y N N N A P S F A I E A A V I R S P H L L D F L E K V T I Y S L L S R W S N T Q Y M N M W 360  
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Db 352 G G H K L E F R T I G G T L N T S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 411  
  
Qy 421 V D F H W K F P T L P I A S D N F Y I L G Y A G V G T O L Q D S E N E L P P E T T G O P N Y E S Y S H R L S H I G L I S 480  
Db 412 V D F H W K F V T H P I A S D N F Y I P G Y A G I G T Q L Q D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 471  
  
Qy 481 A S H V K A L V Y S W T H S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G G D I L R R T N 540  
Db 472 A S H V K A L V Y S W T H S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G G D I L R R K N 531  
  
Qy 541 T G T F G D I R V N I N P P P A Q R Y R V I R Y A S T D T L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600

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Db 532 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATWNRGCDLDYK 591
Qy 601 TFRIGFTTTPSDFSDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
Db 592 TFRIVGFTTTPSDFSDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEEV 651
Qy 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDYFYLDEKRELFEIVKYAKQIHERNM 719
Db 652 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDYFYLDEKRELFEIVKYAKQIHERNM 710

RESULT 5
US-08-286-870A-4
; Sequence 4, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENN, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-870A-4

Query Match 84.4%; Score 3160; DB 3; Length 648;
Best Local Similarity 92.3%; Pred. No. 1.8e-282;
Matches 598; Conservative 30; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MKLKNPKDQHSLSNAKVDKIATDSLKNETDIELKMNNDYLRMSHESIDPFVSASTI 60
Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHECDLKASEVENVEPFVSASTI 60
Qy 61 QTGIGIAGKILGTGVPPFAGQASLYSFLGELWPKGKQWEIFMHEVEEIIINOKILTYA 120
Db 61 QTGIGIAGKILGTGVPPFAGQASLYSFLGELWPKGKQWEIFMHEVEEIIINOKILTYA 120

121 RNKALSDRLGLGDLAVYHESLESWVENRNTNTRARSVVKNOYIALELMFVKQLPSPFAVSG 180
121 RNKALTDLKGDLAVYHDSLESWGNRNTNTRARSVVKQYIALELMFVKQLPSPFAVSG 180
181 EEPVLPPIYAAANLHLLLRDASIIFGKEWGLSASEISTFYNQVERTRDYSHCICKWYN 240
181 EEPVLPPIYAAANLHLLLRDASIIFGKEWGLSSEISTFYNQVERAGDYSCHVKWYS 240
241 TGLNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPSYDTLVPIKTTSLTREVVYDAI 300
241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPIKTTAQLTREVVYDAI 300
301 GTVHPNQAFASATTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYLLSRWSNTQYNNMW 360
301 GTVHPHPSFTTWTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYNNMW 360
361 GGHRLSRPIGGALNTSTQSTNTSINPVIQFTSRDVTYTESLAGLNLFLTPQVNGVPR 420
361 GGHKLEPFTTGGTLNISTQSTNTSINPVTLPFTSRDVTYTESLAGLNLFLTPQVNGVPR 420
421 VDFHWKFTPLPIASDNFYLYGAGVGTQLODSENELPPTTQPNYESYSHRLSHIGLIS 480
421 VDFHWKFTVTHPIASDNFYLYGAGVGTQLODSENELPPTTQPNYESYSHRLSHIGLIS 480
481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILARTN 540
481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILARTN 540
541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATWNRGCDLDYK 600
541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATWNRGCDLDYK 600
601 TFRIGFTTTPSDFSDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 648
601 TFRIVGFTTTPSDFSDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEEV 648

RESULT 6
US-08-286-870A-6
; Sequence 6, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENN, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-870A-6

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-870A-6

Query Match 68.8%; Score 2573; DB 3; Length 535;
Best Local Similarity 91.0%; Pred. No. 2e-228;
Matches 487; Conservative 29; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MKLNPKDQKQSSNAKVDTATDSLKNETDIELKMNEDYLMSEHESIDPPFVSASTI 60
Db 1 MKLNPKDQKQSSNAKVDTATDSLKNETDIELKMNEDYLMSEHESIDPPFVSASTI 60
Qy 61 QTGIGIACKILGTGVPFAGQIASYFSLGELWPKGKQWEIFMEHVEEIIINOKILTYA 120
Db 61 QTGIGIACKILGTGVPFAGQIASYFSLGELWPKGKQWEIFMEHVEEIIINOKISTYA 120
Qy 121 RNKALDRLGGLDALAVYHESLESVENNRNTRARSVVKQYIALELMFVKLPFAVSG 180
Db 121 RNKALDRLGGLDALAVYHESLESVENNRNTRARSVVKQYIALELMFVKLPFAVSG 180
Qy 181 BEVPLLPYIAQAANLHLLLRDASIFGKWEGLSASEISTFTYRQVERTRDYSHCIKWYN 240
Db 181 BEVPLLPYIAQAANLHLLLRDASIFGKWEGLSASEISTFTYRQVERAGDYSCHCKWYS 240
Qy 241 TGLNLRGTNAKSWRVNQPRKDMTLMVLDLVALFPSSYDTLVYPIKTTTSOLTREVYTDAI 300
Db 241 TGLNLRGTNAKSWRVNQPRKDMTLMVLDLVALFPSSYDTLVYPIKTTTSOLTREVYTDAI 300
Qy 301 GTVHPNQAFSTTWYNNNAPSFAIAEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW 360
Db 301 GTVHPNPFSTTWYNNNAPSFAIAEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW 360
Qy 361 GGHLESPIGALNTSTQGSTNTSINPVTLOFTSRDVRVRESLAGLNLFTQPVNGVPR 420
Db 361 GGHLESPIGALNTSTQGSTNTSINPVTLOFTSRDVRVRESLAGLNLFTQPVNGVPR 420
Qy 421 VDFHWKFTPLPIASDNFYVLGAGVGTQLODSENELPPEATTGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTPLPIASDNFYVLGAGVGTQLODSENELPPEATTGQPNYESYSHRLSHIGLIS 480
Qy 481 ASHKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535
Db 481 ASHKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
; Sequence 4, Application US/08100709
; Patent No. 5322487
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia

```

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; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,709
; FILING DATE: 19930729
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Egoif, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-100-709-4

Query Match 65.7%; Score 2459; DB 1; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.7e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

Qy 3 LKNPDKQSSNAKVDTATDSLKNETDIELKMNEDYLMSEHESIDPPFVSASTIQT 62
Db 20 VSNFSTQMNLSFDARI-----EDSLCAEVNNDIPFVSASTVQT 58
Qy 63 GIGIAGKILGTGVPFAGQIASYFSLGELWPKGKQWEIFMEHVEEIIINOKILTYARN 122
Db 59 GINIAGRLGLVGVFAGQIASYFSLGELWPGSDGPDWEIFLEHVEQLIQQOIVENTRN 118
Qy 123 KALSDRLGGLDALAVYHESLESVENNRNTRARSVVKQYIALELMFVKLPFAVSGEE 182
Db 119 TAIARLEGLGRGYSYQQALETWLDNRNDRASRSIILERYVALELDITTAIPFIRNEE 178
Qy 183 VPLPIYQAANLHLLLRDASIFGKWEGLSASEISTFTYRQVERTRDYSHCIKWYNTG 242
Db 179 VPLLMVYQAANLHLLLRDASIFGSEWGMASDVNQYIQEIRYTBESYHNCVQWYNTG 238
Qy 243 LNNLRGTNAKSWRVNQPRKDMTLMVLDLVALFPSSYDTLVYPIKTTTSOLTREVYTDALGT 302
Db 239 LNNLRGTNAESWLRYNQPRDRLTGLVLDLVALFPSSYDTRTPINTSAQLREIYTDPIGR 298
Qy 303 VHPNQAFSTTWYNNNAPSFAIAEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMWGG 362
Db 299 TNAPSGFASTWYNNNAPSFAIAEAAVIRSPHLLDFPEQLTIYSASSRWSSTQHNNYVWG 358
Qy 363 HRLSRPIGALNTSTQGST-NTSINPVTLOFTSRDVRVRESLAGLNLFTQPVNGVPRV 421
Db 359 HRLNFRPIGGTLNTSTQGLTNTSINPVTLOFTSRDVRVRESNAGTNILFTTPVNGVPPWA 418
Qy 422 DFHWKFTPLPIASDNFYVLG-----YAGVGTQLODSENELPPEATTGQPNYESYSHRLS 474
Db 419 RFNF-----INPQNIYERGATTYSQPYQGVGIQLFDSETELPPPTTTPPTTTPPTTTPPTT 472
Qy 475 HIGLISAHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGD 534
Db 473 HIGLIIGNTLRAPVYSWTHRSADRTNTEPNISITQIPLVKALNLHSGVTVVGGPGFTGGD 532
Qy 535 ILRRTNTGTFGDIRNINPPPAQRYRVRIRVASTTDLQFHTSINGKALNQGNFSATMNRG 594
Db 533 ILRRTNTGTFGDIRNINPPPAQRYRVRIRVASTTDLQFHTSINGKALNQGNFSATMNRG 592
Qy 595 EDLDYKFTRTIGTTPFSDVQSTFTTIGANNFSGNEVYIDRIEFVVEVTEYAEYDFE 654
Db 593 DNLBYRFRTAGFTSTPFNFLNAQSTFTTILGAQFSN-QEVYIDRVFVFAEVTEYAEYDLE 651

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QY 655 KAOEKVATLFTSTNPRGLKTDVYHIDQVSNLVESLSDBFYLDKRELEFSEIVKYAKQIH 714  
 DB 652 RAQKAVNALFTSTNPRGLKTDVYHIDQVSNLVESLSDBFYLDKRELEFSEIVKYAKRLS 711  
 QY 715 IERNM 719  
 DB 712 DERNL 716

RESULT 8  
 US-08-176-865-4  
 ; Sequence 4, Application US/08176865  
 ; Patent No. 5616319  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yuping  
 ; APPLICANT: Jan, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESS: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/176,865  
 FILING DATE: 30-DEC-1993  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/100,709  
 FILING DATE: 29-JUL-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Egolf, Christopher  
 REGISTRATION NUMBER: 27633  
 REFERENCE/DOCKET NUMBER: 7205-49  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 215-757-1590  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1229 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-176-865-4

Query Match 65.7%; Score 2459; DB 1; Length 1229;  
 Best Local Similarity 64.8%; Pred. No. 2.7e-217;  
 Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKPNPKHQHSSNNKVKDIATDSLKNETDIELKMNEDYLRMSEHESIDPFVSASTIOT 62  
 DB 20 VSNPSTQWNLSPDARI-----EDSLCAEAVNNDIDPFVSASTVQT 58  
 QY 63 GIGTAGKILGLVPPFAGQIASLYSFLIGELWPKGKSQWEIFMEHVEEIIQKILYARN 122  
 DB 59 GINTAGRLGLVGLVPPFAGQIASLYSFLIGELWPKGSRDPWEIFLHVQLIRQVVTNTRN 118  
 QY 123 KALSDRLGLDALVYTHESLESWVENNTRARVKNQIALELMVQKLPFSVSGEE 182  
 DB 119 TAIARLEGIGRYSYQQALETWLDNRDARSRIILERYVALELDTITTAIPLRIRNEE 178  
 QY 183 VLLPIYAQAANLHLLLRDASIFGKEWGLSASISITFYNRQVTRDYSCHICKWYNTG 242

DB 179 VLLMVAQAANLHLLLRDASLFGSEWGMASDVNQYIQOIRYTERYSNHCQWYNTG 238  
 QY 243 LNNLRGTNAKSVRYNQPKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYDAIGT 302  
 DB 239 LNNLRGTNAESWLRNQFRDLTLGVLVALFPSYDTRTYPIKTTSQLTREVYDPIGR 298  
 QY 303 VHPNQAFASTWYNNNAPSFAIEAAVIRSHPLLDLFLEKVIYISLLSWSNTQYNNMGG 362  
 DB 299 TNAPSGFASTWYNNNAPSFAIEAAVIRSHPLLDLFLEKVIYISLLSWSNTQYNNMGG 358  
 QY 363 HRLSRPIGALNTSTQGST-NTSINPVTLQFTSRDVTRESLAGLNLFLTPVNGVPRV 421  
 DB 359 HRLNFRPIGGLTNTSTQGLTNTSINPVTLQFTSRDVTRESNAGTNILFTTPVNGVPA 418  
 QY 422 DFHWKEPTLPIASDNFYLG-----YAGVGTQIQDSNELPPTTGPQNYVESYHRLS 474  
 DB 419 RENF-----INPQNIYERGATTYSQYQGVGLQFLDSETELPETTERPNYESYHRLS 472  
 QY 475 HGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTG 534  
 DB 473 HGLIIGTILRAPVYSWTHRSADRTNTIGPNRITQIPLVKAFLNLSGAAVVRGPGFTG 532  
 QY 535 ILRRTNTGTFGDIRVNNPFPQRYVRIRYASTTDLQFHTSINGKAINOGNFSATMNRG 594  
 DB 533 ILRRTNTGTFGDIRVNNPFPQRYVRIRYASTTDLQFHTSINGKAINOGNFSATMNRG 592  
 QY 595 EDLYKTFTRTIGTTFPSFSDVOSTTIGANFPSSNEVYIDRIEVPVVEVTEAAYDPE 654  
 DB 593 DNLEYSRFTAGFTPTFNLNAQSTFTLGAQSFEN-QEYVIDRVEFVPAEVTPEAYDLE 651  
 QY 655 KAOEKVATLFTSTNPRGLKTDVYHIDQVSNLVESLSDBFYLDKRELEFSEIVKYAKQIH 714  
 DB 652 RAQKAVNALFTSTNPRGLKTDVYHIDQVSNLVESLSDBFYLDKRELEFSEIVKYAKRLS 711  
 QY 715 IERNM 719  
 DB 712 DERNL 716

RESULT 9  
 US-08-474-038-4  
 ; Sequence 4, Application US/08474038  
 ; Patent No. 5679343  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yuping  
 ; APPLICANT: Jan, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESS: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/474,038  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/176,865  
 FILING DATE: 30-DEC-1993  
 APPLICATION NUMBER: US 08/100,709

```

; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-474-038-4

Query Match 65.7%; Score 2459; DB 1; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.7e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKNDPKHQSLSNAKVKDIATDSLKNETDIELKNNNEDYLRMSHEHSDIPFVSASTIQT 62
DB 20 VSNPSTQWNLSPDARI-----EDSLCVAEVNNDIPFVSASTVQT 58

QY 63 GIGTAGKILGTGVPPFAGQIASLYSFIILGELWPKGKSOWEIFMEHVEEIIINQKILTYARN 122
DB 59 GINIAGRILGVLGVPPFAGQLASFYSFLVGLWPSGRDPWEIFLEHVEQLIRQQVTENTRN 118

QY 123 KALSDRLGLGDLALAVYHESLESWENRNNTARSVVKNQYIALELMFVQKLPSPAVSGEE 182
DB 119 TAIARLEGLGRGYSYQOALETWLDRNDARSIIILERYVALELDITTAIPLFRIRNEE 178

QY 183 VPLLPIYAAANLHLLLRDASIFGKWLGLSASISITFYNRQVTRDRYSDHICIKWYNTG 242
DB 179 VPLLWVYAAANLHLLLRDASLFGSEWGMASDVNQYQYQIRYEEYSHNCVQWYNTG 238

QY 243 LNNLRGTNAKSWRYNQFRKMTLMVLVDLVALFPSYDTLVPIKTTTSOLTREVYDTAIGT 302
DB 239 LNNLRGTNAESWLRYNQFRDLTLGLVDLVALFPSYDTRTYPINTSAQLTREIYDPIGR 298

QY 303 VHPNQAFASITWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYLSLLSSNTOYNNMGG 362
DB 299 TNAPSGFASTWYNNAPSFSAIEAAI FRP PHLLDFPEQLTIYSSASSWSSTQHNWYWG 358

; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-779-046-4

Query Match 65.7%; Score 2459; DB 2; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.7e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKNDPKHQSLSNAKVKDIATDSLKNETDIELKNNNEDYLRMSHEHSDIPFVSASTIQT 62
DB 20 VSNPSTQWNLSPDARI-----EDSLCVAEVNNDIPFVSASTVQT 58

QY 63 GIGTAGKILGTGVPPFAGQIASLYSFIILGELWPKGKSOWEIFMEHVEEIIINQKILTYARN 122
DB 59 GINIAGRILGVLGVPPFAGQLASFYSFLVGLWPSGRDPWEIFLEHVEQLIRQQVTENTRN 118

QY 123 KALSDRLGLGDLALAVYHESLESWENRNNTARSVVKNQYIALELMFVQKLPSPAVSGEE 182
DB 119 TAIARLEGLGRGYSYQOALETWLDRNDARSIIILERYVALELDITTAIPLFRIRNEE 178

QY 183 VPLLPIYAAANLHLLLRDASIFGKWLGLSASISITFYNRQVTRDRYSDHICIKWYNTG 242
DB 179 VPLLWVYAAANLHLLLRDASLFGSEWGMASDVNQYQYQIRYEEYSHNCVQWYNTG 238

QY 243 LNNLRGTNAKSWRYNQFRKMTLMVLVDLVALFPSYDTLVPIKTTTSOLTREVYDTAIGT 302
DB 239 LNNLRGTNAESWLRYNQFRDLTLGLVDLVALFPSYDTRTYPINTSAQLTREIYDPIGR 298

QY 303 VHPNQAFASITWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYLSLLSSNTOYNNMGG 362
DB 299 TNAPSGFASTWYNNAPSFSAIEAAI FRP PHLLDFPEQLTIYSSASSWSSTQHNWYWG 358

```



```

; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation.
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-951-715A-7

Query Match 61.9%; Score 2314.5; DB 1; Length 1207;
Best Local Similarity 65.4%; Pred. No. 5.7e-204;
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;

Qy 40 EDYLRMSHESIDPVSASTQTGTGIGIAGKILGTILGVFPAGQIASLVSFILGELWPKGKS 99
Db 10 EDSLICIAEGNNIDPVSASTVQTGINIAGRILGVLPVFPAGQIASLVSFILGELWPRGRD 69
Qy 100 QWEIFMEHVEEIIINQILTYARNKALSOLRGLGDALAVYHESLESSEWENRNNTRARSVVK 159
Db 70 QWEIFLEHVEGLINQITENARNALARLQGLGDSFRAYQOSLEDWLENRDRDARTSRVLY 129
Qy 160 NOYIALELMFVQKLPSPAVSGEVPPLPIYAQAANLHLLLRDASIFGKEMGLSASEIST 219
Db 130 TOYIALELDPLNAMPPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIOR 189
Qy 220 FYNQVETRDYSDHCIKWYNTGLNLTGKTNKSWRVYQNRKDWLMLDLVALPFSYD 279
Db 190 YYERQVETRDYSDYCVENYNTGLNLTGKTNKSWRVYQNRKDWLMLDLVALPFSYD 249
Qy 280 TLVYPIKTSQLTREYVYDAITGVHPNQAFASFTWYNNAPSFSAIEAAVIRSPLLDFL 339
Db 250 TRTPINTSAQLTREYVYDALGATGVN--MASMWNYNNAFSAIEAAVIRSPLLDFL 307
Qy 340 EKVTIYSLRSWNTQYNNMGGHRESRPICGALNTSTQGSTNTSINPVTLOFTSRDVI 399
Db 308 EQLIFGSASSRWSNTRHMYRWGHTIQSRPIGGGLNTSTHGATNTSINPVTLRASRDVI 367
Qy 400 RTESLAGLNLF--LTQPVNGVPRVDFHWKFP-TLPIASDNFYILGYAGVGTQLQDSNEL 456

; Db 368 RTESVAGVLLWGIYLEPIHGVTFRFNTFNQNTSDRGTANYSQYESFGLQKDSIETEL 427
; Qy 457 PPETTGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAF 516
; Db 428 PPETTERENYESYSHRLSHIGIILQSRVNVVPVSWTHRSADRTNTIGPNRITQIIPMKAS 487
; Qy 517 NLSGAAVVRGPGFTGGDILRRTWGTGPDTRVNIINPPFAQRYRVRIYASTTDLQFHTS 576
; Db 488 ELPOGTTVVRGPGFTGGDILRRTWGTGPGFRIVTVNGELTQRYRIGFRYASTVDFDFVS 547
; Qy 577 INKALINQGNFSATMNGEDLDYKTFRTIGTTFPSPSDVOSTFTTIGAWNFSSGNEVYID 636
; Db 548 RGGTVNVNFRFLRTWNSGDEKYNFVRARTTTFFTQIQDIIRTSIQGLSGNGEVYID 607
; Qy 637 RIEFVPVEVITYEABYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFY 696
; Db 608 KIEIIPVTATFEAEVDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDSDFC 667
; Qy 697 LDEKRELFVIVYAKQIHIERNM 719
; Db 668 LDEKRELLEKVKYAKRLSDERNL 690

RESULT 13
US-08-459-448A-7
; Sequence 7, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
```

REGISTRATION NUMBER: 40403  
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4  
TELEPHONE: (919)541-8582  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-459-448A-7

Query Match 61.9%; Score 2314.5; DB 2; Length 1207;  
Best Local Similarity 65.4%; Pred. No. 5.7e-204;  
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;

QY 40 EDYLRMSHESIDPFVSASTIQTGIGIAGKILGTGVPFAGQIASLYSFILGELWPKGKS 99  
DB 10 EDSLCAIEAGNNIDPFVSASTVQTGINIAGRILGVLGVPFAGQLASFYSFLVGELWPRGRD 69  
QY 100 QWEIFMEHVEBIIINOKILTYARNKALSDRLGGLDALAVYHESLSWENRNNTRARSYVK 159  
DB 70 QWEIFLEHVEQLINQOITENARTALARLOGLGDSFRAYQQSLEDWLENRDDARTSVLY 129  
QY 160 NOYIALELMFVKLPSPFVSGEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSASEIST 219  
DB 130 TOYIALELDFLNAMPFLFAIRNQEVPLLMVYIAQAANLHLLLRDASIFGSEFGLTSQEIQR 189  
QY 220 FYNQVTRTSDYSDHICIKWNTGLNLRGTNAKSWRVYNQFRKDMTLMVLDFLVPFSYD 279  
DB 190 YERQVTRTSDYSDYCVWEYNTGLNLRGTNAKSWRVYNQFRDRLTLGLVDFLVPFSYD 249  
QY 280 TLVPIKTSQITREYVDALGTWHPNOAFSTWYNNAPSFSAIEAAVIRSHLLDFL 339  
DB 250 TRTPINTSAQITREYVDALGTWHPNOAFSTWYNNAPSFSAIEAAVIRSHLLDFL 307  
QY 340 EKVTIYSLSSWNTQYNNMGGHLESRPIGGALNTSTOGSTNTSINPVTLOFTSRDYY 399  
DB 308 EQLTIFSSASSWNSRTHWYWRGHTIQSRPIGGGLNTSTHGTATNTSINPVTLRASRDYV 367  
QY 400 RTESLAGLNLFF--LTQPVNGVPRVDFHWKFF--TLPIASDNFYLYGAGVGTQLODSENEL 456  
DB 368 RTESYAGVLLGVIYLEPHGVPTFRFNTPNQNISDRGTANYSQYSPGLQKDSYTEL 427  
QY 457 PPTTGQPNYSYSHRLSHIGLISASHVKALVYSWTHSADRTNTEBNSITQPLVKAF 516  
DB 428 PPETTERPNYESYSHRLSHIGLILQSVRVNVPYVSWTHSADRTNTIGNRTIQIPMVKAS 487  
QY 517 NLSSCAAVVRGPGFTGGDILRNTGTGDIRVNINPPFAQRYRVRIRYASTTDLOFHTS 576  
DB 488 ELPOQTTVVRGPGFTGGDILRNTGTGDIRVNINPPFAQRYRVRIRYASTVDFFVVS 547  
QY 577 INKAINOCNFSATNRGDEDLYKTRTFTGFTTPFSFSDVQSTFTTIGAMVSSNGNEVID 636  
DB 548 RGGTVNNFRFLRTWNSGDELKYGNFVRAAFTTPTFTTQIQDIIRTSIQGLSGNEVID 607  
QY 637 RIEFPVPEVTEAEYDFEKAQKVTALPTSTNPRGLKTDVKKYHIDQVNLVESISDEFY 696  
DB 608 KIEIIPVTATPEAEYDLERAQAVNALFTNTNPRELKTDTVTDYHIDQVNLVACLSDSEFC 667  
QY 697 LDEKRELPEIVYAKQIHIERNM 719  
DB 668 LDEKRELLEKVKYAKRLSDERML 690

RESULT 14  
US-08-459-595A-7  
Sequence 7, Application US/08459595A  
Patent No. 6018104  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
APPLICANT: Desai, Nalini M.

APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6018104artis Corporation  
STREET: Patent & Trademark Dept., 520 White Plains  
STREET: Rd., POB 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patenlin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,595A  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: 40403  
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8582  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-459-595A-7

Query Match 61.9%; Score 2314.5; DB 3; Length 1207;  
Best Local Similarity 65.4%; Pred. No. 5.7e-204;  
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;  
QY 40 EDYLRMSHESIDPFVSASTIQTGIGIAGKILGTGVPFAGQIASLYSFILGELWPKGKS 99  
DB 10 EDSLCAIEAGNNIDPFVSASTVQTGINIAGRILGVLGVPFAGQLASFYSFLVGELWPRGRD 69  
QY 100 QWEIFMEHVEBIIINOKILTYARNKALSDRLGGLDALAVYHESLSWENRNNTRARSYVK 159  
DB 70 QWEIFLEHVEQLINQOITENARTALARLOGLGDSFRAYQQSLEDWLENRDDARTSVLY 129  
QY 160 NOYIALELMFVKLPSPFVSGEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSASEIST 219  
DB 130 TOYIALELDFLNAMPFLFAIRNQEVPLLMVYIAQAANLHLLLRDASIFGSEFGLTSQEIQR 189  
QY 220 FYNQVTRTSDYSDHICIKWNTGLNLRGTNAKSWRVYNQFRKDMTLMVLDFLVPFSYD 279



Db 190 YERQVTRDYSYCVWYNTGLNSLRGTNAASWVRNQFRDLTLGLVDLVALPSPYD 249  
QY 280 TLVYPIKTSQTLREYVDAIGTVHPNQAFSTWYNNAPSFSAIEAAVIRSPHLLDPL 339  
Db 250 TRTYPINTSAQLTRREYVDAIGATGVN--MASMWNYNNAAPSFSAIEAAVIRSPHLLDPL 307  
QY 340 EKVITYISLLSRWSNTQYNNMGHLESRPIGGALNTSTQGSTNTSINPVTLOFTSRDYY 399  
Db 308 EQLTIFSSASSRWSNTRHMYRWGHTIQSRPIGGGLNTSTHGTATNTSINPVTLRFASTRDYY 367  
QY 400 RTESLAGNLNF--LTQPVNGVRVDFHWKFP--TLPIASDNFYLYGAGVGTQLQDSENEL 456  
Db 368 RTESYAGVLLWGIYLEPHGVPTVRFNTPNQISDRGTANYSQYSPGQLQKDSSETL 427  
QY 457 PPETGQPNYSYSHRLSHIGLISASHVKALVYSWTHRSADRTNTPNSITQIPLVKAF 516  
Db 428 PPETTERPNYSYSHRLSHIGLILQSRVNVVYSWTHRSADRTNTPNRIQIPMVKAS 487  
QY 517 NLSSGAAVVRGPGFTGGDLRRTNTGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTS 576  
Db 488 ELPOGTTVVRGPGFTGGDLRRTNTGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTS 547  
QY 577 INKAINQGNFSATNMRGEDLDYKTFRTIGFTTTPFSFSDVOSTFTTIGAWNFSSGNEVYD 636  
Db 548 RGGTTVNNFRFLRTMNSGDELKYNFVRRFTTPTFTQIQDIIRTSIQGLSGNGEVYD 607  
QY 637 RIEFPVVEVYEAEDYFKAQKVYALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFY 696  
Db 608 KIEIIPVTATPEABYDLERAQEAVALFTNPNRLKTDVTDYHIDQVSNLVACLSDEFY 667  
QY 697 LDEKRELFEIVKAKQIHERNM 719  
Db 668 LDEKRELLEKVKYAKRLSDERNL 690

## RESULT 15

US-08-459-504B-7  
; Sequence 7, Application US/08459504B  
; Patent No. 6075185  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Mallini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6075185artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,504B

; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/459,595  
; FILING DATE: 02-JUN-1995  
; APPLICATION NUMBER: US 07/951,715  
; FILING DATE: 25-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8587  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1207 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-459-504B-7  
Query Match 61.9%; Score 2314.5; DB 3; Length 1207;  
Best Local Similarity 65.4%; Pred. No. 5.7e-204;  
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;  
QY 40 EDYLRMSHESIDPFVSASTQTGTGIGIAGKILGTGVFPAGIASLYSIFILGELPKGKS 99  
Db 10 EDSLCAEAGNIDPFVSASTVQTGTGIGIAGKILGTGVFPAGIASLYSIFILGELPKGGRD 69  
QY 100 QWEIFMEHVEI INKILTYARNKALSDLRIGLGDALAVYHESLESWSVENRNNTRASVVK 159  
Db 70 QWEIFLEHVEQLNQITENARNTALRQGLGDSFRAYQOSLEWLNRRDARTRSVLY 129  
QY 160 NQYIALELMFVQKLPSPFAVSGEVPLPIYAAANLHLLLRDASIFKGEWLSASEIST 219  
Db 130 TQYIALELDLFLNAPLFAIRNQEVPLLMVYAAANLHLLLRDASLFGSEFGLTSQEIOR 189  
QY 220 FYNQVTRDYSYSHRLSHIGLISASHVKALVYSWTHRSADRTNTPNSITQIPLVKAF 279  
Db 190 YERQVTRDYSYCVWYNTGLNSLRGTNAASWVRNQFRDLTLGLVDLVALPSPYD 249  
QY 280 TLVYPIKTSQTLREYVDAIGTVHPNQAFSTWYNNAPSFSAIEAAVIRSPHLLDPL 339  
Db 250 TRTYPINTSAQLTRREYVDAIGATGVN--MASMWNYNNAAPSFSAIEAAVIRSPHLLDPL 307  
QY 340 EKVITYISLLSRWSNTQYNNMGHLESRPIGGALNTSTQGSTNTSINPVTLOFTSRDYY 399  
Db 308 EQLTIFSSASSRWSNTRHMYRWGHTIQSRPIGGGLNTSTHGTATNTSINPVTLRFASTRDYY 367  
QY 400 RTESLAGNLNF--LTQPVNGVRVDFHWKFP--TLPIASDNFYLYGAGVGTQLQDSENEL 456  
Db 368 RTESYAGVLLWGIYLEPHGVPTVRFNTPNQISDRGTANYSQYSPGQLQKDSSETL 427  
QY 457 PPETGQPNYSYSHRLSHIGLISASHVKALVYSWTHRSADRTNTPNSITQIPLVKAF 516  
Db 428 PPETTERPNYSYSHRLSHIGLILQSRVNVVYSWTHRSADRTNTPNRIQIPMVKAS 487  
QY 517 NLSSGAAVVRGPGFTGGDLRRTNTGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTS 576  
Db 488 ELPOGTTVVRGPGFTGGDLRRTNTGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTS 547  
QY 577 INKAINQGNFSATNMRGEDLDYKTFRTIGFTTTPFSFSDVOSTFTTIGAWNFSSGNEVYD 636  
Db 548 RGGTTVNNFRFLRTMNSGDELKYNFVRRFTTPTFTQIQDIIRTSIQGLSGNGEVYD 607  
QY 637 RIEFPVVEVYEAEDYFKAQKVYALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFY 696  
Db 608 KIEIIPVTATPEABYDLERAQEAVALFTNPNRLKTDVTDYHIDQVSNLVACLSDEFY 667

Thu Mar 10 14:26:07 2005

QY 697 LDEKRELF EIVKYAKQIHIERNM 719  
 ||||| | |||||:: |||:  
 Db 668 LDEKRELL EKKVYAKRLSDERNL 690

Search completed: March 9, 2005, 17:27:50  
Job time : 25.1512 secs